

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000987_25579662_f3_575	1558	5330	1221	406	849	8.0e-85

Description

pir:[LN:H69817] [AC:H69817] [PN:aminoacylase homolog yhaA] [GN:yhaA] [CL:hippurate hydrolase] [OR:Bacillus subtilis] [DB:pir2]
 >gp:[GI:e1183009:g2633343] [LN:BSUB0006] [AC:Z99109:AL009126] [GN:yhaA] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.] [NT:similar to aminoacylase] [LE:80123] [RE:81313] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000987_25660937_c3_990	1559	5331	498	165	175	3.5e-13

Description

sp:[LN:OPUC_BACSU] [AC:P46922] [GN:OPUAC] [OR:BACILLUS SUBTILIS] [DE:GLYCINE BETAINE-BINDING PROTEIN PRECURSOR] [SP:P46922] [DB:swissprot]
 >pir:[LN:I40537] [AC:I40537:F69669] [PN:glycine betaine ABC transporter (glycine betaine-binding protein) opuAC precursor] [GN:opuAC] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1182252:g2632586] [LN:BSUB0002] [AC:Z99105:AL009126] [PN:glycine betaine ABC transporter (glycine) [GN:opuAC] [FN:glycine betaine transport (osmoprotection)] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.] [SP:P46922] [LE:128023] [RE:128904] [DI:direct] >gp:[GI:d1009569:g1805372] [LN:D50453] [AC:D50453] [PN:glycine betain-binding protein precursor] [GN:opuAC] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain 168 trpC2) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis DNA for 25-36 degree region containing theamyE-srfA region, complete cds.] [LE:2326] [RE:3207] [DI:direct] >gp:[GI:g984805] [LN:BSU17292] [AC:U17292] [PN:glycine betaine-binding protein precursor] [GN:opuAC] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis ATPase (opuAA), transmembrane protein (opuAB) andglycine betaine-binding protein precursor (opuAC) genes, completecds.] [LE:2332] [RE:3213] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000987_25667753_c2_773	1560	5332	564	187	906	7.3e-91

Description

sp:[LN:NUSG_STACA] [AC:P36264] [GN:NUSG] [OR:STAPHYLOCOCCUS CARNOSUS] [DE:TRANSCRIPTION ANTITERMINATION PROTEIN NUSG] [SP:P36264] [DB:swissprot]
 >pir:[LN:S38870] [AC:S38870] [PN:transcription antitermination factor nusG] [GN:nusG] [CL:transcription antitermination factor nusG] [OR:Staphylococcus carnosus] [DB:pir2] >gp:[GI:g426473] [LN:SCSECE] [AC:X76134] [GN:nusG] [OR:Staphylococcus carnosus] [DB:genpept-bct1] [DE:S.carnosus secE, nusG and rplK genes.] [SP:P36264] [LE:331] [RE:879] [DI:direct]

ORF Name

NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000987_25972086_f1_108	1561	5333	135	44	

Description

NO-HIT

ORF Name

NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000987_26173287_c3_970	1562	5334	363	120	103

Description

sp: [GI:e244712:g2764863] [LN:BSPP1GENM] [AC:X97918] [OR:Bacteriophage SPPI]
 [DB:genpept-phg] [DE:Bacteriophage SPPI complete nucleotide sequence.]
 [NT:gene 16] [LE:9322] [RE:9651] [DI:direct]

ORF Name

NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000987_26206687_c1_642	1563	5335	210	69	278

Description

sp: [LN:SECE_STAAU] [AC:006442] [GN:SECE] [OR:STAPHYLOCOCCUS AUREUS]
 [DE:PREPROTEIN TRANSLOCASE SECE SUBUNIT] [SP:006442] [DB:swissprot]
 >gp: [GI:g2078376] [LN:SAU96619] [AC:U96619] [PN:SecE] [GN:secE]
 [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:Staphylococcus aureus NCTC
 8325 SecE (secE), NusG (nusG) and RplK(rplK) genes, complete cds.] [LE:31]
 [RE:213] [DI:direct]

ORF Name

NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000987_26290912_f3_547	1564	5336	882	293	665

Description

pir: [LN:H69759] [AC:H69759] [PN:conserved hypothetical protein yciA]
 [GN:yciA] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:e1182286:g2632620]
 [LN:BSUB0002] [AC:Z99105:AL009126] [GN:yciA] [FN:unknown] [OR:Bacillus
 subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 2
 of 21): from 194651 to 415810.] [NT:similar to hypothetical proteins]
 [LE:169177] [RE:170094] [DI:direct] >gp: [GI:d1009603:g1805406] [LN:D50453]
 [AC:D50453] [GN:yciA] [OR:Bacillus subtilis] [SR:Bacillus subtilis
 (strain:168 trpC2) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis DNA for
 25-36 degree region containing theamyE-srfA region, complete cds.]
 [LE:43480] [RE:44397] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000987_26306568_c1_724	1565	5337	330	109	83	0.019
<u>Description</u>						

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000987_26350125_c2_834	1566	5338	252	83	79	0.041
Description						

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000987_26360327_c1_725	1567	5339	552	183	515	2.0e-49
Description						

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000987_26369082_c2_837	1568	5340	252	83		
<u>Description</u>						

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000987_26375952_c1_714	1569	5341	627	208	223	1.7e-18

Description

gp:[GI:e1254413:g2924242] [LN:BTP901456] [AC:Y14232] [PN:hypothetical protein] [OR:Bacteriophage TP901-1] [DB:genpept-phg] [DE:Bacteriophage TP901-1 ORFs 1-12.] [NT:ORF11] [LE:5545] [RE:6168] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000987_26569377_c2_810	1570	5342	639	212	625	4.4e-61

Description

sp:[LN:HUMS_BACSU] [AC:P42405:O31477] [GN:YCKG] [OR:BACILLUS SUBTILIS] [EC:4.1.2.-] [DE:3-HEXULOSE 6-PHOSPHATE FORMALDEHYDE LYASE)] [SP:P42405:O31477] [DB:swissprot] >pir:[LN:A69761] [AC:A69761] [PN:D-arabino 3-hexulose 6-phosphate formaldeh homolog yckG] [GN:yckG] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1182298:g2632632] [LN:BSUB0002] [AC:Z99105:AL009126] [GN:yckG] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.] [NT:similar to D-arabino 3-hexulose 6-phosphate] [SP:P42405] [LE:180087] [RE:180719] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000987_26734625_f1_89	1571	5343	351	116	210	4.1e-17

Description

gp:[GI:e308969:g2292761] [LN:BSFI21LYS] [AC:X95646] [PN:cI-like repressor] [GN:orf127] [OR:Streptococcus thermophilus bacteriophage Sfi21] [DB:genpept-phg] [DE:Streptococcus thermophilus bacteriophage Sfi21 DNA; lysogenymodule, 8141 bp.] [NT:putative] [LE:5693] [RE:6076] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000987_26772801_f1_91	1572	5344	504	167	168	6.1e-12

Description

pir:[LN:A71608] [AC:A71608] [PN:probable integral membrane protein PFB0710c] [GN:PFB0710c] [OR:Plasmodium falciparum] [DB:pir2] >gp:[GI:g3845257] [LN:AE001413] [AC:AE001413:AE001362] [PN:predicted integral membrane protein] [GN:PFB0710c] [OR:Plasmodium falciparum] [SR:malaria parasite P. falciparum] [DB:genpept-inv2] [DE:Plasmodium falciparum chromosome 2, section 50 of 73 of thecomplete sequence.] [NT:predicted by GlimmerM] [LE:4351] [RE:5562] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000987_26839638_c1_750	1573	5345	1314	437	1429	2.8e-146

Description

sp:[LN:YWFO_BACSU] [AC:P39651] [GN:YWFO:IPA-93D] [OR:BACILLUS SUBTILIS]
[DE:HYPOTHETICAL 51.0 KD PROTEIN IN PTA 3'REGION] [SP:P39651] [DB:swissprot]
>pir:[LN:G70056] [AC:G70056:S39748] [PN:ywfo protein:hypothetical protein
ipa-93d] [GN:ywfo] [OR:Bacillus subtilis] [DB:pir2]
>gp:[GI:e1186260:g2636296] [LN:BSUB0020] [AC:Z99123:AL009126] [GN:ywfo]
[FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
complete genome (section 20 of 21): from 3798401to 4010550.] [NT:alternate
gene name: ipa-93d; similar to] [SP:P39651] [LE:59934] [RE:61235]
[DI:complement] >gp:[GI:e267329:g1561567] [LN:BSUWFO] [AC:Z80355]
[PN:Unknown] [GN:ywfo] [OR:Bacillus subtilis] [DB:genpept-bct1]
[DE:B.subtilis ywfo, ywgA and ywgB genes.] [SP:P39651] [LE:267] [RE:1568]
[DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000987_26854757_c3_886	1574	5346	660	219	975	3.6e-98

Description

sp:[LN:CYSE_STAXY] [AC:P77985] [GN:CYSE] [OR:STAPHYLOCOCCUS XYLOSUS]
[EC:2.3.1.30] [DE:SERINE ACETYLTRANSFERASE, (SAT)] [SP:P77985]
[DB:swissprot] >gp:[GI:e261410:g1514656] [LN:SXCYSEREG] [AC:Y07614]
[PN:serine O-acetyltransferase] [GN:cysE] [OR:Staphylococcus xylosus]
[DB:genpept-bct1] [EC:2.3.1.30] [DE:S.xylosus cysE gene, genomic region.]
[SP:P77985] [LE:707] [RE:1357] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000987_27318_c2_877	1575	5347	1035	344	1198	8.3e-122

Description

sp:[LN:ADH1_ZYMMO] [AC:P20368] [GN:ADHA] [OR:ZYMOMONAS MOBILIS] [EC:1.1.1.1]
[DE:ALCOHOL DEHYDROGENASE I, (ADH I)] [SP:P20368] [DB:swissprot]
>pir:[LN:A35260] [AC:A35260:E40649:A24801] [PN:alcohol dehydrogenase, 1]
[GN:adhA] [CL:alcohol dehydrogenase:long-chain alcohol dehydrogenase
homology] [OR:Zymomonas mobilis] [EC:1.1.1.1] [DB:pir1] >gp:[GI:g155571]
[LN:ZMOADHA] [AC:M32100] [OR:Zymomonas mobilis] [SR:Z.mobilis (strain CP4)
DNA] [DB:genpept-bct1] [DE:Z.mobilis alcohol dehydrogenase I (adhA) gene,
complete cds.] [NT:alcohol dehydrogenase I (adhA) (EC 1.1.1.1)] [LE:218]
[RE:1231] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000987_276590_c2_821	1576	5348	375	124	279	2.0e-24

Description

pir:[LN:H70070] [AC:H70070] [PN:hypothetical protein ywzC] [GN:ywzC]
[OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1186261:g2636297] [LN:BSUB0020]
[AC:Z99123:AL009126] [GN:ywzC] [FN:unknown] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 20 of 21):
from 3798401to 4010550.] [LE:61397] [RE:61621] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000987_2847887_f2_351	1577	5349	576	191	797	2.6e-79

Description

sp:[LN:ARSB_STAAU] [AC:P30329] [GN:ARSB] [OR:STAPHYLOCOCCUS AUREUS]
[DE:ARSENICAL PUMP MEMBRANE PROTEIN] [SP:P30329] [DB:swissprot]
>pir:[LN:C41903] [AC:C41903] [PN:arsenical pump membrane protein] [GN:arsB
] [CL:arsenical pump membrane protein] [OR:Staphylococcus aureus] [DB:pir1]
>gp:[GI:g150728] [LN:PI2ARSRBC] [AC:M86824] [PN:arsenic efflux pump protein]
[GN:arsB] [FN:arsenic efflux pump component (membrane) [OR:Plasmid pI258]
[SR:Plasmid pI258 DNA] [DB:genpept-bct1] [DE:Plasmid pI258 arsenic
resistance operon (arsRBC) genes, completecds.] [LE:587] [RE:1876]
[DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000987_29320127_f3_442	1578	5350	135	44		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000987_29694425_f1_142	1579	5351	852	283	418	3.8e-39

Description

gp:[GI:g1502421] [LN:BSU59433] [AC:U59433] [PN:3-ketoacyl-acyl carrier
protein reductase] [GN:fabG] [OR:Bacillus subtilis] [DB:genpept-bct2]
[DE:Bacillus subtilis PlsX (plsX), malonyl-CoA:Acyl carrier
proteintransacylase (fabD) and 3-ketoacyl-acyl carrier protein
reductase(fabG) genes, complete cds, and acyl carrier protein (acpP)
gene,partial cds.] [NT:also called 3-oxoacyl-acyl carrier protein] [LE:1813]
[RE:2553] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000987_30178137_c1_706	1580	5352	132	43		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000987_30267937_f3_532	1581	5353	123	40		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000987_30742332_c2_841	1582	5354	228	75	76	0.012

Description

pir:[LN:D71169] [AC:D71169] [PN:hypothetical protein PH0552] [GN:PH0552]
 [OR:Pyrococcus horikoshii] [DB:pir2] >gp:[GI:d1030584:g3256958]
 [LN:AP000002]
 [AC:AP000002:AB009475:AB009476:AB009477:AB009478:AB009479:AB009480]
 [PN:163aa long hypothetical protein] [GN:PH0552] [OR:Pyrococcus horikoshii]
 [SR:Pyrococcus horikoshii (strain:OT3) DNA] [DB:genpept-bct1] [DE:Pyrococcus
 horikoshii OT3 genomic DNA, 287001-544000 nt. position(2/7).] [NT:similar to
 PIR:F64411 percent identity:33.898 in] [LE:205880] [RE:206371] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000987_31256916_c2_774	1583	5355	507	168	681	5.1e-67

Description

pir:[LN:S38871] [AC:S38871] [PN:ribosomal protein L11] [GN:rplK]
 [CL:Escherichia coli ribosomal protein L11] [OR:Staphylococcus carnosus]
 [DB:pir2] >gp:[GI:g581638] [LN:SCSECE] [AC:X76134] [PN:L11 protein]
 [GN:rplK] [OR:Staphylococcus carnosus] [DB:genpept-bct1] [DE:S.carnosus
 secE, nusG and rplK genes.] [SP:P36254] [LE:1061] [RE:1483] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000987_31334838_c3_993	1584	5356	519	172	544	1.7e-52

Description

pir:[LN:E70057] [AC:E70057] [PN:hypothetical protein ywhD] [GN:ywhD]
 [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e267625:g1565239] [LN:BSTHRZ]
 [AC:Z80360] [PN:Unknown] [GN:ywhD] [OR:Bacillus subtilis] [DB:genpept-bct1]
 [DE:B.subtilis thrZ downstream chromosomal region.] [LE:3358] [RE:3876]
 [DI:direct] >gp:[GI:e1186252:g2636288] [LN:BSUB0020] [AC:Z99123:AL009126]
 [GN:ywhD] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus
 subtilis complete genome (section 20 of 21): from 3798401to 4010550.]
 [LE:52838] [RE:53356] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000987_3134386_f3_616	1585	5357	228	75		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000987_31353377_c2_785	1586	5358	474	157	703	2.4e-69

Description

gp:[GI:d1039003:g4512400] [LN:AB017508] [AC:AB017508] [GN:rpsG] [OR:Bacillus
 halodurans] [SR:Bacillus halodurans (strain:C-125) DNA] [DB:genpept-bct1]
 [DE:Bacillus halodurans C-125 genomic DNA, 32 kb fragment, completecds.]
 [NT:rpsG homologue (identity of 84% to B. subtilis)] [LE:8367] [RE:8837]
 [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000987_31562_f2_326	1587	5359	123	40		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000987_32031437_c1_736	1588	5360	2706	901	1163	4.3e-118

Description

sp:[LN:VG12_BPPZA] [AC:P07537] [GN:12] [OR:BACTERIOPHAGE PZA] [DE:PRE-NECK APPENDAGE PROTEIN (LATE PROTEIN GP12)] [SP:P07537] [DB:swissprot]
 >pir:[LN:WMBP12] [AC:G24831] [PN:gene 12 protein] [GN:12] [CL:phage PZA gene 12 protein] [OR:phage PZA] [DB:pir1] >gp:[GI:g216061] [LN:PZACG] [AC:M11813:M13904:M13905] [PN:pre-neck appendage protein] [OR:Bacteriophage PZA] [SR:Bacteriophage PZA DNA] [DB:genpept-phg] [DE:Bacteriophage PZA (from B.subtilis), complete genome.] [LE:11428] [RE:13992] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000987_32251_f1_98	1589	5361	129	42		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000987_32315907_f3_595	1590	5362	126	41		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000987_32595152_c1_739	1591	5363	402	133		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000987_3306563_c1_688	1592	5364	366	121		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000987_33756503_c2_830	1597	5369	273	90	265	6.2e-23

Description

gp:[GI:e1285113:g3005826] [LN:BPA2INT] [AC:Y12813] [PN:hypothetical protein]
 [GN:orfB] [OR:Lactobacillus casei bacteriophage A2] [DB:genpept-phg]
 [DE:Bacteriophage A2 rep, xis and int genes.] [LE:852] [RE:1097]
 [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000987_33786251_c2_865	1598	5370	246	81		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000987_33869193_c1_726	1599	5371	183	60	130	1.2e-08

Description

sp:[LN:RINB_BPPHA] [AC:Q03183] [GN:RINB] [OR:BACTERIOPHAGE PHI-11]
 [DE:TRANSCRIPTIONAL ACTIVATOR RINB] [SP:Q03183] [DB:swissprot]
 >pir:[LN:A49703] [AC:A49703] [PN:int gene activator RinB] [OR:phage phi-11]
 [DB:pir2] >gp:[GI:g166161] [LN:BPHRINAB] [AC:L07580] [PN:Bacteriophage
 phi-11 int gene activator] [GN:rinB] [FN:Activate bacteriophage phi-11 int
 gene] [OR:Staphylococcus bacteriophage phi 11] [SR:Bacteriophage phi-11 DNA]
 [DB:genpept-phg] [DE:Bacteriophage phi-11 rinA and rin B genes, required for
 theactivation of Staphylococcal phage phi-11 int expression.] [LE:60]
 [RE:248] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000987_34025066_c2_856	1600	5372	642	213	89	8.2e-07

Description

gp:[GI:e247172:g1926370] [LN:LBPHIG1E] [AC:X98106] [GN:Rorf232]
 [OR:Bacteriophage phigle] [DB:genpept-phg] [DE:Lactobacillus bacteriophage
 phigle complete genomic DNA.] [LE:4579] [RE:5277] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000987_34242202_c3_956	1601	5373	270	89	78	0.017

Description

sp:[LN:VP8_VARV] [AC:P33039] [GN:L4R:M4R] [OR:VARIOLA VIRUS] [DE:STRUCTURAL PROTEIN VP8 PRECURSOR (25 KD MAJOR CORE PROTEIN) (P25K)] [SP:P33039]
 [DB:swissprot] >pir:[LN:A36845] [AC:A36845:S33090] [PN:M4R
 protein:structural protein VP8] [CL:vaccinia virus 28K protein] [OR:variola virus] [DB:pir2] >gp:[GI:g262435] [LN:S55844] [AC:S55844] [PN:glycoprotein VP8] [GN:L4R] [OR:Variola major virus] [SR:Variola major virus India-1967] [DB:genpept-vrl] [DE:G9R...H7R [variola major virus, India-1967, Genomic, 19 genes,18029 nt].] [NT:This sequence comes from Fig. 2.] [LE:3187] [RE:3942] [DI:direct] >gp:[GI:g438994] [LN:VARCG] [AC:L22579] [OR:Variola major virus] [SR:Variola major virus (strain Bangladesh-1975) DNA] [DB:genpept-vrl] [DE:Variola major virus (strain Bangladesh-1975) complete genome.] [NT:homolog of vaccinia virus CDS L4R (structural] [LE:70583] [RE:71338] [DI:direct] >gp:[GI:g297256] [LN:VVCGAA] [AC:X69198] [GN:M4R] [OR:Variola virus] [DB:genpept-vrl] [DE:Variola virus DNA complete genome.] [SP:P33039] [LE:69950] [RE:70705] [DI:direct] >gp:[GI:g62352] [LN:VVHINDQKH] [AC:X67119] [PN:structural protein VP8] [GN:L4R COP] [OR:Variola virus] [DB:genpept-vrl] [DE:Variola virus (HindIII-Q,K,H,M,L,I,F genome fragment) genes.] [SP:P33039] [LE:19835] [RE:20590] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000987_34242202_f1_156	1602	5374	210	69	69	0.047

Description

sp:[LN:Y076_MYCPN] [AC:P75555] [OR:MYCOPLASMA PNEUMONIAE] [DE:HYPOTHETICAL PROTEIN MG076 HOMOLOG] [SP:P75555] [DB:swissprot] >pir:[LN:S73943] [AC:S73943] [PN:MG076 homolog G07_orf138] [OR:Mycoplasma pneumoniae] [SR:ATCC 29342, , ATCC 29342] [SR:ATCC 29342,] [DB:pir2] >gp:[GI:g1674320] [LN:MPAE000059] [AC:AE000059:U00089] [GN:G07_orf138] [OR:Mycoplasma pneumoniae] [DB:genpept-bct2] [DE:Mycoplasma pneumoniae section 59 of 63 of the complete genome.] [NT:MG076 homolog, from M. genitalium] [LE:168] [RE:584] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000987_34407053_f3_433	1603	5375	783	260	564	1.3e-54

Description

pir:[LN:S76797] [AC:S76797] [PN:hypothetical protein] [CL:conserved hypothetical protein MJ0165: phosphoribosylaminoimidazole carboxylase catalytic chain homology] [OR:Synechocystis sp.] [SR:PCC 6803, , PCC 6803] [SR:PCC 6803,] [DB:pir2] >gp:[GI:d1019442:g1653798] [LN:D90916] [AC:D90916:AB001339] [PN:hypothetical protein] [OR:Synechocystis sp.] [SR:Synechocystis sp. (strain:PCC6803) DNA] [DB:genpept-bct1] [DE:Synechocystis sp. PCC6803 complete genome, 26/27, 3270710-3418851.] [NT:ORF_ID:sll1489] [LE:107538] [RE:108377] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000987_34609703_c3_963	1604	5376	198	65	110	1.6e-06

Description

pir:[LN:T00185] [AC:T00185] [PN:hypothetical protein 52] [OR:Staphylococcus aureus phage phi PVL] [DB:pir3] >gp:[GI:d1032886:g3341959] [LN:AB009866] [AC:AB009866] [OR:bacteriophage phi PVL] [SR:bacteriophage phi PVL (specific_host:Staphylococcus aureus ATC) [DB:genpept-phg] [DE:Bacteriophage phi PVL proviral DNA, complete sequence.] [NT:orf 52] [LE:37356] [RE:37604] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000987_34651555_c1_734	1605	5377	3123	1040	267	2.8e-24

Description

gp:[GI:e244718:g2764872] [LN:BSPP1GENM] [AC:X97918] [OR:Bacteriophage SPP1] [DB:genpept-phg] [DE:Bacteriophage SPP1 complete nucleotide sequence.] [NT:gene 18] [LE:12264] [RE:13373] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000987_35162800_c3_885	1606	5378	1506	501	1701	4.2e-175

Description

sp:[LN:SYE_BACSU] [AC:P22250] [GN:GLTX] [OR:BACILLUS SUBTILIS] [EC:6.1.1.17] [DE:(GLURS)] [SP:P22250] [DB:swissprot] >pir:[LN:SYBSET] [AC:A36090:S66121:E69635] [PN:glutamate--tRNA ligase, gltX:glutamyl-tRNA synthetase gltX] [GN:gltX] [CL:glutamate--tRNA ligase:glutamine--tRNA ligase homology] [OR:Bacillus subtilis] [EC:6.1.1.17] [DB:pir1] >gp:[GI:d1005868:g467480] [LN:BAC180K] [AC:D26185] [PN:glutamyl-tRNA synthetase] [GN:gltX] [OR:Bacillus subtilis] [SR:Bacillus subtilis (sub_species:Marburg, strain:168) DNA] [DB:genpept-bct1] [DE:B. subtilis DNA, 180 kilobase region of replication origin.] [LE:174646] [RE:176097] [DI:direct] >gp:[GI:g143006] [LN:BACGLTXA] [AC:M55073:J05647] [PN:transfer RNA-Gln synthetase] [GN:gltX] [OR:Bacillus subtilis] [SR:Bacillus subtilis 168T DNA] [DB:genpept-bct1] [EC:6.1.1.17] [DE:Bacillus subtilis glutamyl-tRNA synthetase gene, complete cds.] [LE:1] [RE:1452] [DI:direct] >gp:[GI:g289282] [LN:BACGLUSYN] [AC:L14580] [PN:glutamyl-tRNA synthetase] [GN:gltX] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain 168T) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis glutamyl-tRNA transferase (gltX), serineacetyltransferase (cysE), and cysteinyl-tRNA synthetase (cysS)genes, complete cds's.] [LE:1706] [RE:3157] [DI:direct] >gp:[GI:e1182025:g2632359] [LN:BSUB0001] [AC:Z99104:AL009126] [PN:glutamyl-tRNA synthetase] [GN:gltX] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:6.1.1.17] [DE:Bacillus subtilis complete genome (section 1 of 21): from 1 to213080.] [SP:P22250] [LE:111044] [RE:112495] [DI:direct] >gp:[GI:g2653659] [LN:U49789] [AC:U49789] [PN:glutamyl-tRNA synthetase] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis glutamyl-tRNA synthetase gene, complete cds.] [LE:1] [RE:1452] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000987_35350062_f2_317	1607	5379	141	46		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000987_35445875_c1_728	1608	5380	159	52	53	0.016

Description

pir:[LN:C70306] [AC:C70306] [PN:conserved hypothetical protein aq_064c] [GN:aq_064c] [CL:conserved hypothetical secreted protein HP0320] [OR:Aquifex aeolicus] [DB:pir2] >gp:[GI:g2982828] [LN:AE000672] [AC:AE000672:AE000657] [PN:hypothetical protein] [GN:aq_064c] [OR:Aquifex aeolicus] [DB:genpept-bct2] [DE:Aquifex aeolicus section 4 of 109 of the complete genome.] [LE:2190] [RE:2423] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000987_36054813_c2_833	1609	5381	387	128	79	0.034

Description

pir:[LN:S41186] [AC:S43812:S41186] [PN:gene 39 protein] [OR:phage SPP1]
 [DB:pir2] >gp:[GI:e244746:g2764918] [LN:BSPP1GENM] [AC:X97918]
 [OR:Bacteriophage SPP1] [DB:genpept-phg] [DE:Bacteriophage SPP1 complete
 nucleotide sequence.] [NT:gene 39] [LE:36342] [RE:36722] [DI:direct]
 >gp:[GI:g439643] [LN:BSSPP1] [AC:X67865] [GN:39] [OR:Bacteriophage SPP1]
 [DB:genpept-phg] [DE:B.subtilis phage SPP1 DNA sequence coding for products
 required for replication initiation.] [LE:6073] [RE:6453] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000987_36134715_c3_887	1610	5382	771	256	666	2.0e-65

Description

sp:[LN:YACO_BACSU] [AC:Q06753] [GN:YACO] [OR:BACILLUS SUBTILIS] [EC:2.1.1.-]
 [DE:HYPOTHETICAL TRNA/RRNA METHYLTRANSFERASE YACO,] [SP:Q06753]
 [DB:swissprot] >pir:[LN:S66124] [AC:S66124:G69741:I40000] [PN:conserved
 hypothetical protein yaco] [GN:yaco] [CL:conserved hypothetical protein
 HI0860] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:d1005871:g467483]
 [LN:BAC180K] [AC:D26185] [PN:unknown] [OR:Bacillus subtilis] [SR:Bacillus
 subtilis (sub_species:Marburg, strain:168) DNA] [DB:genpept-bct1] [DE:B.
 subtilis DNA, 180 kilobase region of replication origin.] [LE:178868]
 [RE:179617] [DI:direct] >gp:[GI:e1182029:g2632363] [LN:BSUB0001]
 [AC:Z99104:AL009126] [GN:yaco] [FN:unknown] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 1 of 21):
 from 1 to213080.] [NT:similar to hypothetical proteins] [SP:Q06753]
 [LE:115266] [RE:116015] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000987_36228563_c3_960	1611	5383	699	232	110	0.00063

Description

gp:[GI:g2865254] [LN:AF008237] [AC:AF008237:L28928:L28929:L28930:L28931]
 [PN:unknown] [OR:Mitochondrion Chlamydomonas eugametos] [SR:Chlamydomonas
 eugametos] [DB:genpept-pln2] [DE:Chlamydomonas eugametos mitochondrion,
 complete genome.] [NT:orf306; intronic ORF; formerly i3; in frame with]
 [LE:<8260] [RE:9180] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000987_36521067_f3_540	1612	5384	204	67		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000987_3908462_c1_703	1613	5385	144	47		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000987_3909643_f2_217	1614	5386	1197	398	719	4.8e-71

Description

gp:[GI:g4981502] [LN:AE001759] [AC:AE001759:AE000512] [PN:conserved hypothetical protein] [GN:TM0964] [OR:Thermotoga maritima] [DB:genpept-bct2] [DE:Thermotoga maritima section 71 of 136 of the complete genome.] [NT:similar to GP:2622211 percent identity: 60.38;] [LE:5733] [RE:6941] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000987_3912503_c1_698	1615	5387	1500	499	331	1.5e-28

Description

pir:[LN:E69825] [AC:E69825] [PN:amino acid transporter homolog yhdG] [GN:yhdG] [CL:arginine permease] [OR:Bacillus subtilis] [DB:pir2]
>gp:[GI:e1182947:g2633281] [LN:BSUB0006] [AC:Z99109:AL009126] [GN:yhdG] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.] [NT:similar to amino acid transporter] [LE:23330] [RE:24727] [DI:direct]
>gp:[GI:e325026:g2226202] [LN:BSY14082] [AC:Y14082] [PN:hypothetical protein] [GN:yhdG] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis chromosomal DNA, region 72 to 75 degrees: spoVRto sspB.] [NT:Similarity to human retroviral receptor (PIR) [LE:9978] [RE:11375] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000987_3945333_c2_782	1616	5388	168	55		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000987_3961590_c3_922	1617	5389	1164	387	669	9.5e-66

Description

pir:[LN:H69831] [AC:H69831] [PN:acetyl-CoA C-acetyltransferase homolog yhfS] [GN:yhfS] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1183037:g2633371] [LN:BSUB0006] [AC:Z99109:AL009126] [GN:yhfS] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.] [NT:similar to acetyl-CoA C-acetyltransferase] [LE:109360] [RE:110454] [DI:complement] >gp:[GI:e324998:g2226255] [LN:BSY14084] [AC:Y14084] [PN:hypothetical protein] [GN:yhfS] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis chromosomal DNA, region 78-80 degrees: aprE to comK.] [NT:similarity to acetyl-CoAacetyltransferases (ThiL,] [LE:3788] [RE:4882] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000987_39635_f2_316	1618	5390	1245	414	972	7.4e-98

Description

sp:[LN:YKGC_ECOLI] [AC:P77212] [GN:YKGC] [OR:ESCHERICHIA COLI] [DE:INTERGENIC REGION] [SP:P77212] [DB:swissprot] >pir:[LN:H64756] [AC:H64756] [PN:probable mercury(II) reductase, ykgC protein] [GN:ykgC] [OR:Escherichia coli] [EC:1.16.1.1] [DB:pir2] >gp:[GI:g1657503] [LN:ECU73857] [AC:U73857] [OR:Escherichia coli] [DB:genpept-bct1] [DE:Escherichia coli chromosome minutes 6-8.] [NT:similar to S. aureus mercury(II) reductase] [LE:26473] [RE:27825] [DI:complement] >gp:[GI:g1786495] [LN:AE000137] [AC:AE000137:U00096] [PN:putative oxidoreductase] [GN:ykgC] [FN:putative enzyme; Not classified] [OR:Escherichia coli] [DB:genpept-bct2] [DE:Escherichia coli K-12 MG1655 section 27 of 400 of the completegenome.] [NT:f450; 35 pct identical (29 gaps) to 430 residues of] [LE:6292] [RE:7644] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000987_4031952_c2_775	1619	5391	501	166	545	1.3e-52

Description

pir:[LN:D69695] [AC:D69695] [PN:ribosomal protein L10 (BL5) rplJ] [GN:rplJ] [CL:Escherichia coli ribosomal protein L10] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:d1009473:g786163] [LN:BACRPL2] [AC:D50303] [PN:Ribosomal Protein L10] [GN:rplJ] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:168) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis genes for ribosomal proteins L1, L10 and L12,partial and complete cds.] [LE:347] [RE:847] [DI:direct] >gp:[GI:e1182037:g2632371] [LN:BSUB0001] [AC:Z99104:AL009126] [PN:ribosomal protein L10 (BL5)] [GN:rplJ] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 1 of 21): from 1 to213080.] [SP:P42923] [LE:120057] [RE:120557] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000987_40676_c1_644	1620	5392	183	60		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000987_4078305_c3_927	1621	5393	126	41		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000987_4078375_f1_6	1622	5394	129	42		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000987_4078518_f1_143	1623	5395	843	280	521	4.6e-50

Description

sp:[LN:YXEK_BACSU] [AC:P54950] [GN:YXEK:LP9C] [OR:BACILLUS SUBTILIS]
 [DE:HYPOTHETICAL 49.3 KD PROTEIN IN IDH-DEOR INTERGENIC REGION] [SP:P54950]
 [DB:swissprot] >pir:[LN:E70075] [AC:E70075] [PN:monooxygenase homolog yxeK]
 [GN:yxek] [CL:nitrilotriacetate monooxygenase] [OR:Bacillus subtilis]
 [DB:pir2] >gp:[GI:e1184677:g2636498] [LN:BSUB0021] [AC:Z99124:AL009126]
 [GN:yxek] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus
 subtilis complete genome (section 21 of 21): from 3999281to 4214814.]
 [NT:similar to monooxygenase] [SP:P54950] [LE:60328] [RE:61653]
 [DI:complement] >gp:[GI:d1008923:g1408496] [LN:D45912] [AC:D45912] [GN:yxek]
 [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:BGSC 1A1 (Marburg 168;
 trpC2)) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis genome sequence between
 the iol and hut operon,partial and complete cds.] [NT:homologous to dszA
 gene product of Rhodococcus sp.] [LE:9823] [RE:11148] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000987_4181527_c1_720	1624	5396	447	148	93	0.0045

Description

sp:[LN:V17_BPT7] [AC:P03781] [GN:1.7] [OR:BACTERIOPHAGE T7] [DE:GENE 1.7 PROTEIN] [SP:P03781] [DB:swissprot] >pir:[LN:W1BP77]
[AC:G43002:G43004:S42296:A04406] [PN:gene 1.7 protein] [GN:1.7] [CL:phage T7 gene 1.7 protein] [OR:phage T7] [DB:pir1] [MP:20.42-21.89]
>gp:[GI:g15512] [LN:PET7XX] [AC:V01127] [OR:Bacteriophage T7]
[DB:genpept-phg] [DE:Left end of bacteriophage T7 genome. Includes the reading frames of the genes 0.3, 0.4, 0.5, 0.6, 0.65, 0.7, 1, 1.1, 1.2, 1.3 (early proteins) and 1.4, 1.5, 1.6, 1.7, 2, 2.5, 2.8, 3, 3.5, 4A and 4B (late proteins). Gene 1 is the T7 RNA polymerase.] [NT:1.7 protein] [SP:P03781] [LE:8166] [RE:8756] [DI:direct] >gp:[GI:g15576] [LN:T7CG]
[AC:V01146:J02518:X00411] [OR:Bacteriophage T7] [DB:genpept-phg] [DE:Genome of bacteriophage T7.] [NT:gene 1.7] [SP:P03781] [LE:8166] [RE:8756] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000987_4181577_c3_955	1625	5397	1251	416	465	3.9e-44

Description

pir:[LN:H70427] [AC:H70427] [PN:replicative DNA helicase] [GN:dnaB] [CL:phage P22 gene 12 protein] [OR:Aquifex aeolicus] [DB:pir2]
>gp:[GI:g2983861] [LN:AE000742] [AC:AE000742:AE000657] [PN:replicative DNA helicase] [GN:dnaB] [OR:Aquifex aeolicus] [DB:genpept-bct2] [DE:Aquifex aeolicus section 74 of 109 of the complete genome.] [LE:2249] [RE:3655] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000987_4329063_c3_900	1626	5398	1245	414	1786	4.1e-184

Description

gp:[GI:d1039005:g4512402] [LN:AB017508] [AC:AB017508] [GN:tufA] [OR:Bacillus halodurans] [SR:Bacillus halodurans (strain:C-125) DNA] [DB:genpept-bct1] [DE:Bacillus halodurans C-125 genomic DNA, 32 kb fragment, completecds.] [NT:tufA homologue (identity of 91% to B. subtilis)] [LE:11150] [RE:12340] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000987_4334510_c2_822	1627	5399	135	44		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000987_4398453_f3_561	1628	5400	477	158	279	4.5e-24

Description

sp:[LN:NTAA_CHEHE] [AC:P54989] [GN:NTAA:NMOA] [OR:CHELATOBACTER HEINTZII] [EC:1.14.13.-] [DE:MONOOXYGENASE COMPONENT A] (NTA-MO A)] [SP:P54989] [DB:swissprot] >gp:[GI:g1119211] [LN:CBYNNMOB] [AC:L49438] [GN:nmoA] [FN:component A of NTA monooxygenase] [OR:Chelatobacter heintzii] [DB:genpept-bct1] [DE:Chelatobacter heintzii NTA monooxygenase component B (nmoB), NTAmooxygenase component A (nmoA), regulatory protein (nmoR) and transposase (nmoT) genes, complete cds.] [LE:1323] [RE:2684] [DI:direct] >gp:[GI:g1480205] [LN:CHU39411] [AC:U39411] [PN:NTA monooxygenase component A] [GN:ntaA] [OR:Chelatobacter heintzii] [SR:Chelatobacter heintzii strain=ATCC 29600] [DB:genpept-bct1] [DE:Chelatobacter heintzii nitrilotriacetate monooxygenase genes, putative regulatory protein (ntaR), NTA monooxygenase component A (ntaA) and component B (ntaB) genes, complete cds.] [LE:1123] [RE:2484] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000987_446062_c1_748	1629	5401	690	229	1165	2.6e-118

Description

sp:[LN:TRA2_STAAU] [AC:P19380] [OR:STAPHYLOCOCCUS AUREUS] [DE:TRANSPOSASE FOR INSERTION SEQUENCE-LIKE ELEMENT IS431MEC] [SP:P19380] [DB:swissprot] >pir:[LN:S12093] [AC:S12093:JU0116] [PN:probable transposase] [OR:Staphylococcus aureus] [DB:pir2] >gp:[GI:g46602] [LN:SAIS431M] [AC:X53818:M18438] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:S. aureus IS431mec gene associated with methicillin resistance.] [NT:putative transposase (AA 1 - 224)] [SP:P19380] [LE:272] [RE:946] [DI:direct] >gp:[GI:e1237900:g2791991] [LN:SAMECAR1I] [AC:Y14051] [PN:putative transposase] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:Staphylococcus aureus mecA, mecR1, mecI genes and ORF168, ORF142, ORF44, ORF145 and ORF224.] [NT:ORF224] [LE:8096] [RE:8770] [DI:direct] >gp:[GI:d1046034:g5360858] [LN:D86934] [AC:D86934] [PN:transposase for insertion sequence-like element] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus (strain:N315) DNA, clone_lib:library of N31] [DB:genpept] [DE:Staphylococcus aureus genes, mec region, partial and complete cds.] [NT:ORF N062] [LE:48054] [RE:48728] [DI:direct] >gp:[GI:d1046044:g5360868] [LN:D86934] [AC:D86934] [PN:transposase for insertion sequence-like element] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus (strain:N315) DNA, clone_lib:library of N31] [DB:genpept] [DE:Staphylococcus aureus genes, mec region, partial and complete cds.] [NT:ORF N070] [LE:53400] [RE:54074] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000987_4725006_c3_981	1630	5402	537	178		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000987_4727203_c3_925	1631	5403	369	122	86	0.032

Description

gp:[GI:d1004088:g505029] [LN:MUSMNS1] [AC:D14849] [PN:meiosis-specific nuclear structural protein 1] [OR:Mus musculus] [SR:Mus musculus (strain ddY) testis pachytene spermatocyte cDNA t] [DB:genpept-rod] [DE:Mouse mRNA for meiosis-specific nuclear structural protein 1(MNS1), complete cds.] [LE:180] [RE:1655] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000987_4735833_f2_359	1632	5404	711	236	464	5.0e-44

Description

sp:[LN:YAAG_BACSU] [AC:P37530] [GN:YAAG] [OR:BACILLUS SUBTILIS] [DE:HYPOTHETICAL 24.1 KD PROTEIN IN SERS-DNAZ INTERGENIC REGION] [SP:P37530] [DB:swissprot] >pir:[LN:S66045] [AC:S66045:G69736] [PN:deoxypurine kinase subunit homolog yaaG] [GN:yaaG] [CL:Lactobacillus acidophilus deoxyadenosine kinase] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:d1005793:g467405] [LN:BAC180K] [AC:D26185] [PN:unknown] [OR:Bacillus subtilis] [SR:Bacillus subtilis (sub_species:Marburg, strain:168) DNA] [DB:genpept-bct1] [DE:B. subtilis DNA, 180 kilobase region of replication origin.] [LE:86746] [RE:87369] [DI:complement] >gp:[GI:e1181948:g2632282] [LN:BSUB0001] [AC:Z99104:AL009126] [GN:yaaG] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 1 of 21): from 1 to213080.] [NT:similar to deoxypurine kinase subunit] [SP:P37530] [LE:23144] [RE:23767] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000987_4741068_c3_967	1633	5405	609	202	210	4.1e-17

Description

gp:[GI:e247154:g1926352] [LN:LBPHIG1E] [AC:X98106] [PN:minor capsid protein] [GN:Rorf204] [OR:Bacteriophage phigle] [DB:genpept-phg] [DE:Lactobacillus bacteriophage phigle complete genomic DNA.] [LE:24554] [RE:25168] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000987_4741077_c3_952	1634	5406	687	228	238	4.5e-20

Description

gp:[GI:e247139:g1926334] [LN:LBPHIG1E] [AC:X98106] [GN:Rorf242]
[OR:Bacteriophage phigle] [DB:genpept-phg] [DE:Lactobacillus bacteriophage
phigle complete genomic DNA.] [LE:37600] [RE:38328] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000987_4876967_c3_913	1635	5407	579	192	168	1.2e-12

Description

pir:[LN:G69824] [AC:G69824] [PN:conserved hypothetical protein yhdA]
[GN:yhdA] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1182923:g2633257]
[LN:BSUB0005] [AC:Z99108:AL009126] [GN:yhdA] [FN:unknown] [OR:Bacillus
subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 5
of 21): from 802821 to1011250.] [NT:similar to hypothetical proteins]
[LE:207082] [RE:207606] [DI:direct] >gp:[GI:e1182935:g2633269] [LN:BSUB0006]
[AC:Z99109:AL009126] [GN:yhdA] [FN:unknown] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 6 of 21):
from 999501 to1209940.] [NT:similar to hypothetical proteins] [LE:10402]
[RE:10926] [DI:direct] >gp:[GI:e324946:g2226142] [LN:BSY14079] [AC:Y14079]
[PN:hypothetical protein] [GN:yhdA] [OR:Bacillus subtilis] [DB:genpept-bct1]
[DE:Bacillus subtilis chromosomal DNA, region 75 degrees: glpPFDKoperon and
downstream.] [NT:similarity to the hypothetical protein YIEF from]
[LE:10050] [RE:10574] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000987_4882760_c3_1001	1636	5408	183	60		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000987_4886075_f3_559	1637	5409	678	225	794	5.4e-79

Description

sp:[LN:YAAF_BACSU] [AC:P37529] [GN:YAAF] [OR:BACILLUS SUBTILIS]
[DE:HYPOTHETICAL 25.4 KD PROTEIN IN SERS-DNAZ INTERGENIC REGION] [SP:P37529]
[DB:swissprot] >pir:[LN:S66044] [AC:S66044:F69736] [PN:deoxypurine kinase
subunit homolog yaaF] [GN:yaaF] [CL:Lactobacillus acidophilus
deoxyadenosine kinase] [OR:Bacillus subtilis] [DB:pir2]
>gp:[GI:d1005792:g467404] [LN:BAC180K] [AC:D26185] [PN:unknown] [OR:Bacillus
subtilis] [SR:Bacillus subtilis (sub_species:Marburg, strain:168) DNA]
[DB:genpept-bct1] [DE:B. subtilis DNA, 180 kilobase region of replication
origin.] [LE:86096] [RE:86749] [DI:complement] >gp:[GI:e1181947:g2632281]
[LN:BSUB0001] [AC:Z99104:AL009126] [GN:yaaF] [FN:unknown] [OR:Bacillus
subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 1
of 21): from 1 to213080.] [NT:similar to deoxypurine kinase subunit]
[SP:P37529] [LE:22494] [RE:23147] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000987_4892127_c1_746	1638	5410	2706	901	1557	7.6e-160

Description

pir:[LN:H69780] [AC:H69780] [PN:antibiotic transport-associated protein
homolog ydfJ] [GN:ydfJ] [OR:Bacillus subtilis] [DB:pir2]
>gp:[GI:d1020130:g1881350] [LN:AB001488] [AC:AB001488] [GN:ydfJ]
[OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:168) DNA]
[DB:genpept-bct1] [DE:Bacillus subtilis genome sequence, 148 kb sequence of
the regionbetween 35 and 47 degree.] [NT:PROBABLE TRANSPORT PROTEIN, SIMILAR
TO ANTIBIOTIC] [LE:122935] [RE:125109] [DI:direct]
>gp:[GI:e1182509:g2632843] [LN:BSUB0003] [AC:Z99106:AL009126] [GN:ydfJ]
[FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
complete genome (section 3 of 21): from 402751 to611850.] [NT:similar to
antibiotic transport-associated protein] [LE:186681] [RE:188855] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000987_4901703_c2_792	1639	5411	510	169	95	0.0031

Description

pir:[LN:D69887] [AC:D69887] [PN:conserved hypothetical protein ynaD]
 [GN:ynaD] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:g1750115] [LN:BSU66480]
 [AC:U66480] [PN:YnaD] [GN:ynaD] [OR:Bacillus subtilis] [DB:genpept-bct1]
 [DE:Bacillus subtilis SpoVK (spoVK), YnbA (ynbA), YnbB (ynbB), GlnR(glnR),
 glutamine synthetase (glnA), YnaA (ynaA), YnaB (ynaB), YnaC(ynaC), YnaD
 (ynaD), YnaE (ynaE), YnaF (ynaF), YnaG (ynaG), YnaH(ynaH), YnaI (ynaI), YnaJ
 (ynaJ), xylan beta-1,4-xylosidase (xynB),xylose repressor (xylR), xylose
 isomerase (xylA), xylulose kinase(xylB), YncB (yncB), YncC (yncC), YncD
 (yncD) and YncE (yncE)genes, complete cds.] [LE:9169] [RE:9681] [DI:direct]
 >gp:[GI:e1183411:g2634136] [LN:BSUB0010] [AC:Z99113:AL009126] [GN:ynaD]
 [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
 complete genome (section 10 of 21): from 1781201to 2014980.] [NT:similar to
 hypothetical proteins] [LE:101220] [RE:101732] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000987_4946962_c3_907	1640	5412	1068	355	183	1.0e-11

Description

gp:[GI:g3264834] [LN:AF072541] [AC:AF072541] [PN:xylitol dehydrogenase]
 [GN:xdh] [FN:xylose utilisation] [OR:Galactocandida mastotermitis]
 [DB:genpept-pln2] [EC:1.1.1.9] [DE:Galactocandida mastotermitis xylitol
 dehydrogenase (xdh) gene,complete cds.] [NT:a member of the medium chain
 dehydrogenase] [LE:301:373] [RE:312:1422] [DI:directJoin]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000987_4964677_c2_832	1641	5413	444	147	257	4.3e-22

Description

pir:[LN:T00179] [AC:T00179] [PN:ssDNA-binding protein] [OR:Staphylococcus
 aureus phage phi PVL] [DB:pir3] >gp:[GI:d1032880:g3341953] [LN:AB009866]
 [AC:AB009866] [PN:ssDNA binding protein] [OR:bacteriophage phi PVL]
 [SR:bacteriophage phi PVL (specific_host:Staphylococcus aureus ATC]
 [DB:genpept-phg] [DE:Bacteriophage phi PVL proviral DNA, complete sequence.]
 [NT:orf 45] [LE:34657] [RE:35127] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000987_5080092_c2_809	1642	5414	744	247	529	6.5e-51

Description

sp:[LN:YBFT_BACSU] [AC:O31458] [GN:YBFT] [OR:BACILLUS SUBTILIS]
[DE:HYPOTHETICAL 27.3 KD PROTEIN IN GLTP-CWLJ INTERGENIC REGION] [SP:O31458]
[DB:swissprot] >pir:[LN:E69750] [AC:E69750] [PN:glucosamine-6-phosphate
isomerase homolog ybft] [GN:ybft] [CL:glucosamine-6-phosphate isomerase]
[OR:Bacillus subtilis] [DB:pir2] >gp:[GI:d1034099:g3599658] [LN:AB006424]
[AC:AB006424] [GN:ybft] [OR:Bacillus subtilis] [SR:Bacillus subtilis
(strain:168) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis genomic DNA, 70 kb
region between 17 and 23degree.] [LE:59813] [RE:60562] [DI:complement]
>gp:[GI:e1182188:g2632522] [LN:BSUB0002] [AC:Z99105:AL009126] [GN:ybft]
[FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
complete genome (section 2 of 21): from 194651 to415810.] [NT:similar to
glucosamine-6-phosphate isomerase] [SP:O31458] [LE:62162] [RE:62911]
[DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000987_5125076_f3_531	1643	5415	810	269	873	2.3e-87

Description

sp:[LN:YWFI_BACSU] [AC:P39645] [GN:YWFI:IPA-87R] [OR:BACILLUS SUBTILIS]
[DE:HYPOTHETICAL 29.5 KD PROTEIN IN ROCC-PTA INTERGENIC REGION] [SP:P39645]
[DB:swissprot] >pir:[LN:S39742] [AC:S39742:B70056] [PN:ywfi
protein:hypothetical protein ipa-87r] [GN:ywfi] [OR:Bacillus subtilis]
[DB:pir2] >gp:[GI:g414011] [LN:BSGENR] [AC:X73124] [GN:ipa-87r] [OR:Bacillus
subtilis] [DB:genpept-bct1] [DE:B.subtilis genomic region (325 to 333).]
[SP:P39645] [LE:90200] [RE:90964] [DI:complement] >gp:[GI:e1186267:g2636303]
[LN:BSUB0020] [AC:Z99123:AL009126] [GN:ywfi] [FN:unknown] [OR:Bacillus
subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section
20 of 21): from 3798401to 4010550.] [NT:alternate gene name: ipa-87r;
similar to] [SP:P39645] [LE:66995] [RE:67759] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000987_5251588_c1_747	1644	5416	582	193	87	0.0010

Description

gp:[GI:g1079814] [LN:S79230] [AC:S79230] [PN:BM1P1] [GN:CYP106] [OR:Bacillus
megaterium] [DB:genpept-bct2] [DE:CYP106=BM1P2 orf...CYP106=P450BM-1 orf
{regulatory regions}[Bacillus megaterium, mRNA Partial, 3 genes, 1400 nt].]
[NT:positive transcription factor involved in] [LE:763] [RE:1059]
[DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000987_5258515_c3_965	1645	5417	1314	437	1298	2.1e-132

Description

sp:[LN:TERL_BPSPP] [AC:P54308] [GN:2] [OR:BACTERIOPHAGE SPP1] [DE:TERMINASE LARGE SUBUNIT (G2P)] [SP:P54308] [DB:swissprot] >pir:[LN:S24451] [AC:S24451] [PN:terminase] [OR:phage SPP1] [DB:pir2] >gp:[GI:e244468:g2764840] [LN:BSPP1GENM] [AC:X97918] [OR:Bacteriophage SPP1] [DB:genpept-phg] [DE:Bacteriophage SPP1 complete nucleotide sequence.] [NT:gene 2] [SP:P54308] [LE:307] [RE:1575] [DI:direct] >gp:[GI:g15466] [LN:NCSP116] [AC:X56064:S35313] [PN:terminase] [GN:SPP1 gene 2] [OR:Bacteriophage SPP1] [DB:genpept-phg] [DE:B. subtilis bacteriophage SPP1 genes for terminase and portalprotein.] [SP:P54308] [LE:633] [RE:1901] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000987_5370450_f3_432	1646	5418	1284	427	305	3.6e-27

Description

pir:[LN:A69256] [AC:A69256] [PN:hypothetical protein AF0049] [OR:Archaeoglobus fulgidus] [DB:pir2] >gp:[GI:g2650605] [LN:AE001103] [AC:AE001103:AE000782] [PN:A. fulgidus predicted coding region AF0049] [GN:AF0049] [OR:Archaeoglobus fulgidus] [DB:genpept-bct2] [DE:Archaeoglobus fulgidus section 4 of 172 of the complete genome.] [NT:hypothetical protein; identified by GeneMark;] [LE:7830] [RE:9068] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000987_56626_c2_855	1647	5419	336	111	84	0.0020

Description

gp:[GI:g1209829] [LN:BBU45421] [AC:U45421] [GN:REP+] [OR:Borrelia burgdorferi] [SR:Lyme disease spirochete strain=297] [DB:genpept-bct1] [DE:Borrelia burgdorferi 2.9-1 locus, ORF 5-8, ORF-A-D, REP+, REP-, andlipoprotein (LP) genes, complete cds.] [NT:repeat motif-containing gene] [LE:4602] [RE:5156] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000987_587811_f1_125	1648	5420	345	114		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
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AI7503000987_6056625_c1_755	1649	5421	258	85		
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Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
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AI7503000987_6149152_c3_884	1650	5422	1389	462	1543	2.3e-158
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Description

sp:[LN:RADA_BACSU] [AC:P37572] [GN:RADA:SMS] [OR:BACILLUS SUBTILIS] [DE:DNA REPAIR PROTEIN RADA HOMOLOG (DNA REPAIR PROTEIN SMS HOMOLOG)] [SP:P37572] [DB:swissprot] >pir:[LN:S66116] [AC:S66116:I40509:A69709] [PN:DNA repair protein homolog sms] [GN:sms] [CL:DNA repair protein sms] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:d1005863:g467475] [LN:BAC180K] [AC:D26185] [PN:unknown] [OR:Bacillus subtilis] [SR:Bacillus subtilis (sub_species:Marburg, strain:168) DNA] [DB:genpept-bct1] [DE:B. subtilis DNA, 180 kilobase region of replication origin.] [LE:169695] [RE:171071] [DI:direct] >gp:[GI:e1182020:g2632354] [LN:BSUB0001] [AC:Z99104:AL009126] [PN:DNA repair protein homolog] [GN:sms] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 1 of 21): from 1 to213080.] [NT:alternate gene name: yacJ] [SP:P37572] [LE:106093] [RE:107469] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
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AI7503000987_6250050_f2_233	1651	5423	147	48		
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Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
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AI7503000987_6406337_f3_448	1652	5424	210	69		
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Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000987_6407136_c2_840	1653	5425	1455	484	667	1.6e-65

Description

sp:[LN:SIZ_BPSPP] [AC:P54309] [GN:6:SIZ] [OR:BACTERIOPHAGE SPP1] [DE:PORTAL PROTEIN (PORTAL VERTEX PROTEIN) (GP6)] [SP:P54309] [DB:swissprot]
>pir:[LN:S21805] [AC:S21805:S24455:S36725] [PN:portal protein:gene 6 protein] [GN:6] [OR:phage SPP1] [DB:pir2] >gp:[GI:e244702:g2764847] [LN:BSPP1GENM] [AC:X97918] [OR:Bacteriophage SPP1] [DB:genpept-phg] [DE:Bacteriophage SPP1 complete nucleotide sequence.] [NT:gene 6] [SP:P54309] [LE:2334] [RE:3845] [DI:direct] >gp:[GI:g15470] [LN:NCSP116] [AC:X56064:S35313] [PN:portal protein] [GN:SPP1 gene 6] [OR:Bacteriophage SPP1] [DB:genpept-phg] [DE:B. subtilis bacteriophage SPP1 genes for terminase and portalprotein.] [SP:P54309] [LE:2660] [RE:4171] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000987_6443763_c2_769	1654	5426	408	135	298	2.0e-26

Description

pir:[LN:C69742] [AC:C69742] [PN:conserved hypothetical protein yazC] [GN:yazC] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1182028:g2632362] [LN:BSUB0001] [AC:Z99104:AL009126] [GN:yazC] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 1 of 21): from 1 to213080.] [NT:similar to hypothetical proteins] [LE:114851] [RE:115282] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000987_661062_c1_641	1655	5427	1440	479	1568	5.2e-161

Description

sp:[LN:SYC_BACSU] [AC:Q06752] [GN:CYSS:SPNA] [OR:BACILLUS SUBTILIS]
[EC:6.1.1.16] [DE:(CYSRS)] [SP:Q06752] [DB:swissprot] >pir:[LN:C53402]
[AC:C53402:S44447:S66123:B69612] [PN:cysteine--tRNA ligase,
cysS:cysteinyI-tRNA synthetase cysS] [GN:cysS] [CL:cysteine--tRNA ligase]
[OR:Bacillus subtilis] [EC:6.1.1.16] [DB:pir1] >gp:[GI:d1005870:g467482]
[LN:BAC180K] [AC:D26185] [PN:cysteinyI-tRNA synthetase] [GN:cysS]
[OR:Bacillus subtilis] [SR:Bacillus subtilis (sub_species:Marburg,
strain:168) DNA] [DB:genpept-bct1] [DE:B. subtilis DNA, 180 kilobase region
of replication origin.] [LE:177049] [RE:178449] [DI:direct] >gp:[GI:g289284]
[LN:BACGLUSYN] [AC:L14580] [PN:cysteinyI-tRNA synthetase] [OR:Bacillus
subtilis] [SR:Bacillus subtilis (strain 168T) DNA] [DB:genpept-bct1]
[DE:Bacillus subtilis glutamyl-tRNA transferase (gltX),
serineacetyltransferase (cysE), and cysteinyI-tRNA synthetase (cysS)genes,
complete cds's.] [LE:4109] [RE:5509] [DI:direct] >gp:[GI:g499303] [LN:BSCTS]
[AC:X73989] [PN:cysteine--tRNA ligase] [GN:SPNA/CYSS] [OR:Bacillus subtilis]
[DB:genpept-bct1] [EC:6.1.1.16] [DE:B.subtilis gene for cysteinyI-tRNA
synthetase.] [SP:Q06752] [LE:321] [RE:1721] [DI:direct]
>gp:[GI:e1182027:g2632361] [LN:BSUB0001] [AC:Z99104:AL009126]
[PN:cysteinyI-tRNA synthetase] [GN:cysS] [OR:Bacillus subtilis]
[DB:genpept-bct1] [EC:6.1.1.16] [DE:Bacillus subtilis complete genome
(section 1 of 21): from 1 to213080.] [NT:alternate gene name: snpA]
[SP:Q06752] [LE:113447] [RE:114847] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000987_6725707_c2_770	1656	5428	552	183	327	1.7e-29

Description

sp:[LN:YACP_BACSU] [AC:P37574] [GN:YACP] [OR:BACILLUS SUBTILIS]
[DE:HYPOTHETICAL 19.7 KD PROTEIN IN CYSS 3'REGION] [SP:P37574]
[DB:swissprot] >pir:[LN:S66125] [AC:S66125:H69741] [PN:conserved
hypothetical protein yacP] [GN:yacP] [OR:Bacillus subtilis] [DB:pir2]
>gp:[GI:d1005872:g467484] [LN:BAC180K] [AC:D26185] [PN:unknown] [OR:Bacillus
subtilis] [SR:Bacillus subtilis (sub_species:Marburg, strain:168) DNA]
[DB:genpept-bct1] [DE:B. subtilis DNA, 180 kilobase region of replication
origin.] [LE:179624] [RE:180136] [DI:direct] >gp:[GI:e1182030:g2632364]
[LN:BSUB0001] [AC:Z99104:AL009126] [GN:yacP] [FN:unknown] [OR:Bacillus
subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 1
of 21): from 1 to213080.] [NT:similar to hypothetical proteins] [SP:P37574]
[LE:116022] [RE:116534] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000987_6757338_c3_906	1657	5429	1089	362	1129	1.7e-114

Description

pir:[LN:H69750] [AC:H69750] [PN:branched-chain amino acid aminotransferase homolog ybgE] [GN:ybgE] [CL:branched-chain-amino-acid transaminase BAT1] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:d1034103:g3599662] [LN:AB006424] [AC:AB006424] [GN:ybgE] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:168) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis genomic DNA, 70 kb region between 17 and 23degree.] [LE:62005] [RE:63075] [DI:direct] >gp:[GI:e1182191:g2632525] [LN:BSUB0002] [AC:Z99105:AL009126] [GN:ybgE] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.] [NT:similar to branched-chain amino acid] [LE:64355] [RE:65425] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000987_6932750_f2_348	1658	5430	378	125	266	4.8e-23

Description

pir:[LN:C69906] [AC:C69906] [PN:hypothetical protein yojF] [GN:yojF] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1185419:g2634340] [LN:BSUB0011] [AC:Z99114:AL009126] [GN:yojF] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.] [LE:121397] [RE:121747] [DI:complement] >gp:[GI:g3169322] [LN:AF026147] [AC:AF026147] [PN:YojF] [GN:yojF] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis YojA (yojA), YojB (yojB), YojC (yojC), YojD(yojD), YojE (yojE), YojF (yojF), YojG (yojG), YojH (yojH), YojI(yojI), YojJ (yojJ), YojK (yojK), YojL (yojL), YojM (yojM), YojN(yojN), and YojO (yojO) genes, complete cds; and OdhA (odhA) gene,partial cds.] [LE:3518] [RE:3868] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000987_7032188_f2_246	1659	5431	126	41		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000987_7068751_c3_984	1660	5432	945	314	974	4.6e-98

Description

sp:[LN:IOLS BACSU] [AC:P46336] [GN:IOLS:SS92ER] [OR:BACILLUS SUBTILIS]
 [DE:IOLS PROTEIN (VEGETATIVE PROTEIN 147) (VEG147)] [SP:P46336]
 [DB:swissprot] >pir:[LN:D69646] [AC:D69646] [PN:myo-inositol catabolism
 iols] [GN:iols] [CL:conserved hypothetical protein YPL088w] [OR:Bacillus
 subtilis] [DB:pir2] >gp:[GI:d1022457:g904205] [LN:AB005554]
 [AC:AB005554:D45242:D31629] [GN:iols] [OR:Bacillus subtilis] [SR:Bacillus
 subtilis (strain:BGSC 1A1) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis
 genomic DNA, 36 kb region between gnt and ioloperons.] [NT:plausibly
 involved in inositol catabolism] [LE:32539] [RE:33471] [DI:complement]
 >gp:[GI:e1184703:g2636524] [LN:BSUB0021] [AC:Z99124:AL009126] [GN:iols]
 [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete
 genome (section 21 of 21): from 3999281to 4214814.] [NT:alternate gene name:
 yxbF; myo-inositol catabolism] [SP:P46336] [LE:85121] [RE:86053] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000987_7160287_c2_805	1661	5433	126	41		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000987_7164191_c2_798	1662	5434	150	49		

Description

NO-HIT

AI7503000987_7068751_c3_984

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000987_7229680_c1_634	1663	5435	492	163	377	8.3e-35

Description

sp:[LN:CTSR_BACSU] [AC:P37568] [GN:CTSR] [OR:BACILLUS SUBTILIS]
 [DE:TRANSCRIPTIONAL REGULATOR CTSR] [SP:P37568] [DB:swissprot]
 >pir:[LN:S66112] [AC:S66112:D69610] [PN:transcription repressor of class
 III stress genes ctsR] [GN:ctsR] [OR:Bacillus subtilis] [DB:pir2]
 >gp:[GI:d1005859:g467471] [LN:BAC180K] [AC:D26185] [PN:unknown] [OR:Bacillus
 subtilis] [SR:Bacillus subtilis (sub_species:Marburg, strain:168) DNA]
 [DB:genpept-bct1] [DE:B. subtilis DNA, 180 kilobase region of replication
 origin.] [LE:165048] [RE:165512] [DI:direct] >gp:[GI:e1182016:g2632350]
 [LN:BSUB0001] [AC:Z99104:AL009126] [PN:transcriptional regulator] [GN:ctsR]
 [FN:negative regulation of class III stress genes] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 1 of 21):
 from 1_ to213080.] [NT:alternate gene name: yacG] [SP:P37568] [LE:101446]
 [RE:101910] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000987_7275263_c1_733	1664	5436	441	146	158	1.3e-11

Description

gp:[GI:e244713:g2764865] [LN:BSPP1GENM] [AC:X97918] [OR:Bacteriophage SPP1]
 [DB:genpept-phg] [DE:Bacteriophage SPP1 complete nucleotide sequence.]
 [NT:gene 17] [LE:10063] [RE:10467] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000987_782590_f1_114	1665	5437	171	56	56	0.044

Description

gp:[GI:e289995:g1764015] [LN:CICOS41] [AC:Z83760] [PN:COS41.5] [OR:Ciona
 intestinalis] [DB:genpept-inv1] [DE:Ciona intestinalis DNA sequence from
 cosmid COS41.] [NT:weak similarity to membrane transport proteins]
 [LE:11497:13519:14634] [RE:13190:13703:14681] [DI:complementJoin]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000987_783425_c1_675	1666	5438	165	54		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000987_818942_c3_989	1667	5439	477	158	173	3.4e-17

Description

sp:[LN:OPUC_BACSU] [AC:P46922] [GN:OPUAC] [OR:BACILLUS SUBTILIS] [DE:GLYCINE BETAINE-BINDING PROTEIN PRECURSOR] [SP:P46922] [DB:swissprot]
>pir:[LN:I40537] [AC:I40537:F69669] [PN:glycine betaine ABC transporter (glycine betaine-binding protein) opuAC precursor] [GN:opuAC] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1182252:g2632586] [LN:BSUB0002] [AC:Z99105:AL009126] [PN:glycine betaine ABC transporter (glycine) [GN:opuAC] [FN:glycine betaine transport (osmoprotection)] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.] [SP:P46922] [LE:128023] [RE:128904] [DI:direct] >gp:[GI:d1009569:g1805372] [LN:D50453] [AC:D50453] [PN:glycine betain-binding protein precursor] [GN:opuAC] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:168 trpC2) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis DNA for 25-36 degree region containing theamyE-srfA region, complete cds.] [LE:2326] [RE:3207] [DI:direct] >gp:[GI:g984805] [LN:BSU17292] [AC:U17292] [PN:glycine betaine-binding protein precursor] [GN:opuAC] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis ATPase (opuAA), transmembrane protein (opuAB) andglycine betaine-binding protein precursor (opuAC) genes, completecds.] [LE:2332] [RE:3213] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000987_819575_c2_850	1668	5440	1857	618	158	1.4e-08

Description

gp:[GI:e247163:g1926361] [LN:LBPHIG1E] [AC:X98106] [GN:Rorf372] [OR:Bacteriophage phigle] [DB:genpept-phg] [DE:Lactobacillus bacteriophage phigle complete genomic DNA.] [LE:13476] [RE:14594] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000987_821012_c1_664	1669	5441	1725	574	469	6.8e-44

Description

pir:[LN:S49240] [AC:S49240] [PN:hypothetical protein 3 (capsulation locus)] [OR:Haemophilus influenzae] [DB:pir2] >gp:[GI:g547513] [LN:HIACAPIID] [AC:Z37516] [OR:Haemophilus influenzae] [DB:genpept-bct1] [DE:Haemophilus influenzae serotype a capsulation locus region II DNA.] [NT:orf3] [LE:2838] [RE:5207] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000987_833125_f3_493	1670	5442	285	94		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000987_892842_c3_926	1671	5443	387	128	337	1.4e-30

Description

sp:[LN:YWDK_BACSU] [AC:P39619] [GN:YWDK:IPA-61D] [OR:BACILLUS SUBTILIS]
[DE:HYPOTHETICAL 12.0 KD PROTEIN IN UNG-ROCA INTERGENIC REGION] [SP:P39619]
[DB:swissprot] >pir:[LN:S39716] [AC:S39716:F70054] [PN:ywdK
protein:hypothetical protein ipa-61d] [GN:ywdK] [OR:Bacillus subtilis]
[DB:pir2] >gp:[GI:g413985] [LN:BSGENR] [AC:X73124] [GN:ipa-61d] [OR:Bacillus
subtilis] [DB:genpept-bct1] [DE:B.subtilis genomic region (325 to 333).]
[SP:P39619] [LE:63169] [RE:63510] [DI:direct] >gp:[GI:e1186292:g2636328]
[LN:BSUB0020] [AC:Z99123:AL009126] [GN:ywdK] [FN:unknown] [OR:Bacillus
subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section
20 of 21): from 3798401to 4010550.] [NT:alternate gene name: ipa-61d;
similar to] [SP:P39619] [LE:94452] [RE:94793] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000987_972187_f2_208	1672	5444	924	307	834	3.1e-83

Description

gp:[GI:g2689564] [LN:U93688] [AC:U93688] [PN:integrase] [GN:int]
[OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus toxic
shock syndrome toxin-1 (tst), enterotoxin (ent), and integrase (int) genes,
complete cds.] [NT:similar to staphylococcal phage integrase] [LE:13871]
[RE:15091] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000987_9765677_c3_949	1673	5445	804	267	226	8.4e-19

Description

gp:[GI:g928839] [LN:BK5TATTP] [AC:L44593] [FN:unidentified] [OR:Lactococcus
lactis phage BK5-T] [SR:Bacteriophage BK5-T DNA] [DB:genpept-phg]
[DE:Bacteriophage BK5-T ORF'410, 3' end pf cds, 20 ORFs, repressorprotein,
and Cro repressor protein genes, complete cds, ORF70'gene, 5' end of cds.]
[NT:ORF266; putative] [LE:14882] [RE:15682] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000987_977181_c1_702	1674	5446	180	59		
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Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000987_978377_c1_689	1675	5447	264	87	75	0.0037
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Description

sp:[LN:VG05_VACCC] [AC:P21026] [GN:G5R] [OR:VACCINIA VIRUS] [SR:COPENHAGEN,]
[DE:PROTEIN G5] [SP:P21026] [DB:swissprot] >pir:[LN:A42512] [AC:A42512]
[PN:G5R protein] [OR:vaccinia virus] [DB:pir2] >gp:[GI:g335417] [LN:VACCG]
[AC:M35027] [OR:Vaccinia virus] [SR:Vaccinia virus (strain Copenhagen) DNA,
clone VC-2] [DB:genpept-vrl] [DE:Vaccinia virus, complete genome.] [NT:G5R;
putative] [LE:75218] [RE:76522] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000987_9819392_c3_908	1676	5448	789	262	179	6.4e-13
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Description

gp:[GI:g1463023] [LN:CELF45E1] [AC:U28732] [GN:F45E1.3] [OR:Caenorhabditis
elegans] [SR:Caenorhabditis elegans strain=Bristol N2] [DB:genpept-inv1]
[DE:Caenorhabditis elegans cosmid F45E1.] [LE:13873:15298:15662:15851]
[RE:14009:15615:15806:16024] [DI:directJoin]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000987_9924055_c2_765	1677	5449	216	71		
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Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000987_9926903_c2_835	1678	5450	309	102	79	0.0032
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Description

pir:[LN:F45681] [AC:F45681] [PN:orf 61.2] [OR:phage T2] [DB:pir2]
>gp:[GI:g298525] [LN:S57515] [AC:S57515] [GN:orf 61.2] [OR:coliphage T2]
[DB:genpept-phg] [DE:orf 61.2 {intergenic region between 41 and 61}
[bacteriophage T2,Genomic, 323 nt].] [NT:This sequence comes from Fig. A3.]
[LE:12] [RE:323] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000987_994052_c3_979	1679	5451	1536	511	130	0.00012

Description

gp:[GI:g4049717] [LN:AF063866] [AC:AF063866] [PN:ORF MSV156 hypothetical protein] [GN:MSV156] [OR:Melanoplus sanguinipes entomopoxvirus] [DB:genpept-vr1] [DE:Melanoplus sanguinipes entomopoxvirus, complete genome.] [LE:140126] [RE:143509] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000988_22939705_c3_35	1680	5452	402	133	99	0.00020

Description

gp:[GI:g2689564] [LN:U93688] [AC:U93688] [PN:integrase] [GN:int] [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus toxic shock syndrome toxin-1 (tst), enterotoxin (ent), and integrase (int) genes, complete cds.] [NT:similar to staphylococcal phage integrase] [LE:13871] [RE:15091] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000988_235762_f2_11	1681	5453	159	52		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000988_23626577_c2_32	1682	5454	210	69	56	0.0035

Description

gp:[GI:d1009788:g829068] [LN:SHFORF] [AC:D50601] [PN:ORF10] [OR:Shigella sonnei] [SR:Shigella sonnei (individual_isolate HW383) DNA, clone pJK1142] [DB:genpept-bct1] [DE:Shigella sonnei DNA for 26 ORFs, complete cds.] [LE:5933] [RE:6628] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000988_24297062_f1_1	1683	5455	183	60		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000988_24642202_c1_30	1684	5456	648	215	822	5.8e-82

Description

gp:[GI:g2689554] [LN:U93688] [AC:U93688] [OR:Staphylococcus aureus]
[DB:genpept-bct2] [DE:Staphylococcus aureus toxic shock syndrome toxin-1
(tst),enterotoxin (ent), and integrase (int) genes, complete cds.] [NT:orf7]
[LE:6109] [RE:6708] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000988_25665687_c2_33	1685	5457	876	291	322	5.6e-29

Description

gp:[GI:g2689560] [LN:U93688] [AC:U93688] [OR:Staphylococcus aureus]
[DB:genpept-bct2] [DE:Staphylococcus aureus toxic shock syndrome toxin-1
(tst),enterotoxin (ent), and integrase (int) genes, complete cds.]
[NT:orf13] [LE:9717] [RE:10004] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000988_34428905_f1_3	1686	5458	165	54		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000988_35428187_c3_37	1687	5459	438	145		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000988_36601678_c1_29	1688	5460	1728	575	102	0.010

Description

gp:[GI:g1004289] [LN:PPRNAE14B] [AC:Z50050] [PN:Xylanase B] [OR:Penicillium
purporogenum] [DB:genpept-pln1] [EC:3.2.1.8] [DE:P.purpurogenum mRNA for
endo-1,4-beta-xylanase.] [LE:11] [RE:637] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000988_4303175_f1_10	1689	5461	180	59		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000988_9923176_f3_20	1690	5462	162	53	56	0.013

Description

sp:[LN:NU5M_CAEL] [AC:P24896] [GN:ND5] [OR:CAENORHABDITIS ELEGANS]
[EC:1.6.5.3] [DE:NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5,] [SP:P24896]
[DB:swissprot] >pir:[LN:S26037] [AC:S26037:S25810] [PN:NADH dehydrogenase
(ubiquinone), chain 5] [GN:ND5] [CL:NADH dehydrogenase (ubiquinone) chain
5] [OR:mitochondrion Caenorhabditis elegans] [EC:1.6.5.3] [DB:pir2]
>gp:[GI:g515886] [LN:MTCE] [AC:X54252:S93745] [OR:Mitochondrion
Caenorhabditis elegans] [SR:Caenorhabditis elegans] [DB:genpept-inv1] [DE:C.
elegans complete mitochondrial genome.] [NT:ND5 protein (AA 1 - 527)]
[SP:P24896] [LE:11691] [RE:13274] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000990_10003756_f3_471	1691	5463	138	45		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000990_10193763_c2_864	1692	5464	186	61		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000990_10194713_f1_31	1693	5465	147	48		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000990_10241287_c2_822	1694	5466	663	220	74	0.037

Description

gp:[GI:g924349] [LN:HIV1U13473] [AC:U13473] [PN:envelope glycoprotein V1V2
region] [GN:env] [OR:Human immunodeficiency virus type 1] [DB:genpept-vr1]
[DE:Human immunodeficiency virus type 1 isolate 037 clone 03 from Uganda,
envelope glycoprotein (env) gene, V1V2 region, partial cds.] [LE:<1]
[RE:>285] [DI:direct]

AI7503000990_10268812_c2_820	1695	5467	144	47
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NO-HIT

AI7503000990_10360902_f3_536	1696	5468	183	60
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NO-HIT

AI7503000990_1042202_c3_948	1697	5469	1074	357	625	4.4e-61
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sp:[LN:POTD_ECOLI] [AC:P23861] [GN:POTD] [OR:ESCHERICHIA COLI]
[DE:SPERMIDINE/PUTRESCINE-BINDING PERIPLASMIC PROTEIN PRECURSOR (SPBP)]
[SP:P23861] [DB:swissprot] >pir:[LN:D40840] [AC:D40840:H64856 ]
[PN:spermidine/putrescine-binding protein precursor:spermidine/putrescine
transport protein D] [GN:potD ] [OR:Escherichia coli] [DB:pir2]
>gp:[GI:d1036929:g1651550] [LN:D90747] [AC:D90747:AB001340]
[PN:Spermidine/putrescine transport protein D] [GN:potD] [OR:Escherichia
coli] [SR:Escherichia coli(strain:K12) DNA, clone:Kohara clone #238]
[DB:genpept-bct1] [DE:Escherichia coli genomic DNA. (25.2 - 25.6 min).]
[NT:ORF_ID:o238#12; similar to PIR Accession Number] [LE:13470] [RE:14516]
[DI:complement] >gp:[GI:g1787367] [LN:AE000212] [AC:AE000212:U00096]
[PN:spermidine/putrescine periplasmic transport] [GN:potD] [FN:transport;
Transport of small molecules: Amino] [OR:Escherichia coli] [DB:genpept-bct2]
[DE:Escherichia coli K-12 MG1655 section 102 of 400 of the completegenome.]
[NT:f348; 100 pct identical to POTD_ECOLI SW: P23861] [LE:7785] [RE:8831]
[DI:complement] >gp:[GI:g147329] [LN:ECOPOTABCD] [AC:M64519] [PN:transport
protein] [GN:potD] [OR:Escherichia coli] [SR:E.coli (strain DR112) DNA,
clone pPT104] [DB:genpept-bct2] [DE:E.coli transport protein (potA, potB,
potC and potD) genes,complete cds.] [LE:3144] [RE:4190] [DI:direct]

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ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000990_10579000_c1_734	1698	5470	957	318	728	5.3e-72

Description

sp:[LN:COXX_BACSU] [AC:P24009] [GN:CTAB] [OR:BACILLUS SUBTILIS] [DE:PROBABLE CYTOCHROME C OXIDASE ASSEMBLY FACTOR] [SP:P24009] [DB:swissprot]
>pir:[LN:C69609] [AC:C69609:S14395] [PN:cytochrome caa3 oxidase (assembly factor) ctaB] [GN:ctaB] [CL:heme O synthase] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e334763:g2339991] [LN:BS16823KB] [AC:Z98682] [PN:CtaB protein] [GN:ctaB] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis genomic DNA 23.9kB fragment.] [SP:P24009] [LE:4441] [RE:5358] [DI:direct] >gp:[GI:g994794] [LN:BSCTABF] [AC:X54140] [PN:cytochrome a assembly facto] [GN:ctaB] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:1.9.3.1] [DE:B. subtilis ctaB-F genes for cytochrome a assembly factor andcytochrome-c oxidase (EC 1.9.3.1) subunits II, I, II, and IVB.] [NT:putative] [SP:P24009] [LE:408] [RE:1325] [DI:direct]
>gp:[GI:e1185078:g2633859] [LN:BSUB0008] [AC:Z99111:AL009126] [PN:cytochrome caa3 oxydase assembly factor] [GN:ctaB] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.] [SP:P24009] [LE:163924] [RE:164841] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000990_1063753_c2_874	1699	5471	1374	457	2070	3.3e-214

Description

sp:[LN:MURD_STAAU] [AC:O33595:O07323] [GN:MURD] [OR:STAPHYLOCOCCUS AUREUS] [EC:6.3.2.9] [DE:ADDING ENZYME)] [SP:O33595:O07323] [DB:swissprot]
>pir:[LN:JC6560] [AC:JC6560] [PN:UDP-N-acetylmuramoylalanine--D-glutamate ligase, :UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase] [GN:murD] [OR:Staphylococcus aureus] [EC:6.3.2.9] [DB:pir2] >gp:[GI:g2271510] [LN:AF009671] [AC:AF009671] [PN:UDP-N-acetylmuramoyl-L-alanine : D-glutamate] [GN:murD] [FN:catalyzes ATP-dependent D-glutamate addition] [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus UDP-N-acetylmuramoyl-L-alanine : D-glutamateligase (murD) gene, complete cds.] [NT:MurD] [LE:1] [RE:1350] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000990_10740628_f3_637	1700	5472	183	60		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000990_10928_c3_958	1701	5473	1242	413	239	1.1e-17

Description

pir:[LN:T03492] [AC:T03492] [PN:hypothetical protein] [OR:Rhodobacter capsulatus] [DB:pir2] [MP:1] >gp:[GI:g3128293] [LN:AF010496] [AC:AF010496] [PN:hypothetical protein] [OR:Rhodobacter capsulatus] [DB:genpept-bct2] [DE:Rhodobacter capsulatus strain SB1003, partial genome.] [LE:54291] [RE:55613] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000990_10969052_c3_935	1702	5474	1725	574	2602	1.4e-270

Description

sp:[LN:PT1_STAAU] [AC:P51183] [GN:PTS1] [OR:STAPHYLOCOCCUS AUREUS] [EC:2.7.3.9] [DE:(PHOSPHOTRANSFERASE SYSTEM, ENZYME I)] [SP:P51183] [DB:swissprot] >gp:[GI:g1070386] [LN:SAPTSHI] [AC:X93205] [PN:phosphoenolpyruvate-protein phosphatase] [GN:ptsI] [OR:Staphylococcus aureus] [DB:genpept-bct1] [EC:2.7.3.9] [DE:S.aureus ptsH and ptsI genes.] [SP:P51183] [LE:462] [RE:2180] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000990_10972150_c3_1037	1703	5475	2055	684	3024	0.0

Description

sp:[LN:RECG_STAAU] [AC:O50581] [GN:RECG] [OR:STAPHYLOCOCCUS AUREUS] [EC:3.6.1.-] [DE:ATP-DEPENDENT DNA HELICASE RECG,] [SP:O50581] [DB:swissprot] >gp:[GI:d1025491:g2826896] [LN:AB000439] [AC:AB000439] [PN:RecG] [GN:recG] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus (strain:RN4220) DNA] [DB:genpept-bct1] [DE:Staphylococcus aureus recG gene, complete cds.] [LE:319] [RE:2379] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000990_1173177_f3_667	1704	5476	1053	350	691	4.4e-68

sp:[LN:YAAF_ECOLI] [AC:P22564] [GN:YAAF] [OR:ESCHERICHIA COLI]
[DE:HYPOTHETICAL 32.6 KD PROTEIN IN LYTB-DAPB INTERGENIC REGION] [SP:P22564]
[DB:swissprot] >pir:[LN:JE0404] [AC:JE0404:S40553:F64723:S22291]
[PN:probable glycosidase, yaaF] [GN:yaaF] [CL:yaaF protein] [OR:Escherichia
coli] [EC:3.2.-.-] [DB:pir2] >gp:[GI:g41934] [LN:ECLSPDAP] [AC:X54945]
[GN:ORF 3] [OR:Escherichia coli] [DB:genpept-bct1] [DE:E. coli lsp-dapB
interval.] [NT:product appears to be membrane bound] [SP:P22564] [LE:1613]
[RE:2527] [DI:direct] >gp:[GI:d1001780:g216457] [LN:ECO110K]
[AC:D10483:J01597:J01683:J01706:K01298:K01990:M10420:M10611:M12544]
[OR:Escherichia coli] [SR:Escherichia coli (strain:K-12) DNA]
[DB:genpept-bct1] [DE:E.coli K12 genome, 0-2.4min. region.] [NT:hypothetical
32.6K protein(PIR:JE0404)] [LE:26947] [RE:27861] [DI:direct]
>gp:[GI:g1786213] [LN:AE000113] [AC:AE000113:U00096] [PN:orf, hypothetical
protein] [GN:yaaF] [FN:orf; Unknown] [OR:Escherichia coli] [DB:genpept-bct2]
[DE:Escherichia coli K-12 MG1655 section 3 of 400 of the completegenome.]
[NT:o304; 100 pct identical to YAAF_ECOLI SW: P22564] [LE:6634] [RE:7548]
[DI:direct]

gp:[GI:g4097530] [LN:LLU64311] [AC:U64311]
[PN:phosphoribosylaminoimidazolesuccinocarboxamide] [GN:purC]
[OR:Lactococcus lactis] [DB:genpept-bct2] [EC:6.3.2.6] [DE:Lactococcus
lactis phosphoribosylaminoimidazolesuccinocarboxamidesynthetase (purC),
phosphoribosylformylglycinamidine synthetase I(purQ),
phosphoribosylformylglycinamidine synthetase II (purL),
andphosphoribosylpyrophosphate amidotransferase (purF) genes, completedcds;
and unknown gene.] [NT:SAICAR synthetase] [LE:792] [RE:1502] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000990_11806512_f3_562	1707	5479	207	68	86	0.0050

Description

gp:[GI:e1344613:g3874900] [LN:CEC41G6] [AC:Z81047] [GN:C41G6.8]
 [OR:Caenorhabditis elegans] [DB:genpept-inv1] [DE:Caenorhabditis elegans
 cosmid C41G6, complete sequence.] [LE:18951:19702:20184]
 [RE:19549:20043:20463] [DI:directJoin]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000990_1204567_c2_897	1708	5480	750	249	481	8.0e-46

Description

pir:[LN:G69878] [AC:G69878] [PN:conserved hypothetical protein yloO]
 [GN:yloO] [CL:conserved hypothetical protein yloO:conserved hypothetical
 protein yloO homology] [OR:Bacillus subtilis] [DB:pir2]
 >gp:[GI:e1185167:g2633948] [LN:BSUB0009] [AC:Z99112:AL009126] [GN:yloO]
 [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
 complete genome (section 9 of 21): from 1598421to 1807200.] [NT:similar to
 hypothetical proteins] [LE:51363] [RE:52127] [DI:direct]
 >gp:[GI:e323505:g2337805] [LN:BSY13937] [AC:Y13937] [PN:putative Ptc1
 protein] [GN:yloO] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1]
 [DE:Bacillus subtilis genomic DNA from the spoVM region.] [LE:13135]
 [RE:13899] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000990_1209638_c1_775	1709	5481	540	179	642	6.9e-63

Description

sp:[LN:LSPA_STAAU] [AC:P31024] [GN:LSPA:LSP] [OR:STAPHYLOCOCCUS AUREUS]
 [EC:3.4.23.36] [DE:PEPTIDASE) (SIGNAL PEPTIDASE II) (SPASE II)] [SP:P31024]
 [DB:swissprot] >pir:[LN:S20433] [AC:S20433] [PN:lipoprotein signal
 peptidase,] [CL:lipoprotein signal peptidase] [OR:Staphylococcus aureus]
 [EC:3.4.23.36] [DB:pir2] >gp:[GI:g153045] [LN:STALSP] [AC:M83994:M84707]
 [PN:prolipoprotein signal peptidase] [GN:lsp] [OR:Staphylococcus aureus]
 [SR:Staphylococcus aureus DNA] [DB:genpept-bct1] [DE:Staphylococcus aureus
 prolipoprotein signal peptidase (lsp) gene,complete cds.] [LE:1213]
 [RE:1704] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000990_1209682_c2_856	1710	5482	2409	802	1984	4.3e-205

Description

sp:[LN:SYFB_BACSU] [AC:P17922:P94540] [GN:PHET] [OR:BACILLUS SUBTILIS]
[EC:6.1.1.20] [DE:TRNA LIGASE BETA CHAIN) (PHERS)] [SP:P17922:P94540]
[DB:swissprot] >pir:[LN:YFBSB] [AC:A69676:I40460:S11731]
[PN:phenylalanine--trna ligase, beta chain:phenylalanyl-trna synthetase beta
chain] [GN:pheT] [CL:phenylalanine--trna ligase beta chain] [OR:Bacillus
subtilis] [EC:6.1.1.20] [DB:pir1] >gp:[GI:e1184112:g2635328] [LN:BSUB0015]
[AC:Z99118:AL009126] [PN:phenylalanyl-trna synthetase (beta subunit)]
[GN:pheT] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:6.1.1.20]
[DE:Bacillus subtilis complete genome (section 15 of 21): from 2795131to
3013540.] [SP:P17922] [LE:130980] [RE:133394] [DI:complement]
>gp:[GI:e1165325:g1770031] [LN:BSZ75208] [AC:Z75208] [PN:phenylalanyl-trna
synthetase beta subunit] [GN:pheT] [OR:Bacillus subtilis] [DB:genpept-bct1]
[EC:6.1.1.20] [DE:B.subtilis genomic sequence 89009bp.]
[NT:phenylalanyl-trna synthetase beta subunit] [SP:P17922] [LE:36513]
[RE:38927] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000990_13720312_c3_1024	1711	5483	240	79	117	3.0e-07

Description

pir:[LN:C69878] [AC:C69878] [PN:hypothetical protein yloH] [GN:yloH]
[OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1185160:g2633941] [LN:BSUB0009]
[AC:Z99112:AL009126] [GN:yloH] [FN:unknown] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 9 of 21):
from 1598421to 1807200.] [LE:43546] [RE:43749] [DI:direct]
>gp:[GI:e323522:g2337798] [LN:BSY13937] [AC:Y13937] [PN:putative rpoZ
protein] [GN:yloH] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1]
[DE:Bacillus subtilis genomic DNA from the spoVM region.] [LE:5318]
[RE:5521] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000990_13757785_f3_639	1712	5484	135	44		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000990_1376317_c2_881	1713	5485	564	187	481	8.0e-46

Description

gp:[GI:e199384:g1514599] [LN:LPPYRBSOP] [AC:Z54240] [GN:pyrR] [FN:regulatory protein] [OR:Lactobacillus plantarum] [DB:genpept-bct1] [DE:L.plantarum pyrimidine biosynthetic operon (pyrR, pyrB, pyrC,pyrAA, pyrAB, pyrD, pyrF, and pyrE) genes.] [LE:781] [RE:1323] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000990_13797076_c3_915	1714	5486	135	44		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000990_13864213_f3_624	1715	5487	234	77	186	1.4e-14

Description

pir:[LN:D69871] [AC:D69871] [PN:hypothetical protein ykzG] [GN:ykzG] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1185044:g2633825] [LN:BSUB0008] [AC:Z99111:AL009126] [GN:ykzG] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.] [LE:129406] [RE:129615] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000990_13869091_f2_433	1716	5488	294	97	246	6.4e-21

Description

sp:[LN:QOX4_BACSU] [AC:P34959] [GN:QOXD:IPA-40D] [OR:BACILLUS SUBTILIS] [EC:1.9.3.-] [DE:SUBUNIT QOXD)] [SP:P34959] [DB:swissprot] >pir:[LN:D38129] [AC:D38129:S39695:H69687] [PN:quinol oxidase aa3-600 chain IV] qoxD:cytochrome aa3 quinol oxidase (subunit IV) qoxD] [GN:qoxD] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:g143399] [LN:BACQOXA] [AC:M86548] [PN:quinol oxidase] [GN:QOXD] [OR:Bacillus subtilis] [SR:Bacillus subtilis DNA] [DB:genpept-bct1] [DE:Bacillus subtilis AA3-600 quinol oxidase (QOXA, QOXB, QOXC, QOXD)genes, complete cds.] [LE:4425] [RE:4799] [DI:direct] >gp:[GI:g413964] [LN:BSGENR] [AC:X73124] [GN:ipa-40d qoxD] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis genomic region (325 to 333).] [SP:P34959] [LE:42877] [RE:43251] [DI:direct] >gp:[GI:e1186313:g2636349] [LN:BSUB0020] [AC:Z99123:AL009126] [PN:cytochrome aa3 quinol oxidase (subunit IV)] [GN:qoxD] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.] [NT:alternate gene name: ipa-40d] [SP:P34959] [LE:114711] [RE:115085] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000990_13916017_c1_738	1717	5489	123	40		
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000990_14460882_c2_840	1718	5490	240	79	321	7.2e-29
<u>Description</u>						

gp:[GI:g1022726] [LN:SHU35635] [AC:U35635] [PN:unknown] [OR:Staphylococcus haemolyticus] [SR:Staphylococcus haemolyticus strain=Y176] [DB:genpept-bct1] [DE:Staphylococcus haemolyticus IS1272 ORF1 and ORF2 genes, completedcs.] [NT:ORF1] [LE:1101] [RE:1922] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000990_14557882_f3_532	1719	5491	126	41		
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000990_14642135_c3_957	1720	5492	1905	634	2456	4.1e-255
<u>Description</u>						

sp:[LN:TYPA_BACSU] [AC:O07631] [GN:TYPA] [OR:BACILLUS SUBTILIS] [DE:GTP-BINDING PROTEIN TYPA/BIPA HOMOLOG] [SP:O07631] [DB:swissprot] >pir:[LN:E69872] [AC:E69872] [PN:GTP-binding elongation factor homolog ylaG] [GN:ylaG] [CL:translation elongation factor Tu homology] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1185067:g2633848] [LN:BSUB0008] [AC:Z99111:AL009126] [GN:ylaG] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 8 of 21): from 1394791 to 1603020.] [NT:similar to GTP-binding elongation factor] [SP:O07631] [LE:150736] [RE:152574] [DI:direct] >gp:[GI:e1191893:g2224766] [LN:BSZ97025] [AC:Z97025] [GN:ylaG] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis nprE, yla[A,B,C,D,E,F,G,H,I,J,K,L,M,N,O] and pycAgenes.] [NT:product highly similar to elongation factor EF-G] [SP:O07631] [LE:4995] [RE:6833] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000990_14644066_c2_865	1721	5493	189	62	79	0.0032

Description

gp:[GI:g3212079] [LN:AF068633] [AC:AF068633] [PN:phenol soluble modulin beta 1] [FN:inflammatory protein] [OR:Staphylococcus epidermidis] [DB:genpept-bct2] [DE:Staphylococcus epidermidis phenol soluble modulin beta 1 and phenolsoluble modulin beta 2 genes, complete cds.] [NT:PSM beta 1] [LE:669] [RE:803] [DI:direct] >gp:[GI:g3212080] [LN:AF068633] [AC:AF068633] [PN:phenol soluble modulin beta 2] [FN:inflammatory protein] [OR:Staphylococcus epidermidis] [DB:genpept-bct2] [DE:Staphylococcus epidermidis phenol soluble modulin beta 1 and phenolsoluble modulin beta 2 genes, complete cds.] [NT:PSM beta 2] [LE:859] [RE:993] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000990_14650302_c1_688	1722	5494	264	87	179	8.0e-14

Description

sp:[LN:YEXA_BACSU] [AC:P12049] [GN:YEXA] [OR:BACILLUS SUBTILIS] [DE:HYPOTHETICAL 9.7 KD PROTEIN IN PURC-PURL INTERGENIC REGION] [SP:P12049] [DB:swissprot] >pir:[LN:E29326] [AC:E29326:E69799] [PN:conserved hypothetical protein yexA:hypothetical protein (pur operon)] [GN:yexA] [CL:conserved hypothetical protein MJ1593] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1182626:g2632960] [LN:BSUB0004] [AC:Z99107:AL009126] [GN:yexA] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.] [NT:similar to hypothetical proteins] [LE:101124] [RE:101378] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000990_14664012_f2_323	1723	5495	468	155	341	5.4e-31

Description

pir:[LN:E69875] [AC:E69875] [PN:hypothetical protein ylbP] [GN:ylbP] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e334785:g2340013] [LN:BS16823KB] [AC:Z98682] [PN:YlbP protein] [GN:ylbP] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis genomic DNA 23.9kB fragment.] [LE:21896] [RE:22378] [DI:complement] >gp:[GI:e1185100:g2633881] [LN:BSUB0008] [AC:Z99111:AL009126] [GN:ylbP] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.] [LE:181379] [RE:181861] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000990_14851587_c3_1010	1724	5496	126	41		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000990_14875002_f2_408	1725	5497	141	46	85	0.0044

Description

gp:[GI:g488889] [LN:A12521] [AC:A12521] [PN:Acidic Basic Repeat Antigen
Rhoptry (ABRA)] [OR:Plasmodium falciparum] [SR:malaria parasite P.
falciparum] [DB:genpept-pat] [DE:Ag189 clone.] [LE:1:61] [RE:45:963]
[DI:directJoin]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000990_156502_f1_179	1726	5498	243	80		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000990_16593800_f2_359	1727	5499	144	47		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000990_19537562_f2_429	1728	5500	198	65		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000990_19537878_f1_177	1729	5501	159	52		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000990_19556326_f1_94	1730	5502	141	46		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000990_19557752_c1_777	1731	5503	912	303	844	2.7e-84

Description

sp:[LN:PYRB_BACSU] [AC:P05654] [GN:PYRB] [OR:BACILLUS SUBTILIS] [EC:2.1.3.2] [DE:TRANSCARBAMYLASE) (ATCASE)] [SP:P05654] [DB:swissprot] >pir:[LN:OWBSAC] [AC:A25015:C39845:B69686] [PN:aspartate carbamoyltransferase, catalytic chain:aspartate transcarbamoylase] [GN:pyrB] [CL:ornithine carbamoyltransferase: aspartate/ornithine carbamoyltransferase homology] [OR:Bacillus subtilis] [EC:2.1.3.2] [DB:pir1] [MP:37 min] >gp:[GI:g143384] [LN:BACPYRB] [AC:M13128] [OR:Bacillus subtilis] [SR:B.subtilis (strain JH861) DNA, clone pLS201] [DB:genpept-bct1] [DE:B.subtilis pyrB gene encoding aspartate transcarbamoylase, completecds.] [NT:aspartate transcarbamoylase (EC 2.1.3.2)] [LE:96] [RE:1010] [DI:direct] >gp:[GI:e1185141:g2633922] [LN:BSUB0009] [AC:Z99112:AL009126] [PN:aspartate carbamoyltransferase] [GN:pyrB] [FN:pyrimidine biosynthesis] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:2.1.3.2] [DE:Bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.] [SP:P05654] [LE:21455] [RE:22369] [DI:direct] >gp:[GI:g143387] [LN:BACPYROP] [AC:M59757] [PN:aspartate transcarbamylase] [GN:pyrB] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis ORF1A (pyrR), putative membrane-bound uracilpermease (pyrP), aspartate transcarbamylase (pyrB), dihydroorotase (pyrC), glutaminase of carbamyl phosphate synthetase (pyrAA), carbamyl phosphate synthetase (pyrAB), dihydroorotase dehydrogenase (pyrD), OMP decarboxylase (pyrF), and OMP-PRPP transferase (pyrE) genes, complete cds; and unknown gene.] [LE:2859] [RE:3773] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000990_19565627_c2_879	1732	5504	132	43		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000990_19609530_f1_155	1733	5505	147	48		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000990_19804703_c2_811	1734	5506	747	248	696	1.3e-68

Description

sp:[LN:PURQ_BACSU] [AC:P12041] [GN:PURQ] [OR:BACILLUS SUBTILIS] [EC:6.3.5.3] [DE:SYNTHASE I]) [SP:P12041] [DB:swissprot] >pir:[LN:SYBS1G] [AC:F29326:H69684] [PN:phosphoribosylformylglycinamide synthase, component I] [GN:purQ] [CL:phosphoribosylformylglycinamide synthase component I] [OR:Bacillus subtilis] [EC:6.3.5.3] [DB:pir1] [MP:18 min] >gp:[GI:g143368] [LN:BACPURF] [AC:J02732:K00047] [OR:Bacillus subtilis] [SR:B.subtilis (strain DE1 (prototroph DER. or W168)) DNA, clone pPZ] [DB:genpept-bct1] [DE:B.subtilis pur operon encoding purine biosynthesis enzymes, 12genes.] [NT:phosphoribosylformyl glycinamide synthetase I] [LE:4393] [RE:5076] [DI:direct] >gp:[GI:e1182627:g2632961] [LN:BSUB0004] [AC:Z99107:AL009126] [PN:phosphoribosylformylglycinamide synthetase II] [GN:purL] [FN:purine biosynthesis] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:6.3.5.3] [DE:Bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.] [SP:P12041] [LE:101375] [RE:102058] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000990_19957802_c1_752	1735	5507	1896	631	2764	9.5e-288

Description

gp:[GI:e1333202:g3776112] [LN:SATRXA] [AC:AJ223480] [PN:excinuclease ABC, subunit C] [GN:uvrC] [FN:excision of ultraviolet light-induced] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:Staphylococcus aureus trxA and uvrC genes and partial mutS and dhsCgenes.] [NT:alternative gene name: uvrB] [LE:2972] [RE:4753] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000990_20312515_f2_242	1736	5508	141	46		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000990_20500055_f1_218	1737	5509	132	43		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000990_20502217_c3_990	1738	5510	1626	541	718	6.1e-71

Description

pir:[LN:G69875] [AC:G69875] [PN:hypothetical protein yllA] [GN:yllA]
 [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1185102:g2633883] [LN:BSUB0008]
 [AC:Z99111:AL009126] [GN:yllA] [FN:unknown] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 8 of 21):
 from 1394791to 1603020.] [LE:182988] [RE:184607] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000990_2067627_c2_849	1739	5511	129	42		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000990_20890875_c2_801	1740	5512	147	48		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000990_209840_f1_44	1741	5513	195	64		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000990_20994212_f1_151	1742	5514	207	68	71	0.022

Description

pir:[LN:D69872] [AC:D69872] [PN:hypothetical protein ylaF] [GN:ylaF]
 [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1185066:g2633847] [LN:BSUB0008]
 [AC:Z99111:AL009126] [GN:ylaF] [FN:unknown] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 8 of 21):
 from 1394791to 1603020.] [LE:150435] [RE:150623] [DI:complement]
 >gp:[GI:e324391:g2224765] [LN:BSZ97025] [AC:Z97025] [GN:ylaF] [OR:Bacillus
 subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis nprE,
 yla[A,B,C,D,E,F,G,H,I,J,K,L,M,N,O] and pycAgenes.] [LE:4694] [RE:4882]
 [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000990_211677_c3_989	1743	5515	702	233	436	4.7e-41

Description

pir:[LN:E69814] [AC:E69814] [PN:conserved hypothetical protein yfnB]
 [GN:yfnB] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1182712:g2633046]
 [LN:BSUB0004] [AC:Z99107:AL009126] [GN:yfnB] [FN:unknown] [OR:Bacillus
 subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 4
 of 21): from 600701 to813890.] [NT:similar to hypothetical proteins]
 [LE:203465] [RE:204172] [DI:complement] >gp:[GI:e1182723:g2633057]
 [LN:BSUB0005] [AC:Z99108:AL009126] [GN:yfnB] [FN:unknown] [OR:Bacillus
 subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 5
 of 21): from 802821 to1011250.] [NT:similar to hypothetical proteins]
 [LE:1345] [RE:2052] [DI:complement] >gp:[GI:d1020926:g2116760] [LN:D86418]
 [AC:D86418] [PN:YfnB] [OR:Bacillus subtilis] [SR:Bacillus subtilis
 (strain:AC327) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis genomic DNA
 69-70 degree region, partialsequence.] [LE:9019] [RE:9726] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000990_21648962_c3_930	1744	5516	1827	608	1793	7.4e-185

Description

gp:[GI:g517205] [LN:SPU09352] [AC:U09352] [PN:67 kDa Myosin-crossreactive
 streptococcal] [OR:Streptococcus pyogenes] [DB:genpept-bct1]
 [DE:Streptococcus pyogenes 42 KD protein (ORF1) gene and 67
 KDMYosin-crossreactive streptococcal antigen gene, complete cds.] [NT:ORF2]
 [LE:1734] [RE:3506] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000990_21656327_c1_761	1745	5517	936	311	1464	5.4e-150

Description

gp:[GI:g2149891] [LN:SAU94706] [AC:U94706] [PN:unknown] [GN:y11C]
 [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus
 strain ATCC 8325-4 cell wall/cell divisiongene cluster, y11B, y11C, y11D,
 pbpA, mraY, murD, div1B, ftsA andftsZ genes, complete cds.] [LE:987]
 [RE:1922] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000990_21759653_f3_666	1746	5518	609	202	552	2.4e-53

Description

sp:[LN:QOX3_BACSU] [AC:P34958] [GN:QOXC:IPA-39D] [OR:BACILLUS SUBTILIS] [EC:1.9.3.-] [DE:SUBUNIT QOXC)] [SP:P34958] [DB:swissprot] >pir:[LN:C38129] [AC:C38129:S39694:G69687] [PN:bo-type ubiquinol oxidase; chain III] goxC:cytochrome aa3 quinol oxidase (subunit III) goxC] [GN:goxC] [CL:cytochrome-c oxidase chain III] [OR:Bacillus subtilis] [EC:1.10.3.-] [DB:pir2] >gp:[GI:g143398] [LN:BACQOXA] [AC:M86548] [PN:quinol oxidase] [GN:QOXC] [OR:Bacillus subtilis] [SR:Bacillus subtilis DNA] [DB:genpept-bct1] [DE:Bacillus subtilis AA3-600 quinol oxidase (QOXA, QOXB, QOXC, QOXD)genes, complete cds.] [LE:3809] [RE:4423] [DI:direct] >gp:[GI:g413963] [LN:BSGENR] [AC:X73124] [GN:ipa-39d goxC] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis genomic region (325 to 333).] [SP:P34958] [LE:42261] [RE:42875] [DI:direct] >gp:[GI:e1186314:g2636350] [LN:BSUB0020] [AC:Z99123:AL009126] [PN:cytochrome aa3 quinol oxidase (subunit III)] [GN:goxC] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.] [NT:alternate gene name: ipa-39d] [SP:P34958] [LE:115087] [RE:115701] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000990_21915911_f1_197	1747	5519	894	297	229	4.0e-19

Description

pir:[LN:G69858] [AC:G69858] [PN:hypothetical protein ykoC] [GN:ykoC] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1181521:g2632041] [LN:BSAJ2571] [AC:AJ002571] [PN:YkoC] [GN:ykoC] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis 168 56 kb DNA fragment between xlyA and ykoR.] [LE:40195] [RE:40959] [DI:complement] >gp:[GI:e1183341:g2633675] [LN:BSUB0007] [AC:Z99110:AL009126] [GN:ykoC] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.] [LE:193144] [RE:193908] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000990_22000943_f1_216	1748	5520	222	73		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000990_22400283_c2_830	1749	5521	981	326	1329	1.1e-135

Description

pir: [LN:C36718] [AC:C36718:A69674] [PN:pyruvate dehydrogenase (lipoamide), E1 beta chain precursor pdhB] [GN:pdhB] [CL:pyruvate dehydrogenase (lipoamide) beta chain] [OR:Bacillus subtilis] [EC:1.2.4.1] [DB:pir2]
 >gp: [GI:g143378] [LN:BACPYDHY] [AC:M57435:M31542] [PN:pyruvate decarboxylase (E-1) beta subunit] [GN:pdhB] [OR:Bacillus subtilis] [SR:B.subtilis (strain 168) BRB1 (sacA321 metB5) cell line DNA, clone] [DB:genpept-bct1] [EC:1.2.4.1] [DE:B.subtilis pyruvate dehydrogenase complex genes, complete cds;PAL-related lipoprotein (slp) gene, complete cds, lysinedecarboxylase (cad) gene, partial cds.] [LE:2796] [RE:3773] [DI:direct]
 >gp: [GI:e1185049:g2633830] [LN:BSUB0008] [AC:Z99111:AL009126] [PN:pyruvate dehydrogenase (E1 beta subunit)] [GN:pdhB] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:1.2.4.1] [DE:Bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.] [SP:P21882] [LE:134060] [RE:135037] [DI:direct] >gp: [GI:g3282143] [LN:AF012285] [AC:AF012285:AF012284:U51911] [PN:pyruvate decarboxylase E-1 beta subunit] [GN:pdhB] [OR:Bacillus subtilis] [DB:genpept-bct2] [EC:1.2.4.1] [DE:Bacillus subtilis mobA-nprE gene region.] [NT:similar to pyruvate decarboxylase (E-1) beta] [LE:34548] [RE:35525] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000990_2242938_c3_1009	1750	5522	933	310	1055	1.2e-106

Description

sp: [LN:YLYB_BACSU] [AC:Q45480:O31732] [GN:YLYB] [OR:BACILLUS SUBTILIS] [DE:HYPOTHETICAL 33.7 KD PROTEIN IN LSP-PYRR INTERGENIC REGION (ORF-X)] [SP:Q45480:O31732] [DB:swissprot] >gp: [GI:g1373157] [LN:BSU48870] [AC:U48870] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis signal peptidase II (lsp) gene, complete cds, isoleucyl-tRNA synthetase (ileS) and pyrR genes, partial cds.] [NT:orf-X; hypothetical protein; Method: conceptual] [LE:1658] [RE:2569] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000990_22461078_c1_769	1751	5523	735	244	814	4.1e-81

Description

gp: [GI:g1314301] [LN:SAU41072] [AC:U41072] [PN:unknown] [GN:ORF] [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus isoleucyl-tRNA synthetase (ileS) gene, partial cds.] [LE:106] [RE:723] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000990_22462802_c3_1026	1752	5524	1203	400	1070	3.1e-108

Description

pir:[LN:D69878] [AC:D69878] [PN:pantothenate metabolism flavoprotein homolog yloI] [GN:yloI] [CL:pantothenate metabolism flavoprotein dfp] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1185161:g2633942] [LN:BSUB0009] [AC:Z99112:AL009126] [GN:yloI] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.] [NT:similar to pantothenate metabolism flavoprotein] [LE:43830] [RE:45050] [DI:direct] >gp:[GI:e323501:g2337799] [LN:BSY13937] [AC:Y13937] [PN:putative Dfp protein] [GN:yloI] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis genomic DNA from the spoVM region.] [LE:5602] [RE:6822] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000990_22478427_c3_987	1753	5525	138	45	115	4.8e-07

Description

sp:[LN:GGI2_STAHA] [AC:P11698] [OR:STAPHYLOCOCCUS HAEMOLYTICUS] [DE:ANTIBACTERIAL PROTEIN 2 (GONOCOCCAL GROWTH INHIBITOR 2)] [SP:P11698] [DB:swissprot] >pir:[LN:BXSA2] [AC:S00600] [PN:antibacterial protein 2:gonococcal growth inhibitor 2] [CL:Staphylococcus haemolyticus antibacterial protein] [OR:Staphylococcus haemolyticus] [DB:pir1]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000990_22542567_c2_855	1754	5526	759	252	562	2.1e-54

Description

pir:[LN:G69984] [AC:G69984] [PN:rRNA methylase homolog ysgA] [GN:ysgA] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1184114:g2635330] [LN:BSUB0015] [AC:Z99118:AL009126] [GN:ysgA] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.] [NT:similar to rRNA methylase] [LE:134799] [RE:135545] [DI:complement] >gp:[GI:e1165323:g1770029] [LN:BSZ75208] [AC:Z75208] [PN:hypothetical protein] [GN:ysgA] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis genomic sequence 89009bp.] [NT:Homology to SpoU-type rRNA methyltransferases;] [LE:34362] [RE:35108] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000990_22775126_f2_411	1755	5527	633	210	263	1.0e-22

Description

pir:[LN:A69859] [AC:A69859] [PN:hypothetical protein ykoE] [GN:ykoE]
[OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1181523:g2632043] [LN:BSAJ2571]
[AC:AJ002571] [PN:YkoE] [GN:ykoE] [FN:unknown] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis 168 56 kb DNA fragment between xlyA
and ykoR.] [LE:42565] [RE:43164] [DI:complement] >gp:[GI:e1183343:g2633677]
[LN:BSUB0007] [AC:Z99110:AL009126] [GN:ykoE] [FN:unknown] [OR:Bacillus
subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 7
of 21): from 1194391to 1411140.] [LE:195514] [RE:196113] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000990_22931642_c2_802	1756	5528	1224	407	1250	2.6e-127

Description

gp:[GI:d1024918:g2696796] [LN:AB009635] [AC:AB009635] [PN:Fmt] [GN:fmt]
[OR:Staphylococcus aureus] [SR:Staphylococcus aureus (strain:KSA8) DNA]
[DB:genpept-bct1] [DE:Staphylococcus aureus DNA for Fmt, complete cds.]
[LE:1234] [RE:2427] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000990_23438887_c1_748	1757	5529	300	99	196	1.3e-15

Description

pir:[LN:A69985] [AC:A69985] [PN:hypothetical protein yshA] [GN:yshA]
[OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1184110:g2635326] [LN:BSUB0015]
[AC:Z99118:AL009126] [GN:yshA] [FN:unknown] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 15 of 21):
from 2795131to 3013540.] [LE:129612] [RE:129869] [DI:complement]
>gp:[GI:e1165327:g1770033] [LN:BSZ75208] [AC:Z75208] [PN:hypothetical
protein] [GN:yshA] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis
genomic sequence 89009bp.] [NT:unknown function; putative] [LE:40038]
[RE:40295] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000990_23442177_f3_600	1758	5530	669	222	429	2.6e-40

Description

pir:[LN:D69864] [AC:D69864] [PN:hypothetical protein yktB] [GN:yktB]
[OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1185055:g2633836] [LN:BSUB0008]
[AC:Z99111:AL009126] [GN:yktB] [FN:unknown] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 8 of 21):
from 1394791to 1603020.] [LE:140850] [RE:141488] [DI:complement]
>gp:[GI:g3282149] [LN:AF012285] [AC:AF012285:AF012284:U51911] [PN:unknown]
[GN:yktB] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus
subtilis mobA-nprE gene region.] [LE:41338] [RE:41976] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000990_23448838_f1_217	1759	5531	873	290	786	3.8e-78

Description

sp:[LN:FOLD_BACSU] [AC:P54382] [GN:FOLD] [OR:BACILLUS SUBTILIS]
[EC:1.5.1.5:3.5.4.9] [DE:METHENYLTETRAHYDROFOLATE CYCLOHYDROLASE,]
[SP:P54382] [DB:swissprot] >pir:[LN:E69626] [AC:E69626]
[PN:methylenetetrahydrofolate dehydrogenase (NADP+), /
methenyltetrahydrofolate cyclohydrolase,] [GN:fold]
[CL:methylenetetrahydrofolate dehydrogenase (NAD+):
methylenetetrahydrofolate dehydrogenase (NAD+) homology] [OR:Bacillus
subtilis] [EC:1.5.1.5:3.5.4.9] [DB:pir2] >gp:[GI:d1013251:g1303916]
[LN:BACJH642] [AC:D84432:D82370] [PN:YqiA] [OR:Bacillus subtilis]
[SR:Bacillus subtilis (strain:JH642(trpC2 PheA1)) DNA] [DB:genpept-bct1]
[DE:Bacillus subtilis DNA, 283 Kb region containing skin element.]
[LE:190351] [RE:191202] [DI:direct] >gp:[GI:e1185699:g2634865] [LN:BSUB0013]
[AC:Z99116:AL009126] [PN:methenyltetrahydrofolate cyclohydrolase] [GN:fold]
[FN:purines and amino acids biosynthesis] [OR:Bacillus subtilis]
[DB:genpept-bct1] [EC:1.5.1.5:3.5.4.9] [DE:Bacillus subtilis complete genome
(section 13 of 21): from 2395261to 2613730.] [NT:alternate gene name: yqiA;]
[SP:P54382] [LE:132419] [RE:133270] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000990_23453767_f1_62	1760	5532	138	45		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000990_23492327_f1_37	1761	5533	204	67	126	3.3e-08

Description

pir:[LN:S75993] [AC:S75993] [PN:hypothetical protein] [OR:Synechocystis sp.] [SR:PCC 6803, , PCC 6803] [SR:PCC 6803,] [DB:pir2]
>gp:[GI:d1011491:g1001353] [LN:SYCSLLH] [AC:D64006:AB001339]
[PN:hypothetical protein] [GN:clpP] [OR:Synechocystis sp.] [SR:Synechocystis sp. (strain:PCC6803) DNA] [DB:genpept-bct1] [DE:Synechocystis sp. PCC6803 complete genome, 25/27, 3138604-3270709.] [NT:ORF_ID:s110498] [LE:80076]
[RE:80528] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000990_23532327_c2_829	1762	5534	1113	370	1432	1.3e-146

Description

sp:[LN:ODPA_BACST] [AC:P21873] [GN:PDHA] [OR:BACILLUS STEAROTHERMOPHILUS]
[EC:1.2.4.1] [DE:PYRUVATE DEHYDROGENASE E1 COMPONENT, ALPHA SUBUNIT,]
[SP:P21873] [DB:swissprot]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000990_23550313_f2_329	1763	5535	141	46		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000990_23572178_c2_861	1764	5536	846	281	1070	3.1e-108

Description

sp:[LN:DHSB_BACSU] [AC:P08066] [GN:SDHB] [OR:BACILLUS SUBTILIS]
[EC:1.3.99.1] [DE:SUCCINATE DEHYDROGENASE IRON-SULFUR PROTEIN,] [SP:P08066]
[DB:swissprot]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000990_23572253_c1_796	1765	5537	741	246	623	7.1e-61

Description

pir:[LN:B69693] [AC:B69693:JC4821] [PN:ribonuclease III,:RNase D:RNase O]
 [GN:rncS:srb] [CL:ribonuclease III:double-stranded RNA-binding repeat
 homology] [OR:Bacillus subtilis] [EC:3.1.26.3] [DB:pir2]
 >gp:[GI:e1185184:g2633965] [LN:BSUB0009] [AC:Z99112:AL009126]
 [PN:ribonuclease III] [GN:rncS] [OR:Bacillus subtilis] [DB:genpept-bct1]
 [EC:3.1.26.3] [DE:Bacillus subtilis complete genome (section 9 of 21): from
 1598421to 1807200.] [NT:alternate gene name: rnc] [LE:66689] [RE:67438]
 [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000990_23632962_c2_880	1766	5538	810	269	270	1.8e-23

Description

sp:[LN:YFIE_BACSU] [AC:P54721] [GN:YFIE] [OR:BACILLUS SUBTILIS]
 [DE:HYPOTHETICAL 31.5 KD PROTEIN IN GLVBC 3'REGION] [SP:P54721]
 [DB:swissprot] >pir:[LN:H69802] [AC:H69802] [PN:conserved hypothetical
 protein yfiE] [GN:yfiE] [OR:Bacillus subtilis] [DB:pir2]
 >gp:[GI:e1182814:g2633148] [LN:BSUB0005] [AC:Z99108:AL009126] [GN:yfiE]
 [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
 complete genome (section 5 of 21): from 802821 to1011250.] [NT:similar to
 hypothetical proteins from B. subtilis] [SP:P54721] [LE:94696] [RE:95553]
 [DI:direct] >gp:[GI:d1009744:g1486247] [LN:D50543] [AC:D50543] [PN:unknown]
 [GN:yfiE] [FN:unknown] [OR:Bacillus subtilis] [SR:Bacillus subtilis
 (strain:168, haplotype:haploid) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis
 DNA for 76-degree region, complete cds.] [LE:8372] [RE:9229] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000990_23642217_c1_790	1767	5539	648	215	396	8.1e-37

Description

pir:[LN:C69879] [AC:C69879] [PN:hypothetical protein yloS] [GN:yloS]
 [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1185171:g2633952] [LN:BSUB0009]
 [AC:Z99112:AL009126] [GN:yloS] [FN:unknown] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 9 of 21):
 from 1598421to 1807200.] [LE:55709] [RE:56353] [DI:direct]
 >gp:[GI:e323508:g2337809] [LN:BSY13937] [AC:Y13937] [PN:YloS protein]
 [GN:yloS] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus
 subtilis genomic DNA from the spoVM region.] [LE:17481] [RE:18125]
 [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000990_23647178_c2_903	1768	5540	633	210	398	5.0e-37

Description

pir:[LN:A69880] [AC:A69880] [PN:hypothetical protein ylpC] [GN:ylpC]
[OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1185179:g2633960] [LN:BSUB0009]
[AC:Z99112:AL009126] [GN:ylpC] [FN:unknown] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 9 of 21):
from 1598421to 1807200.] [LE:62946] [RE:63512] [DI:direct]
>gp:[GI:e323513:g2337817] [LN:BSY13937] [AC:Y13937] [PN:YlpC protein]
[GN:ylpC] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus
subtilis genomic DNA from the spoVM region.] [LE:24718] [RE:25284]
[DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000990_23650293_c1_785	1769	5541	627	208	693	2.7e-68

Description

pir:[LN:B69878] [AC:B69878] [PN:guanylate kinase homolog yloD] [GN:yloD]
[CL:guanylate kinase:guanylate kinase homology] [OR:Bacillus subtilis]
[DB:pir2] >gp:[GI:e1185159:g2633940] [LN:BSUB0009] [AC:Z99112:AL009126]
[GN:yloD] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus
subtilis complete genome (section 9 of 21): from 1598421to 1807200.]
[NT:similar to guanylate kinase] [LE:42808] [RE:43542] [DI:direct]
>gp:[GI:e323500:g2337797] [LN:BSY13937] [AC:Y13937] [PN:putative Gmk
protein] [GN:yloD] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1]
[DE:Bacillus subtilis genomic DNA from the spoVM region.] [LE:4580]
[RE:5314] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000990_23695900_c2_812	1770	5542	1551	516	1490	9.5e-153

Description

gp:[GI:g4097534] [LN:LLU64311] [AC:U64311] [PN:phosphoribosylpyrophosphate
amidotransferase] [GN:purF] [OR:Lactococcus lactis] [DB:genpept-bct2]
[EC:2.4.2.14] [DE:Lactococcus lactis
phosphoribosylaminoimidazolesuccinocarboxamidesynthetase (purC),
phosphoribosylformylglycinamide synthetase I(purQ),
phosphoribosylformylglycinamide synthetase II (purL),
andphosphoribosylpyrophosphate amidotransferase (purF) genes, completecds;
and unknown gene.] [NT:PRPP ATase] [LE:4921] [RE:6441] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000990_23730340_c1_716	1771	5543	1422	473	2270	2.1e-235

Description

pir:[LN:S19723] [AC:S19723] [PN:dihydrolipoamide dehydrogenase,:pyruvate dehydrogenase complex chain E3] [GN:pdhD] [CL:dihydrolipoamide dehydrogenase:dihydrolipoamide dehydrogenase homology] [OR:Staphylococcus aureus] [EC:1.8.1.4] [DB:pir1] >gp:[GI:g48874] [LN:SAPDHDNA] [AC:X58434:S73625] [PN:dihydrolipoamide dehydrogenase: subunit E3] [GN:pdhD] [OR:Staphylococcus aureus] [DB:genpept-bct1] [EC:1.8.1.4] [DE:S.aureus pdhB, pdhC and pdhD genes for pyruvate decarboxylase, dihydrolipoamide acetyltransferase and dihydrolipoamidedehydrogenase.] [LE:1853] [RE:3259] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000990_23836036_c2_887	1772	5544	192	63	153	1.2e-09

Description

sp:[LN:CARB_BACCL] [AC:P46537] [GN:PYRAB] [OR:BACILLUS CALDOLYTICUS] [EC:6.3.5.5] [DE:(EC 6.3.5.5) (CARBAMOYL-PHOSPHATE SYNTHETASE AMMONIA CHAIN)] [SP:P46537] [DB:swissprot] >pir:[LN:I40169] [AC:I40169:S34321] [PN:carbamoyl-phosphate synthase (glutamine-hydrolyzing),] [GN:pyrAb] [CL:carbamoyl-phosphate synthase (glutamine-hydrolyzing) large chain:biotin carboxylase homology:carbamoyl-phosphate synthase (glutamine-hydrolyzing) large chain homology] [OR:Bacillus caldolyticus] [EC: 6.3.5.5] [DB:pir2] >gp:[GI:g312443] [LN:BCPYR] [AC:X73308] [PN:carbamoyl-phosphate synthase] [GN:PyrAb] [OR:Bacillus caldolyticus] [DB:genpept-bct1] [EC:6.3.5.5] [DE:B.caldolyticus pyrimidine biosynthesis genes.] [SP:P46537] [LE:3658] [RE:6855] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000990_23928937_c3_953	1773	5545	141	46		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000990_24025253_f1_219	1774	5546	321	106	198	1.3e-14

Description

pir:[LN:T00323] [AC:T00323] [PN:chitinase, B] [OR:Clostridium
paraputrificum] [EC:3.2.1.14] [DB:pir3] >gp:[GI:d1024701:g2696017]
[LN:AB001874] [AC:AB001874] [PN:chitinase B] [GN:chiB] [OR:Clostridium
paraputrificum] [SR:Clostridium paraputrificum (strain:M21) DNA]
[DB:genpept-bct1] [EC:3.2.1.14] [DE:Clostridium paraputrificum gene for
chitinase B, complete cds.] [LE:1] [RE:2496] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000990_24025467_c2_863	1775	5547	522	173	238	4.5e-20

Description

sp:[LN:YSNB_BACSU] [AC:P94559] [GN:YSNB] [OR:BACILLUS SUBTILIS]
[DE:HYPOTHETICAL 19.2 KD PROTEIN IN RPH-ILVB INTERGENIC REGION] [SP:P94559]
[DB:swissprot] >pir:[LN:D69986] [AC:D69986] [PN:conserved hypothetical
protein ysnB] [GN:ysnB] [CL:conserved hypothetical protein MG207:
phosphoesterase core homology] [OR:Bacillus subtilis] [DB:pir2]
>gp:[GI:e1184084:g2635300] [LN:BSUB0015] [AC:Z99118:AL009126] [GN:ysnB]
[FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
complete genome (section 15 of 21): from 2795131to 3013540.] [NT:similar to
hypothetical proteins] [SP:P94559] [LE:103990] [RE:104505] [DI:complement]
>gp:[GI:e1165358:g1770061] [LN:BSZ75208] [AC:Z75208] [PN:hypothetical
protein] [GN:ysnB] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis
genomic sequence 89009bp.] [NT:homology to HI0260 of Haemophilus
influenzae;] [SP:P94559] [LE:65402] [RE:65917] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000990_24220002_f1_67	1776	5548	129	42		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000990_24240676_f3_477	1777	5549	246	81		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000990_24257877_c2_854	1781	5553	129	42		
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Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000990_24261068_c1_758	1782	5554	147	48	215	1.2e-17
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Description

gp:[GI:g3212079] [LN:AF068633] [AC:AF068633] [PN:phenol soluble modulin beta 1] [FN:inflammatory protein] [OR:Staphylococcus epidermidis] [DB:genpept-bct2] [DE:Staphylococcus epidermidis phenol soluble modulin beta 1 and phenolsoluble modulin beta 2 genes, complete cds.] [NT:PSM beta 1] [LE:669] [RE:803] [DI:direct] >gp:[GI:g3212080] [LN:AF068633] [AC:AF068633] [PN:phenol soluble modulin beta 2] [FN:inflammatory protein] [OR:Staphylococcus epidermidis] [DB:genpept-bct2] [DE:Staphylococcus epidermidis phenol soluble modulin beta 1 and phenolsoluble modulin beta 2 genes, complete cds.] [NT:PSM beta 2] [LE:859] [RE:993] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000990_24261068_c3_988	1783	5555	147	48	215	1.2e-17
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Description

gp:[GI:g3212079] [LN:AF068633] [AC:AF068633] [PN:phenol soluble modulin beta 1] [FN:inflammatory protein] [OR:Staphylococcus epidermidis] [DB:genpept-bct2] [DE:Staphylococcus epidermidis phenol soluble modulin beta 1 and phenolsoluble modulin beta 2 genes, complete cds.] [NT:PSM beta 1] [LE:669] [RE:803] [DI:direct] >gp:[GI:g3212080] [LN:AF068633] [AC:AF068633] [PN:phenol soluble modulin beta 2] [FN:inflammatory protein] [OR:Staphylococcus epidermidis] [DB:genpept-bct2] [DE:Staphylococcus epidermidis phenol soluble modulin beta 1 and phenolsoluble modulin beta 2 genes, complete cds.] [NT:PSM beta 2] [LE:859] [RE:993] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000990_24275137_f1_21	1784	5556	132	43		
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Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000990_24297217_c1_780	1785	5557	3114	1037	3756	0.0

Description

sp:[LN:CARB_BACCL] [AC:P46537] [GN:PYRAB] [OR:BACILLUS CALDOLYTICUS] [EC:6.3.5.5] [DE:(EC 6.3.5.5) (CARBAMOYL-PHOSPHATE SYNTHETASE AMMONIA CHAIN)] [SP:P46537] [DB:swissprot] >pir:[LN:I40169] [AC:I40169:S34321] [PN:carbamoyl-phosphate synthase (glutamine-hydrolyzing),] [GN:pyrAb] [CL:carbamoyl-phosphate synthase (glutamine-hydrolyzing) large chain:biotin carboxylase homology:carbamoyl-phosphate synthase (glutamine-hydrolyzing) large chain homology] [OR:Bacillus caldolyticus] [EC: 6.3.5.5] [DB:pir2] >gp:[GI:g312443] [LN:BCPYR] [AC:X73308] [PN:carbamoyl-phosphate synthase] [GN:PyrAb] [OR:Bacillus caldolyticus] [DB:genpept-bct1] [EC:6.3.5.5] [DE:B.caldolyticus pyrimidine biosynthesis genes.] [SP:P46537] [LE:3658] [RE:6855] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000990_24330337_f3_557	1786	5558	957	318	555	1.1e-53

Description

pir:[LN:H69984] [AC:H69984] [PN:conserved hypothetical protein ysgB] [GN:ysgB] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1184111:g2635327] [LN:BSUB0015] [AC:Z99118:AL009126] [GN:ysgB] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.] [NT:similar to hypothetical proteins] [LE:130003] [RE:130944] [DI:direct] >gp:[GI:e1165326:g1770032] [LN:BSZ75208] [AC:Z75208] [PN:hypothetical protein] [GN:ysgB] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis genomic sequence 89009bp.] [NT:unknown function; putative] [LE:38963] [RE:39904] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000990_24351577_c1_677	1787	5559	171	56		

Description

NO-HIT

AI7503000990_24351577_c1_677

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000990_24355342_c1_799	1788	5560	1014	338	1265	6.6e-129

sp:[LN:SR54_BACSU] [AC:P37105] [GN:FFH] [OR:BACILLUS SUBTILIS] [DE:SIGNAL
RECOGNITION PARTICLE PROTEIN (FIFTY-FOUR HOMOLOG)] [SP:P37105]
[DB:swissprot] >pir:[LN:B47154] [AC:B47154:H69621] [PN:signal recognition
particle chain ffh] [GN:ffh] [CL:signal recognition particle 54K protein]
[OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1185189:g2633970] [LN:BSUB0009]
[AC:Z99112:AL009126] [PN:signal recognition particle] [GN:ffh] [OR:Bacillus
subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 9
of 21): from 1598421to 1807200.] [LE:73153] [RE:74493] [DI:direct]
>gp:[GI:d1022545:g2309080] [LN:D14356] [AC:D14356] [PN:Ffh] [GN:ffh]
[OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:168) DNA]
[DB:genpept-bct1] [DE:Bacillus subtilis orf1, ffh, rpsP genes for ORF1, Ffh
and 30Sribosomal protein S16, complete cds.] [LE:711] [RE:2051] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000990_24406291_c2_902	1789	5561	417	138	369	5.9e-34

pir:[LN:D69879] [AC:D69879] [PN:alkaline-shock protein homolog yloU]
[GN:yloU] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1185174:g2633955]
[LN:BSUB0009] [AC:Z99112:AL009126] [GN:yloU] [FN:unknown] [OR:Bacillus
subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 9
of 21): from 1598421to 1807200.] [NT:similar to alkaline-shock protein]
[LE:57043] [RE:57405] [DI:direct] >gp:[GI:e323527:g2337812] [LN:BSY13937]
[AC:Y13937] [PN:putative Asp23 protein] [GN:yloU] [FN:unknown] [OR:Bacillus
subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis genomic DNA from the spoVM
region.] [LE:18815] [RE:19177] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000990_24406563_c1_742	1790	5562	141	46		

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000990_24407313_f3_590	1791	5563	126	41		

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000990_24407327_c3_1017	1792	5564	612	203	621	1.2e-60

Description

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sp:[LN:PYRE_BACSU] [AC:P25972] [GN:PYRE:PYRX] [OR:BACILLUS SUBTILIS]
[EC:2.4.2.10] [DE:OROTATE PHOSPHORIBOSYLTRANSFERASE, (OPRT) (OPRTASE)]
[SP:P25972] [DB:swissprot] >pir:[LN:F69686] [AC:F69686:A30492 ] [PN:orotate
phosphoribosyltransferase,] [GN:pyrE ] [CL:orotate
phosphoribosyltransferase:orotate phosphoribosyltransferase homology]
[OR:Bacillus subtilis] [EC:2.4.2.10] [DB:pir1] >gp:[GI:e1185148:g2633929]
[LN:BSUB0009] [AC:Z99112:AL009126] [PN:orotate phosphoribosyltransferase]
[GN:pyrE] [FN:pyrimidine biosynthesis] [OR:Bacillus subtilis]
[DB:genpept-bct1] [EC:2.4.2.10] [DE:Bacillus subtilis complete genome
(section 9 of 21): from 1598421to 1807200.] [NT:alternate gene name: pyrX]
[SP:P25972] [LE:30299] [RE:30949] [DI:direct] >gp:[GI:g143394] [LN:BACPYROP]
[AC:M59757] [PN:OMP-PRPP transferase] [GN:pyrE] [OR:Bacillus subtilis]
[DB:genpept-bct2] [DE:Bacillus subtilis ORF1A (pyrR), putative
membrane-bound uracilpermease (pyrP), aspartate transcarbamylase (pyrB),
dihydroorotase (pyrC), glutaminase of carbamyl phosphate synthetase
(pyrAA), carbamyl phosphate synthetase (pyrAB), dihydroorotase
dehydrogenase (pyrD), OMP decarboxylase (pyrF), and OMP-PRPP transferase
(pyrE)genes, complete cds; and unknown gene.] [LE:11703] [RE:12353]
[DI:direct]

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000990_24407760_c1_773	1793	5565	123	40		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000990_24407936_c2_896	1794	5566	1122	373	1380	4.3e-141

Description

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sp:[LN:YLON_BACSU] [AC:O34617] [GN:YLON] [OR:BACILLUS SUBTILIS]
[DE:HYPOTHETICAL 41.6 KD PROTEIN IN FMT-SPOVM INTERGENIC REGION] [SP:O34617]
[DB:swissprot] >pir:[LN:F69878] [AC:F69878 ] [PN:conserved hypothetical
protein ylon] [GN:ylon ] [CL:conserved hypothetical protein HI0365]
[OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1185166:g2633947] [LN:BSUB0009]
[AC:Z99112:AL009126] [GN:ylon] [FN:unknown] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 9 of 21):
from 1598421to 1807200.] [NT:similar to hypothetical proteins] [SP:O34617]
[LE:50265] [RE:51356] [DI:direct] >gp:[GI:e323524:g2337804] [LN:BSY13937]
[AC:Y13937] [PN:Ylon protein] [GN:ylon] [FN:unknown] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis genomic DNA from the spoVM region.]
[SP:O34617] [LE:12037] [RE:13128] [DI:direct]

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ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000990_24412812_c3_986	1795	5567	225	74		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000990_24415885_c3_960	1796	5568	1227	408	869	6.1e-87

Description

gp:[GI:g4096797] [LN:SCU40157] [AC:U40157] [OR:Staphylococcus carnosus] [DB:genpept-bct2] [DE:Staphylococcus carnosus condensing-enzyme-like protein (orf1) and SpoVE-like protein (orf2) genes, complete cds.] [NT:orf2; unknown function; similar to SpoVE, RodA,] [LE:1676] [RE:2779] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000990_24422077_c3_1013	1797	5569	1101	366	1196	1.4e-121

Description

sp:[LN:CARA_BACCL] [AC:P52557] [GN:PYRAA] [OR:BACILLUS CALDOLYTICUS] [EC:6.3.5.5] [DE:(EC 6.3.5.5) (CARBAMOYL-PHOSPHATE SYNTHETASE GLUTAMINE CHAIN)] [SP:P52557] [DB:swissprot] >pir:[LN:I40168] [AC:I40168:S34320] [PN:carbamoyl-phosphate synthase (glutamine-hydrolyzing),] [GN:pyrAa] [CL:carbamoyl-phosphate synthase (glutamine-hydrolyzing) small chain:carbamoyl-phosphate synthase (glutamine-hydrolyzing) small chain homology:trpG homology] [OR:Bacillus caldolyticus] [EC: 6.3.5.5] [DB:pir2] >gp:[GI:g312442] [LN:BCPYR] [AC:X73308] [PN:carbamoyl-phosphate synthase] [GN:PyrAa] [OR:Bacillus caldolyticus] [DB:genpept-bct1] [EC:6.3.5.5] [DE:B.caldolyticus pyrimidine biosynthesis genes.] [SP:P52557] [LE:2571] [RE:3665] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000990_24424038_c1_791	1798	5570	1692	563	1538	7.8e-158

Description

pir:[LN:E69879] [AC:E69879] [PN:conserved hypothetical protein yloV] [GN:yloV] [CL:Mycoplasma genitalium hypothetical protein MG369] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1185175:g2633956] [LN:BSUB0009] [AC:Z99112:AL009126] [GN:yloV] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 9 of 21): from 1598421 to 1807200.] [NT:similar to hypothetical proteins] [LE:57421] [RE:59082] [DI:direct] >gp:[GI:e323510:g2337813] [LN:BSY13937] [AC:Y13937] [PN:YloV protein] [GN:yloV] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis genomic DNA from the spoVM region.] [LE:19193] [RE:20854] [DI:direct]

AI7503000990_24475252_f2_371	1799	5571	159	52
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NO-HIT

AI7503000990_24484828_c2_832	1800	5572	552	183	311	8.2e-28
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gp:[GI:g4981179] [LN:AE001739] [AC:AE001739:AE000512] [PN:conserved
hypothetical protein] [GN:TM0656] [OR:Thermotoga maritima] [DB:genpept-bct2]
[DE:Thermotoga maritima section 51 of 136 of the complete genome.]
[NT:similar to SP:P38522 GB:U00096 PID:1742120] [LE:1379] [RE:1909]
[DI:complement]

AI7503000990_24485950_c3_951	1801	5573	537	178	91	0.015
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gp:[GI:g5306139] [LN:AF160864] [AC:AF160864] [PN:NADH dehydrogenase subunit
2] [GN:nad2] [OR:Mitochondrion Tetrahymena pyriformis] [SR:Tetrahymena
pyriformis] [DB:genpept] [EC:1.6.5.3] [DE:Tetrahymena pyriformis
mitochondrial DNA, complete genome.] [LE:10108] [RE:10644] [DI:complement]

AI7503000990_24609637_c3_1001	1802	5574	798	265	916	6.4e-92
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gp:[GI:g4009492] [LN:AF068904] [AC:AF068904] [PN:Ylmd] [GN:yldmD]
[OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus cell
division protein FtsZ (ftsZ) gene,partial cds; Ylmd (ylmD), YlmE (ylmE),
YlmF (ylmF), YlmG (ylmG),and YlmH (ylmH) genes, complete cds; and cell
division proteinDivIVA (divIVA) gene, partial cds.] [NT:similar to Bacillus
subtilis Ylmd] [LE:437] [RE:1228] [DI:direct]

AI7503000990_24610885_f2_352	1803	5575	423	140
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NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000990_24632827_c1_786	1804	5576	963	320	917	5.0e-92

Description

pir:[LN:A69626] [AC:A69626] [PN:methionyl-tRNA formyltransferase, fmt] [GN:fmt] [CL:methionyl-tRNA formyltransferase: phosphoribosylglycinamide formyltransferase homology] [OR:Bacillus subtilis] [EC:2.1.2.9] [DB:pir2] >gp:[GI:e1185164:g2633945] [LN:BSUB0009] [AC:Z99112:AL009126] [PN:methionyl-tRNA formyltransferase] [GN:fmt] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:2.1.2.9] [DE:Bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.] [NT:alternate gene name: yloL] [LE:47978] [RE:48931] [DI:direct] >gp:[GI:e323503:g2337802] [LN:BSY13937] [AC:Y13937] [PN:putative Fmt protein] [GN:yloL] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis genomic DNA from the spoVM region.] [LE:9750] [RE:10703] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000990_24642042_c2_853	1805	5577	561	186	255	7.1e-22

Description

pir:[LN:C69875] [AC:C69875] [PN:hypothetical protein ylbN] [GN:ylbN] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e334782:g2340010] [LN:BS16823KB] [AC:Z98682] [PN:YlbN protein] [GN:ylbN] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis genomic DNA 23.9kB fragment.] [LE:20393] [RE:20911] [DI:direct] >gp:[GI:e1185097:g2633878] [LN:BSUB0008] [AC:Z99111:AL009126] [GN:ylbN] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.] [LE:179876] [RE:180394] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000990_24642817_c2_862	1806	5578	810	269	1197	1.1e-121

Description

sp:[LN:MURI_STAHA] [AC:P52974] [GN:DGA] [OR:STAPHYLOCOCCUS HAEMOLYTICUS] [EC:5.1.1.3] [DE:GLUTAMATE RACEMASE,] [SP:P52974] [DB:swissprot] >gp:[GI:g520574] [LN:SHU12405] [AC:U12405] [PN:glutamate racemase] [GN:dga] [OR:Staphylococcus haemolyticus] [DB:genpept-bct1] [DE:Staphylococcus haemolyticus Y176 glutamate racemase (dga) gene,complete cds.] [LE:263] [RE:1063] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000990_24643836_c3_943	1807	5579	633	210	227	6.6e-19

Description

pir:[LN:D69870] [AC:D69870:A36718] [PN:conserved hypothetical protein ykyA:hypothetical protein (aceA 5' region)] [GN:ykyA] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1185047:g2633828] [LN:BSUB0008] [AC:Z99111:AL009126] [GN:ykyA] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.] [NT:alternate gene name: ykrC; similar to hypothetical] [LE:131900] [RE:132517] [DI:direct] >gp:[GI:g3282141] [LN:AF012285] [AC:AF012285:AF012284:U51911] [PN:unknown] [GN:ykrC] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis mobA-nprE gene region.] [NT:similar to Orf5 encoded by GenBank Accession] [LE:32388] [RE:33005] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000990_24645025_c3_1012	1808	5580	1284	427	1287	3.1e-131

Description

sp:[LN:PYRC_BACCL] [AC:P46538] [GN:PYRC] [OR:BACILLUS CALDOLYTICUS] [EC:3.5.2.3] [DE:DIHYDROOROTASE, (DHOASE)] [SP:P46538] [DB:swissprot] >pir:[LN:I40167] [AC:I40167:S34319] [PN:dihydroorotase,] [GN:pyrC] [CL:Bacillus dihydroorotase:Bacillus dihydroorotase homology] [OR:Bacillus caldolyticus] [EC:3.5.2.3] [DB:pir2] >gp:[GI:g312441] [LN:BCPYR] [AC:X73308] [PN:dihydroorotase] [GN:PyrC] [OR:Bacillus caldolyticus] [DB:genpept-bct1] [EC:3.5.2.3] [DE:B.caldolyticus pyrimidine biosynthesis genes.] [SP:P46538] [LE:1285] [RE:2568] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000990_24648412_c1_798	1809	5581	402	133	302	7.4e-27

Description

sp:[LN:YLXM_BACSU] [AC:P37104] [GN:YLXM] [OR:BACILLUS SUBTILIS] [DE:HYPOTHETICAL 13.2 KD PROTEIN IN FFH 5'REGION] [SP:P37104] [DB:swissprot] >pir:[LN:A47154] [AC:A47154:A69882] [PN:conserved hypothetical protein ylxM] [GN:ylxM] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1185188:g2633969] [LN:BSUB0009] [AC:Z99112:AL009126] [GN:ylxM] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.] [NT:similar to hypothetical proteins] [LE:72807] [RE:73139] [DI:direct] >gp:[GI:d1023083:g2424968] [LN:D14356] [AC:D14356] [PN:ORF1] [GN:orf1] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:168) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis orf1, ffh, rpsP genes for ORF1, Ffh and 30Sribosomal protein S16, complete cds.] [LE:365] [RE:697] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000990_24652178_c2_847	1810	5582	477	158	174	2.7e-13

Description

pir:[LN:F69930] [AC:F69930] [PN:conserved hypothetical protein yozB]
 [GN:yozB] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1185386:g2634307]
 [LN:BSUB0011] [AC:Z99114:AL009126] [GN:yozB] [FN:unknown] [OR:Bacillus
 subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section
 11 of 21): from 2000171to 2207900.] [NT:similar to hypothetical proteins]
 [LE:85155] [RE:85691] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000990_24730340_c3_937	1811	5583	672	223	731	2.6e-72

Description

sp:[LN:YKQB_BACSU] [AC:P39760] [GN:YKQB] [OR:BACILLUS SUBTILIS]
 [DE:HYPOTHETICAL 24.3 KD PROTEIN IN KINC-ADEC INTERGENIC REGION (ORF4)]
 [SP:P39760] [DB:swissprot] >pir:[LN:A69862] [AC:A69862:PC6016]
 [PN:conserved hypothetical protein ykqB] [GN:ykqB] [CL:conserved
 hypothetical protein MG323] [OR:Bacillus subtilis] [DB:pir2]
 >gp:[GI:d1007628:g520844] [LN:BACAMOKOOO] [AC:D37799] [PN:orf4] [OR:Bacillus
 subtilis] [SR:Bacillus subtilis (sub_species:Marburg, strain:168]
 [DB:genpept-bct1] [DE:Bacillus subtilis genes for ampS, mreBH, orf1, kinC,
 orf3, orf4 andorf5.] [LE:5175] [RE:5840] [DI:direct]
 >gp:[GI:e1185041:g2633822] [LN:BSUB0008] [AC:Z99111:AL009126] [GN:ykqB]
 [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
 complete genome (section 8 of 21): from 1394791to 1603020.] [NT:alternate
 gene name: ylxV, yzaC; similar to] [SP:P39760] [LE:125146] [RE:125811]
 [DI:direct] >gp:[GI:g3282136] [LN:AF012285] [AC:AF012285:AF012284:U51911]
 [PN:unknown] [GN:ykqA] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct2]
 [DE:Bacillus subtilis mobA-nprE gene region.] [NT:similar to product of orf4
 encoded by GenBank] [LE:25634] [RE:26299] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000990_24801713_c3_946	1812	5584	1314	437	1906	7.9e-197

Description

sp:[LN:ODP2_STAAU] [AC:Q59821] [GN:PDHC] [OR:STAPHYLOCOCCUS AUREUS]
 [EC:2.3.1.12] [DE:COMPLEX, (E2)] [SP:Q59821] [DB:swissprot] >pir:[LN:S19722]
 [AC:S19722] [PN:dihydrolipoamide S-acetyltransferase, chain E2]
 [CL:dihydrolipoamide acetyltransferase: lipoyl/biotin-binding homology]
 [OR:Staphylococcus aureus] [EC:2.3.1.12] [DB:pir2] >gp:[GI:g581570]
 [LN:SAPDHDNA] [AC:X58434:S73625] [PN:dihydrolipoamide acetyltransferase:
 subunit E2] [GN:pdhC] [OR:Staphylococcus aureus] [DB:genpept-bct1]
 [EC:2.3.1.12] [DE:S.aureus pdhB, pdhC and pdhD genes for pyruvate
 decarboxylase, dihydrolipoamide acetyltransferase and
 dihydrolipoamidedehydrogenase.] [SP:Q59821] [LE:557] [RE:1849] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000990_24806587_c2_848	1813	5585	1056	351	399	3.9e-37

Description

pir:[LN:H69873] [AC:H69873] [PN:conserved hypothetical protein ylbC] [GN:ylbC] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e334771:g2339999] [LN:BS16823KB] [AC:Z98682] [PN:YlbC protein] [GN:ylbC] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis genomic DNA 23.9kB fragment.] [LE:11510] [RE:12550] [DI:direct] >gp:[GI:e1185086:g2633867] [LN:BSUB0008] [AC:Z99111:AL009126] [GN:ylbC] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.] [NT:similar to hypothetical proteins from B. subtilis] [LE:170993] [RE:172033] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000990_24851577_c3_971	1814	5586	564	187	405	9.0e-38

Description

pir:[LN:E69874] [AC:E69874] [PN:conserved hypothetical protein ylbH] [GN:ylbH] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e334776:g2340004] [LN:BS16823KB] [AC:Z98682] [PN:YlbH protein] [GN:ylbH] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis genomic DNA 23.9kB fragment.] [LE:14650] [RE:15144] [DI:direct] >gp:[GI:e1185091:g2633872] [LN:BSUB0008] [AC:Z99111:AL009126] [GN:ylbH] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.] [NT:similar to hypothetical proteins] [LE:174133] [RE:174627] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000990_25425202_c1_749	1815	5587	522	173	196	1.3e-15

Description

pir:[LN:B69985] [AC:B69985] [PN:hypothetical protein yshB] [GN:yshB] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1184109:g2635325] [LN:BSUB0015] [AC:Z99118:AL009126] [GN:yshB] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.] [LE:129072] [RE:129605] [DI:complement] >gp:[GI:e1165328:g1770034] [LN:BSZ75208] [AC:Z75208] [PN:hypothetical protein] [GN:yshB] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis genomic sequence 89009bp.] [NT:unknown function; putative] [LE:40302] [RE:40835] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000990_25475250_c3_985	1816	5588	1827	608	2503	4.3e-260

Description

pir:[LN:A27763] [AC:A27763:C69704] [PN:succinate dehydrogenase, flavoprotein:fumarate reductase:fumaric hydrogenase:succinic dehydrogenase] [GN:sdhA:sdhB] [CL:fumarate reductase flavoprotein:3-oxosteroid 1-dehydrogenase homology:fumarate reductase flavoprotein homology] [OR:Bacillus subtilis] [EC:1.3.99.1] [DB:pir2]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000990_25509640_f1_185	1817	5589	240	79	75	0.0084

Description

sp:[LN:YRUB_CLOPA] [AC:P23171] [OR:CLOSTRIDIUM PASTEURIANUM] [DE:(ORF B)] [SP:P23171] [DB:swissprot] >pir:[LN:S29118] [AC:S29118] [PN:hypothetical protein 2] [OR:Clostridium pasteurianum] [DB:pir2] >gp:[GI:g144907] [LN:CLORUB] [AC:M60116] [OR:Clostridium pasteurianum] [SR:C.pasteurianum (strain ATCC 6013) DNA] [DB:genpept-bct1] [DE:C.pasteurianum open reading frame A, B, C, and rubredoxin gene,complete cds.] [NT:open reading frame B] [LE:1126] [RE:1353] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000990_25604677_c1_736	1818	5590	450	149	322	5.6e-29

Description

pir:[LN:C69874] [AC:C69874] [PN:conserved hypothetical protein ylbF] [GN:ylbF] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e334774:g2340002] [LN:BS16823KB] [AC:Z98682] [PN:YlbF protein] [GN:ylbF] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis genomic DNA 23.9kB fragment.] [LE:13551] [RE:14000] [DI:direct] >gp:[GI:e1185089:g2633870] [LN:BSUB0008] [AC:Z99111:AL009126] [GN:ylbF] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.] [NT:similar to hypothetical proteins] [LE:173034] [RE:173483] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000990_25635962_c3_1008	1819	5591	486	161	274	6.9e-24

Description

gp:[GI:e244971:g1340128] [LN:SA1234] [AC:X97985] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:S.aureus orfs 1,2,3 & 4.] [NT:ORF1] [LE:537] [RE:1304] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000990_25816552_c3_1004	1820	5592	777	258	984	4.0e-99

Description

gp:[GI:g4009496] [LN:AF068904] [AC:AF068904] [PN:YlmH] [GN:ylmH]
 [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus cell
 division protein FtsZ (ftsZ) gene,partial cds; YlmD (ylmD), YlmE (ylmE),
 YlmF (ylmF), YlmG (ylmG),and YlmH (ylmH) genes, complete cds; and cell
 division proteinDivIVA (divIVA) gene, partial cds.] [NT:similar to Bacillus
 subtilis YlmH] [LE:2865] [RE:3671] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000990_25818811_c2_841	1821	5593	153	50	162	5.1e-12

Description

gp:[GI:g1022725] [LN:SHU35635] [AC:U35635] [PN:unknown] [OR:Staphylococcus
 haemolyticus] [SR:Staphylococcus haemolyticus strain=Y176] [DB:genpept-bct1]
 [DE:Staphylococcus haemolyticus IS1272 ORF1 and ORF2 genes, completecds.]
 [NT:ORF2] [LE:394] [RE:1083] [DI:complement] >gp:[GI:g295162] [LN:STAMECRA]
 [AC:L14017] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus (strain
 COL) DNA] [DB:genpept-bct1] [DE:Staphylococcus aureus methicillin-resistance
 protein (mecR) geneand unknown ORF, complete cds.] [NT:unknown ORF1;
 putative] [LE:1492] [RE:2181] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000990_25939030_f2_399	1822	5594	183	60		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000990_25972207_f1_6	1823	5595	126	41		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000990_25976401_f3_533	1824	5596	150	49		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000990_26354550_c1_740	1825	5597	192	63		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000990_26423305_c1_767	1826	5598	336	111	386	9.3e-36

Description

gp:[GI:g4009495] [LN:AF068904] [AC:AF068904] [PN:YlmG] [GN:ylmG]
[OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus cell
division protein FtsZ (ftsZ) gene,partial cds; YlmD (ylmD), YlmE (ylmE),
YlmF (ylmF), YlmG (ylmG),and YlmH (ylmH) genes, complete cds; and cell
division proteinDivIVA (divIVA) gene, partial cds.] [NT:similar to Bacillus
subtilis YlmG] [LE:2492] [RE:2782] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000990_26597077_c2_875	1827	5599	1398	465	1113	8.5e-113

Description

gp:[GI:g2149896] [LN:SAU94706] [AC:U94706] [PN:cell division protein]
[GN:div1B] [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus
aureus strain ATCC 8325-4 cell wall/cell divisiongene cluster, yllB, yllC,
yllD, pbpA, mraY, murD, div1B, ftsA andftsZ genes, complete cds.] [LE:7179]
[RE:8498] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000990_26598402_c3_1011	1828	5600	1314	437	1251	2.0e-127

Description

sp:[LN:PYRP_BACCL] [AC:P41006] [GN:PYRP] [OR:BACILLUS CALDOLYTICUS]
[DE:URACIL PERMEASE (URACIL TRANSPORTER)] [SP:P41006] [DB:swissprot]
>pir:[LN:S38893] [AC:S38893] [PN:uracil transport protein:uracil permease]
[CL:uracil transport protein uraA] [OR:Bacillus caldolyticus] [DB:pir2]
>gp:[GI:g431231] [LN:BCPYRQP] [AC:X76083] [PN:uracil permease] [GN:pyrP]
[OR:Bacillus caldolyticus] [DB:genpept-bct1] [DE:B.caldolyticus (DSM405)
pyrR, pyrP and pyrB (partial) genes.] [SP:P41006] [LE:1490] [RE:2788]
[DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000990_26614167_c1_795	1829	5601	240	79	238	4.5e-20

Description

sp:[LN:ACP_BACSU] [AC:P80643:P51832] [GN:ACPA:ACPP] [OR:BACILLUS SUBTILIS]
 [DE:ACYL CARRIER PROTEIN (ACP)] [SP:P80643:P51832] [DB:swissprot]
 >pir:[LN:JC4822] [AC:JC4822:A69582] [PN:acyl carrier protein:8.5K protein]
 [GN:acpA:srb] [CL:acyl carrier protein:acyl carrier protein homology]
 [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1185183:g2633964] [LN:BSUB0009]
 [AC:Z99112:AL009126] [PN:acyl carrier protein] [GN:acpA] [FN:fatty acid
 biosynthesis] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
 complete genome (section 9 of 21): from 1598421to 1807200.] [NT:alternate
 gene name: acpP] [SP:P80643] [LE:66316] [RE:66549] [DI:direct]
 >gp:[GI:d1011632:g1237013] [LN:D64116] [AC:D64116] [PN:ORF2] [GN:orf2]
 [OR:Bacillus subtilis] [SR:Bacillus subtilis DNA] [DB:genpept-bct1]
 [DE:Bacillus subtilis genes for ORF1, ORF2, ORF3, ORF4 and Srb, partialand
 complete cds.] [LE:140] [RE:373] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000990_26828187_f1_147	1830	5602	504	167	187	1.1e-14

Description

pir:[LN:B69873] [AC:B69873] [PN:hypothetical protein ylaL] [GN:ylaL]
 [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1185072:g2633853] [LN:BSUB0008]
 [AC:Z99111:AL009126] [GN:ylaL] [FN:unknown] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 8 of 21):
 from 1394791to 1603020.] [LE:155412] [RE:155897] [DI:complement]
 >gp:[GI:e324323:g2224771] [LN:BSZ97025] [AC:Z97025] [GN:ylaL] [OR:Bacillus
 subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis nprE,
 yla[A,B,C,D,E,F,G,H,I,J,K,L,M,N,O] and pycAgenes.] [LE:9671] [RE:10156]
 [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000990_2751260_f3_673	1831	5603	153	50		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000990_2766500_c3_938	1832	5604	153	50	113	2.8e-06

Description

gp:[GI:g1022726] [LN:SHU35635] [AC:U35635] [PN:unknown] [OR:Staphylococcus haemolyticus] [SR:Staphylococcus haemolyticus strain=Y176] [DB:genpept-bct1] [DE:Staphylococcus haemolyticus IS1272 ORF1 and ORF2 genes, completecds.] [NT:ORF1] [LE:1101] [RE:1922] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000990_2789801_f2_436	1833	5605	366	121	163	1.2e-11

Description

pir:[LN:D70070] [AC:D70070] [PN:transcription regulator homolog ywtF] [GN:ywtF] [CL:Bacillus subtilis probable transcription regulator yvhJ] [OR:Bacillus subtilis] [DB:pir2]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000990_2835285_f3_466	1834	5606	147	48		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000990_29319086_c1_739	1835	5607	519	172	467	2.4e-44

Description

pir:[LN:F69874] [AC:F69874] [PN:lipopolysaccharide core biosynthesis homolog ylbI] [GN:ylbI] [CL:lipopolysaccharide core biosynthesis protein kdtB] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e334777:g2340005] [LN:BS16823KB] [AC:Z98682] [PN:YlbI protein] [GN:ylbI] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis genomic DNA 23.9kB fragment.] [LE:15208] [RE:15693] [DI:direct] >gp:[GI:e1185092:g2633873] [LN:BSUB0008] [AC:Z99111:AL009126] [GN:ylbI] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.] [NT:similar to lipopolysaccharide core biosynthesis] [LE:174691] [RE:175176] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000990_29320217_f2_271	1836	5608	207	68		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000990_29384818_c2_845	1837	5609	3465	1154	3900	0.0

Description

pir:[LN:F69685] [AC:F69685] [PN:pyruvate carboxylase pycA] [GN:pycA]
[CL:pyruvate carboxylase:biotin carboxylase homology:lipoyl/biotin-binding
homology] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1185076:g2633857]
[LN:BSUB0008] [AC:Z99111:AL009126] [PN:pyruvate carboxylase] [GN:pycA]
[OR:Bacillus subtilis] [DB:genpept-bct1] [EC:6.4.1.1] [DE:Bacillus subtilis
complete genome (section 8 of 21): from 1394791to 1603020.] [NT:alternate
gene name: ylaP] [LE:158800] [RE:162246] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000990_29410908_c2_867	1838	5610	129	42		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000990_29488551_f2_398	1839	5611	234	77	59	0.020

Description

gp:[GI:g453389] [LN:BCU05814] [AC:U05814] [PN:cytochrome C oxidase subunit
III] [GN:COIII] [FN:electron transport] [OR:Kinetoplast Blastocrithidia
culicis] [SR:Blastocrithidia culicis] [DB:genpept-inv1] [DE:Blastocrithidia
culicis ATCC30268 kinetoplast NADH dehydrogenasesubunit 7 (ND7) gene,
partial cds, and cytochrome C oxidase subunitIII (COIII) gene, complete
cds.] [LE:223] [RE:1089] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000990_30656300_c3_1030	1840	5612	1353	450	912	1.7e-91

Description

sp:[LN:SUN_BACSU] [AC:P94464] [GN:SUN:FMU] [OR:BACILLUS SUBTILIS] [DE:SUN
PROTEIN] [SP:P94464] [DB:swissprot] >pir:[LN:E69878] [AC:E69878]
[PN:RNA-binding Sun protein homolog yloM] [GN:yloM] [CL:hypothetical
protein HI0624] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1185165:g2633946]
[LN:BSUB0009] [AC:Z99112:AL009126] [GN:yloM] [FN:unknown] [OR:Bacillus
subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 9
of 21): from 1598421to 1807200.] [NT:alternate gene name: sun; similar to
RNA-binding] [SP:P94464] [LE:48918] [RE:50261] [DI:direct]
>gp:[GI:e323504:g2337803] [LN:BSY13937] [AC:Y13937] [PN:putative Fmu
protein] [GN:yloM] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1]
[DE:Bacillus subtilis genomic DNA from the spoVM region.] [SP:P94464]
[LE:10690] [RE:12033] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000990_30663955_c2_809	1841	5613	1152	383	767	3.9e-76

Description

sp:[LN:PURK_BACSU] [AC:P12045] [GN:PURK] [OR:BACILLUS SUBTILIS]
[EC:4.1.1.21] [DE:(AIR CARBOXYLASE) (AIRC)] [SP:P12045] [DB:swissprot]
>pir:[LN:DCBSPK] [AC:B29326:G69684] [PN:phosphoribosylaminoimidazole
carboxylase, carbon dioxide-fixation chain:phosphoribosylaminoimidazole
carboxylase chain II] [GN:purK] [CL:phosphoribosylaminoimidazole
carboxylase carbon dioxide-fixation chain:phosphoribosylaminoimidazole
carboxylase carbon dioxide-fixation chain homology] [OR:Bacillus subtilis]
[EC:4.1.1.21] [DB:pir1] [MP:18 min] >gp:[GI:g143365] [LN:BACPURF]
[AC:J02732:K00047] [OR:Bacillus subtilis] [SR:B.subtilis (strain DE1
(prototroph DER. or W168)) DNA, clone pPZ] [DB:genpept-bct1] [DE:B.subtilis
pur operon encoding purine biosynthesis enzymes, 12genes.]
[NT:phosphoribosyl aminoimidazole carboxylase II] [LE:920] [RE:2059]
[DI:direct] >gp:[GI:e1182623:g2632957] [LN:BSUB0004] [AC:Z99107:AL009126]
[PN:phosphoribosylaminoimidazole carboxylase II] [GN:purK] [FN:purine
biosynthesis] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:4.1.1.21]
[DE:Bacillus subtilis complete genome (section 4 of 21): from 600701
to813890.] [SP:P12045] [LE:97902] [RE:99041] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000990_30745680_f2_431	1842	5614	2007	668	2279	2.3e-236

Description

sp:[LN:QOX1_BACSU] [AC:P34956] [GN:QOXB:IPA-38D] [OR:BACILLUS SUBTILIS]
[EC:1.9.3.-] [DE:SUBUNIT QOXB) (OXIDASE AA(3) SUBUNIT 1)] [SP:P34956]
[DB:swissprot] >pir:[LN:B38129] [AC:B38129:S39693:F69687] [PN:bo-type
ubiquinol oxidase, chain I:cytochrome aa3 quinol oxidase chain I:quinol
oxidase aa3-600] [GN:qoxB] [CL:cytochrome-c oxidase chain I:cytochrome-c
oxidase chain I homology] [OR:Bacillus subtilis] [EC:1.10.3.-] [DB:pir2]
>gp:[GI:g143397] [LN:BACQOXA] [AC:M86548] [PN:quinol oxidase] [GN:QOXB]
[OR:Bacillus subtilis] [SR:Bacillus subtilis DNA] [DB:genpept-bct1]
[DE:Bacillus subtilis AA3-600 quinol oxidase (QOXA, QOXB, QOXC, QOXD)genes,
complete cds.] [LE:1846] [RE:3795] [DI:direct] >gp:[GI:g413962] [LN:BSGENR]
[AC:X73124] [GN:ipa-38d qoxB] [OR:Bacillus subtilis] [DB:genpept-bct1]
[DE:B.subtilis genomic region (325 to 333).] [SP:P34956] [LE:40298]
[RE:42247] [DI:direct] >gp:[GI:e1186315:g2636351] [LN:BSUB0020]
[AC:Z99123:AL009126] [PN:cytochrome aa3 quinol oxidase (subunit I)]
[GN:qoxB] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
complete genome (section 20 of 21): from 3798401to 4010550.] [NT:alternate
gene name: ipa-38d] [SP:P34956] [LE:115715] [RE:117664] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000990_31272062_f1_183	1843	5615	171	56		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000990_32242890_f2_397	1844	5616	1701	566	1986	2.6e-205

Description

sp:[LN:YKQC_BACSU] [AC:Q45493] [GN:YKQC] [OR:BACILLUS SUBTILIS]
[DE:HYPOTHETICAL 61.5 KD PROTEIN IN ADEC-PDHA INTERGENIC REGION] [SP:Q45493]
[DB:swissprot] >pir:[LN:B69862] [AC:B69862] [PN:conserved hypothetical
protein ykqC] [GN:ykqC] [CL:conserved hypothetical protein MG139]
[OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1185043:g2633824] [LN:BSUB0008]
[AC:Z99111:AL009126] [GN:ykqC] [FN:unknown] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 8 of 21):
from 1394791to 1603020.] [NT:similar to hypothetical proteins] [SP:Q45493]
[LE:127733] [RE:129400] [DI:complement] >gp:[GI:g3282138] [LN:AF012285]
[AC:AF012285:AF012284:U51911] [PN:unknown] [GN:ykqC] [FN:unknown]
[OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis mobA-nprE
gene region.] [NT:similar to aminopeptidase AMPS with Swiss-Prot] [LE:28221]
[RE:29888] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000990_32667138_f1_135	1845	5617	177	58		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000990_32756_f3_601	1846	5618	1401	466	748	4.0e-74

Description

pir:[LN:S62667] [AC:S62667] [PN:Nramp1 protein] [CL:natural
resistance-associated macrophage protein 1] [OR:Oryza sativa] [SR:, rice]
[DB:pir2]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000990_3314128_f2_238	1847	5619	234	77		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000990_33153_c2_834	1848	5620	900	299	454	5.8e-43

Description

gp:[GI:g4981938] [LN:AE001791] [AC:AE001791:AE000512]
 [PN:spermidine/putrescine ABC transporter, permease] [GN:TM1377]
 [OR:Thermotoga maritima] [DB:genpept-bct2] [DE:Thermotoga maritima section
 103 of 136 of the complete genome.] [NT:similar to GB:L42023 SP:P45170
 PID:1007357] [LE:8884] [RE:9672] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000990_33367325_c1_706	1849	5621	168	55		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000990_33594187_c1_728	1850	5622	303	100	150	7.1e-10

Description

gp:[GI:g2668605] [LN:AF015453] [AC:AF015453] [PN:unknown] [OR:Lactobacillus
 rhamnosus] [DB:genpept-bct2] [DE:Lactobacillus rhamnosus
 6-phospho-beta-glucosidase homolog gene,partial cds; GNTR transcriptional
 regulator homolog and surfacelocated protein genes, complete cds.]
 [NT:3.0E-ORF-1] [LE:2236] [RE:>3603] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000990_33595178_f3_476	1851	5623	129	42		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000990_33651636_c3_981	1852	5624	1776	591	1528	9.0e-157

Description

pir:[LN:C69985] [AC:C69985] [PN:probable DNA-dependent DNA polymerase beta chain yshC] [GN:yshC] [OR:Bacillus subtilis] [DB:pir2]
 >gp:[GI:e1184108:g2635324] [LN:BSUB0015] [AC:Z99118:AL009126] [GN:yshC] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.] [NT:similar to DNA polymerase beta] [LE:127286] [RE:128998] [DI:complement]
 >gp:[GI:e1165329:g1770035] [LN:BSZ75208] [AC:Z75208] [PN:hypothetical protein] [GN:yshC] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis genomic sequence 89009bp.] [NT:unknown function;putative] [LE:40909] [RE:42621] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000990_34017812_f3_480	1853	5625	1722	573	1369	6.3e-140

Description

pir:[LN:G69877] [AC:G69877] [PN:fibronectin-binding protein homolog yloA] [GN:yloA] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e332190:g2462963] [LN:BSPYREYLO] [AC:AJ000974] [PN:putative fibronectin-binding protein] [GN:yloA] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis pyrE to yloA gene region.] [NT:protein A-like] [LE:6297] [RE:8015] [DI:complement] >gp:[GI:e1185156:g2633937] [LN:BSUB0009] [AC:Z99112:AL009126] [GN:yloA] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.] [NT:similar to fibronectin-binding protein] [LE:37110] [RE:38828] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000990_34100626_f3_494	1854	5626	159	52		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000990_34175686_c1_686	1855	5627	513	170	502	4.7e-48

Description

sp:[LN:PUR6_BACSU] [AC:P12044] [GN:PURE] [OR:BACILLUS SUBTILIS]
[EC:4.1.1.21] [DE:(EC 4.1.1.21) (AIR CARBOXYLASE) (AIRC)] [SP:P12044]
[DB:swissprot] >pir:[LN:DEBSPE] [AC:A29326:D69684]
[PN:phosphoribosylaminoimidazole carboxylase, catalytic
chain:phosphoribosylaminoimidazole carboxylase chain I] [GN:purE]
[CL:phosphoribosylaminoimidazole carboxylase catalytic
chain:phosphoribosylaminoimidazole carboxylase catalytic chain homology]
[OR:Bacillus subtilis] [EC:4.1.1.21] [DB:pir1] [MP:18 min] >gp:[GI:g143364]
[LN:BACPURF] [AC:J02732:K00047] [OR:Bacillus subtilis] [SR:B.subtilis
(strain DE1 (prototroph DER. or W168)) DNA, clone pPZ] [DB:genpept-bct1]
[DE:B.subtilis pur operon encoding purine biosynthesis enzymes, 12genes.]
[NT:phosphoribosyl aminoimidazole carboxylase I] [LE:439] [RE:927]
[DI:direct] >gp:[GI:e1182622:g2632956] [LN:BSUB0004] [AC:Z99107:AL009126]
[PN:phosphoribosylaminoimidazole carboxylase I] [GN:purE] [FN:purine
biosynthesis] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:4.1.1.21]
[DE:Bacillus subtilis complete genome (section 4 of 21): from 600701
to813890.] [SP:P12044] [LE:97421] [RE:97909] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000990_34407750_f2_368	1856	5628	162	53	119	1.8e-07

Description

pir:[LN:G69872] [AC:G69872] [PN:hypothetical protein ylaI] [GN:ylaI]
[OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1185069:g2633850] [LN:BSUB0008]
[AC:Z99111:AL009126] [GN:ylaI] [FN:unknown] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 8 of 21):
from 1394791to 1603020.] [LE:153004] [RE:153213] [DI:complement]
>gp:[GI:e324322:g2224768] [LN:BSZ97025] [AC:Z97025] [GN:ylaI] [OR:Bacillus
subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis nprE,
yla[A,B,C,D,E,F,G,H,I,J,K,L,M,N,O] and pycAgenes.] [LE:7263] [RE:7472]
[DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000990_34642213_c2_877	1857	5629	615	204	681	5.1e-67

Description

gp:[GI:g4009494] [LN:AF068904] [AC:AF068904] [PN:YlmF] [GN:ylmF]
[OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus cell
division protein FtsZ (ftsZ) gene,partial cds; YlmD (ylmD), YlmE (ylmE),
YlmF (ylmF), YlmG (ylmG),and YlmH (ylmH) genes, complete cds; and cell
division proteinDivIVA (divIVA) gene, partial cds.] [NT:similar to Bacillus
subtilis YlmF] [LE:1926] [RE:2480] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000990_34644125_c2_876	1858	5630	1416	471	1792	9.5e-185

Description

sp:[LN:FTSA_STAAU] [AC:O07325] [GN:FTSA] [OR:STAPHYLOCOCCUS AUREUS] [DE:CELL DIVISION PROTEIN FTSA] [SP:O07325] [DB:swissprot] >gp:[GI:g2149897] [LN:SAU94706] [AC:U94706] [PN:cell division protein] [GN:ftsA] [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus strain ATCC 8325-4 cell wall/cell division gene cluster, yllB, yllC, yllD, pbpA, mraY, murD, div1B, ftsA andftsZ genes, complete cds.] [LE:8604] [RE:10019] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000990_34646937_c3_983	1859	5631	336	111	512	4.1e-49

Description

gp:[GI:e1333201:g3776111] [LN:SATRXA] [AC:AJ223480] [PN:thioredoxin] [GN:trxA] [FN:thiol:disulfide interchange] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:Staphylococcus aureus trxA and uvrC genes and partial mutS and dhsC genes.] [LE:2334] [RE:2648] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000990_34650452_c1_782	1860	5632	225	74	87	0.00078

Description

gp:[GI:g488925] [LN:A13473] [AC:A13473] [PN:41kd antigen] [OR:Plasmodium falciparum] [SR:malaria parasite P. falciparum] [DB:genpept-pat] [DE:P.falciparum gene for 41kd antigen, clone 41-14.] [LE:<1] [RE:>532] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000990_35285902_c2_859	1861	5633	150	49	46	0.042

Description

sp:[LN:PGH2_MUSVI] [AC:O62725] [GN:PTGS2:COX2] [OR:MUSTELA VISON] [SR:,AMERICAN MINK] [EC:1.14.99.1] [DE:SYNTHASE 2) (PGH SYNTHASE 2) (PGHS-2) (PHS II)] [SP:O62725] [DB:swissprot] >gp:[GI:g2959708] [LN:AF047841] [AC:AF047841] [PN:prostaglandin synthase 2] [OR:Mustela vison] [SR:American mink] [DB:genpept-mam] [DE:Mustela vison prostaglandin synthase 2 mRNA, complete cds.] [NT:cyclooxygenase 2] [LE:11] [RE:1825] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000990_353427_f2_302	1862	5634	165	54		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000990_35365635_c2_846	1863	5635	156	51		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000990_35947191_c2_835	1864	5636	1155	384	149	6.3e-07

Description

gp:[GI:g1633572] [LN:KSU52064] [AC:U52064] [OR:Kaposi's sarcoma-associated herpesvirus] [SR:Kaposi's sarcoma-associated herpesvirus - Human herpesvirus 8] [DB:genpept-vrl] [DE:Kaposi's sarcoma-associated herpes-like virus ORF73 homolog gene,complete cds.] [NT:Herpesvirus saimiri ORF73 homolog] [LE:1] [RE:3489] [DI:direct] >gp:[GI:g1718329] [LN:KSU75698] [AC:U75698] [OR:Kaposi's sarcoma-associated herpesvirus] [SR:Kaposi's sarcoma-associated herpesvirus - Human herpesvirus 8] [DB:genpept-vrl] [DE:Kaposi's sarcoma-associated herpesvirus long unique region, 80putative ORF's and kaposin gene, complete cds.] [NT:ORF 73; extensive acidic domains, potential leucine] [LE:123809] [RE:127297] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000990_35978392_c1_788	1865	5637	2007	668	949	2.0e-95

Description

pir:[LN:H69878] [AC:H69878] [PN:protein kinase homolog yloP] [GN:yloP] [CL:protein kinase homology] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1185168:g2633949] [LN:BSUB0009] [AC:Z99112:AL009126] [GN:yloP] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.] [NT:similar to protein kinase] [LE:52121] [RE:54067] [DI:direct] >gp:[GI:e323506:g2337806] [LN:BSY13937] [AC:Y13937] [PN:putative Pkn2 protein] [GN:yloP] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis genomic DNA from the spoVM region.] [LE:13893] [RE:15839] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000990_35980062_f2_357	1866	5638	162	53		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000990_36129451_c1_702	1867	5639	288	95	408	4.3e-38

Description

sp:[LN:PTHP_STACA] [AC:P23534] [GN:PTSH] [OR:STAPHYLOCOCCUS CARNOSUS]
[DE:PHOSPHOCARRIER PROTEIN HPR (HISTIDINE-CONTAINING PROTEIN)] [SP:P23534]
[DB:swissprot] >pir:[LN:A42374] [AC:S15367:A42374] [PN:phosphotransferase
system phosphohistidine-containing protein :phosphotransferase system HPr]
[CL:phosphotransferase system phosphohistidine-containing
protein:phosphotransferase system phosphohistidine-containing protein
homology] [OR:Staphylococcus carnosus] [DB:pir1] >gp:[GI:g46908] [LN:SCPTSH]
[AC:X60766] [PN:Histidine-containing protein (HPr)] [GN:ptsH]
[OR:Staphylococcus carnosus] [DB:genpept-bct1] [DE:S.carnosus ptsH gene for
histidine-containing protein (HPr).] [SP:P23534] [LE:270] [RE:536]
[DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000990_36141893_c3_1039	1868	5640	1248	415	1166	2.1e-118

Description

gp:[GI:e1185186:g2633967] [LN:BSUB0009] [AC:Z99112:AL009126] [PN:signal
recognition particle (docking protein)] [GN:ftsY] [FN:involved in secretion
of extracellular proteins] [OR:Bacillus subtilis] [DB:genpept-bct1]
[DE:Bacillus subtilis complete genome (section 9 of 21): from 1598421to
1807200.] [NT:alternate gene name: srb] [SP:P51835] [LE:71119] [RE:72108]
[DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000990_36142817_c1_717	1869	5641	1149	382	925	7.1e-93

Description

pir:[LN:A70180] [AC:A70180] [PN:spermidine/putrescine ABC transporter, ATP-binding protein (potA) homolog] [CL:ATP-binding cassette homology] [OR:Borrelia burgdorferi] [SR:, Lyme disease spirochete] [DB:pir2]
 >gp:[GI:g2688562] [LN:AE001165] [AC:AE001165:AE000783]
 [PN:spermidine/putrescine ABC transporter,] [GN:BB0642] [OR:Borrelia burgdorferi] [SR:Lyme disease spirochete] [DB:genpept-bct2] [DE:Borrelia burgdorferi (section 51 of 70) of the complete genome.] [NT:similar to GB:M64519 SP:P23858 PID:147326 GB:U00096] [LE:11911] [RE:12954]
 [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000990_36147150_c1_757	1870	5642	609	202	492	5.4e-47

Description

pir:[LN:C69986] [AC:C69986] [PN:conserved hypothetical protein ysnA] [GN:ysnA] [CL:Methanococcus jannaschii conserved hypothetical protein MJ0226] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1184085:g2635301] [LN:BSUB0015] [AC:Z99118:AL009126] [GN:ysnA] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.] [NT:similar to hypothetical proteins] [LE:104515] [RE:105111] [DI:complement] >gp:[GI:e1165357:g1770060] [LN:BSZ75208] [AC:Z75208] [PN:hypothetical protein] [GN:ysnA] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis genomic sequence 89009bp.] [NT:homology to ORFol97 of Escherichia coli; unknown] [LE:64796] [RE:65392] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000990_36601687_c1_692	1874	5646	1260	419	1016	1.6e-102

Description

sp:[LN:PUR2_BACSU] [AC:P12039] [GN:PURD] [OR:BACILLUS SUBTILIS]
[EC:6.3.4.13] [DE:RIBONUCLEOTIDE SYNTHETASE] (PHOSPHORIBOSYLGLYCINAMIDE
SYNTHETASE)] [SP:P12039] [DB:swissprot] >pir:[LN:AJBSAG] [AC:B29183:C69684]
[PN:phosphoribosylamine--glycine ligase,:phosphoribosylglycinamide
synthetase] [GN:purD] [CL:phosphoribosylamine--glycine ligase:
phosphoribosylamine--glycine ligase homology] [OR:Bacillus subtilis]
[EC:6.3.4.13] [DB:pir1] [MP:18 min] >gp:[GI:g2465561] [LN:AF011544]
[AC:AF011544] [PN:phosphoribosylglycinamide synthetase] [GN:purD]
[OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
phosphoribosylaminoimidazole-carboxamideformyltransferase (purH-J) gene,
partial cds,phosphoribosylglycinamide synthetase (purD), YecA (yecA),
putativeadenine deaminase (yecB), YecC (yecC), and YecD (yecD)
genes,complete cds, and putative glutamate synthase (yecE) gene,
partialcds.] [NT:identified by complementation of E.coli TX267,] [LE:263]
[RE:1531] [DI:direct] >gp:[GI:g143374] [LN:BACPURF] [AC:J02732:K00047]
[OR:Bacillus subtilis] [SR:B.subtilis (strain DE1 (prototroph DER. or W168))
DNA, clone pPZ] [DB:genpept-bct1] [DE:B.subtilis pur operon encoding purine
biosynthesis enzymes, 12genes.] [NT:phosphoribosyl glycinamide synthetase
(PUR-D; gtg] [LE:11971] [RE:13239] [DI:direct] >gp:[GI:e1182633:g2632967]
[LN:BSUB0004] [AC:Z99107:AL009126] [PN:phosphoribosylglycinamide synthetase]
[GN:purD] [FN:purine biosynthesis] [OR:Bacillus subtilis] [DB:genpept-bct1]
[EC:6.3.4.13] [DE:Bacillus subtilis complete genome (section 4 of 21): from
600701 to813890.] [SP:P12039] [LE:108953] [RE:110221] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000990_3912890_f3_463	1875	5647	222	73	246	6.4e-21

Description

sp:[LN:RL28_BACST] [AC:P23374] [GN:RPMB] [OR:BACILLUS STEAROTHERMOPHILUS]
[DE:50S RIBOSOMAL PROTEIN L28] [SP:P23374] [DB:swissprot] >pir:[LN:A48396]
[AC:A48396] [PN:ribosomal protein L28] [CL:Escherichia coli ribosomal
protein L28] [OR:Bacillus stearothermophilus] [DB:pir2]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000990_3945257_f3_664	1876	5648	1176	391	738	4.6e-73

Description

pir:[LN:E69687] [AC:E69687:A38129:S39692] [PN:cytochrome aa3 quinol oxidase (subunit II) qoxA:quinol oxidase aa3-600 chain qoxA] [GN:qoxA] [CL:bo-type ubiquinol oxidase chain II precursor: cytochrome-c oxidase chain II homology] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1186316:g2636352] [LN:BSUB0020] [AC:Z99123:AL009126] [PN:cytochrome aa3 quinol oxidase (subunit II)] [GN:qoxA] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.] [NT:alternate gene name: ipa-37d] [LE:117692] [RE:118657] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000990_3960881_f3_483	1877	5649	129	42		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000990_39808_f3_498	1878	5650	135	44		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000990_3992193_f3_496	1879	5651	177	58		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000990_4067342_c3_977	1880	5652	1086	361	1267	4.1e-129

Description

sp:[LN:SYFA_BACSU] [AC:P17921:P94539] [GN:PHES] [OR:BACILLUS SUBTILIS] [EC:6.1.1.20] [DE:-TRNA LIGASE ALPHA CHAIN) (PHERS)] [SP:P17921:P94539] [DB:swissprot] >pir:[LN:YFBSA] [AC:H69675:I40459:S11730] [PN:phenylalanine--trna ligase, alpha chain:phenylalanyl-trna synthetase alpha chain] [GN:pheS] [CL:phenylalanine--trna ligase alpha chain] [OR:Bacillus subtilis] [EC:6.1.1.20] [DB:pir1] >gp:[GI:e1184113:g2635329] [LN:BSUB0015] [AC:Z99118:AL009126] [PN:phenylalanyl-trna synthetase (alpha subunit)] [GN:pheS] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:6.1.1.20] [DE:Bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.] [SP:P17921] [LE:133410] [RE:134444] [DI:complement] >gp:[GI:e1165324:g1770030] [LN:BSZ75208] [AC:Z75208] [PN:phenylalany-trna synthetase beta subunit] [GN:pheS] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:6.1.1.20] [DE:B.subtilis genomic sequence 89009bp.] [NT:phenylalanyl-trna synthetase beta subunit] [SP:P17921] [LE:35463] [RE:36497] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000990_4103438_c3_970	1881	5653	255	84	110	1.6e-06

Description

pir:[LN:D69874] [AC:D69874] [PN:conserved hypothetical protein ylbG] [GN:ylbG] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e334775:g2340003] [LN:BS16823KB] [AC:Z98682] [PN:YlbG protein] [GN:ylbG] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis genomic DNA 23.9kB fragment.] [LE:14055] [RE:14327] [DI:direct] >gp:[GI:e1185090:g2633871] [LN:BSUB0008] [AC:Z99111:AL009126] [GN:ylbG] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.] [NT:similar to hypothetical proteins] [LE:173538] [RE:173810] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000990_4298177_c1_776	1882	5654	126	41		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000990_4300332_c1_700	1883	5655	1329	442	98	0.00059

Description

gp:[GI:g5306148] [LN:AF160864] [AC:AF160864] [PN:orf365] [GN:orf365]
[OR:Mitochondrion Tetrahymena pyriformis] [SR:Tetrahymena pyriformis]
[DB:genpept] [DE:Tetrahymena pyriformis mitochondrial DNA, complete genome.]
[NT:Open reading frame ymf65 (CPGN); ATA initiation] [LE:15906] [RE:17003]
[DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000990_4306562_c1_760	1884	5656	306	101	469	1.5e-44

Description

sp:[LN:YLLB_STAAU] [AC:O07319] [GN:YLLB] [OR:STAPHYLOCOCCUS AUREUS]
[DE:HYPOTHETICAL 17.4 KD PROTEIN] [SP:O07319] [DB:swissprot]
>gp:[GI:g2149890] [LN:SAU94706] [AC:U94706] [PN:unknown] [GN:y11B]
[OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus
strain ATCC 8325-4 cell wall/cell division gene cluster, y11B, y11C, y11D,
pbpA, mraY, murD, div1B, ftsA and ftsZ genes, complete cds.] [LE:537]
[RE:971] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000990_4339053_c3_934	1885	5657	144	47		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000990_4457788_f2_344	1886	5658	1716	571	285	5.3e-21

Description

pir:[LN:D71623] [AC:D71623] [PN:erythrocyte membrane protein PfEMP3
PFB0095c] [GN:PFB0095c] [OR:Plasmodium falciparum] [DB:pir2]
>gp:[GI:g3845093] [LN:AE001371] [AC:AE001371:AE001362] [PN:erythrocyte
membrane protein PfEMP3] [GN:PFB0095c] [OR:Plasmodium falciparum]
[SR:malaria parasite P. falciparum] [DB:genpept-inv2] [DE:Plasmodium
falciparum chromosome 2, section 8 of 73 of the complete sequence.]
[NT:identified by sequence similarity] [LE:1407:8817] [RE:8621:8927]
[DI:complementJoin]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000990_4509661_c1_783	1887	5659	411	136	168	1.2e-12

Description

gp:[GI:e1453986:g4835313] [LN:SC5H1] [AC:AL049863] [PN:hypothetical protein]
[GN:SC5H1.10c] [OR:Streptomyces coelicolor] [DB:genpept-bct1]
[DE:Streptomyces coelicolor cosmid 5H1.] [NT:SC5H1.10c, hypothetical
protein, len: 160 aa;] [LE:8093] [RE:8575] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000990_4532967_c3_982	1888	5660	2358	785	3159	0.0

Description

gp:[GI:e1333200:g3776110] [LN:SATRXA] [AC:AJ223480] [PN:MutS-like protein]
[GN:mutS] [FN:DNA mismatch repair protein] [OR:Staphylococcus aureus]
[DB:genpept-bct1] [DE:Staphylococcus aureus trxA and uvrC genes and partial
mutS and dhsCgenes.] [LE:<1] [RE:2161] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000990_4696068_c1_741	1889	5661	186	61	237	5.7e-20

Description

sp:[LN:RL32_BACST] [AC:P07840] [GN:RPMF] [OR:BACILLUS STEAROTHERMOPHILUS]
[DE:50S RIBOSOMAL PROTEIN L32 (RIBOSOMAL PROTEIN I) (BL37)] [SP:P07840]
[DB:swissprot] >pir:[LN:R5BS37] [AC:S07236] [PN:ribosomal protein
L32:ribosomal protein BL37:ribosomal protein I] [CL:Escherichia coli
ribosomal protein L32] [OR:Bacillus stearothermophilus] [DB:pir1]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000990_4725000_c1_797	1890	5662	3636	1211	2426	6.2e-252

Description

pir:[LN:G69708] [AC:G69708:JC4819:PC4029] [PN:chromosome segregation SMC
protein:minichromosome stabilizing protein SMC] [GN:smc] [CL:conserved
hypothetical P115 protein] [OR:Bacillus subtilis] [DB:pir2]
>gp:[GI:e1185185:g2633966] [LN:BSUB0009] [AC:Z99112:AL009126] [PN:chromosome
segregation SMC protein homolg] [GN:smc] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 9 of 21):
from 1598421to 1807200.] [NT:alternate gene name: ylqA] [LE:67539]
[RE:71099] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000990_4725415_c2_873	1891	5663	2337	778	3205	0.0

Description

gp:[GI:d1023422:g2463561] [LN:AB007500] [AC:AB007500:D28879]
 [PN:penicillin-binding protein 1] [GN:pbpA] [OR:Staphylococcus aureus]
 [SR:Staphylococcus aureus (strain:NCTC8325) DNA] [DB:genpept-bct1]
 [DE:Staphylococcus aureus genes for penicillin-binding protein 1, MraY,MurD,
 partial and complete cds.] [LE:594] [RE:2828] [DI:direct] >gp:[GI:g2149893]
 [LN:SAU94706] [AC:U94706] [PN:penicillin-binding protein 1] [GN:pbpA]
 [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus
 strain ATCC 8325-4 cell wall/cell divisiongene cluster, yllB, yllC, yllD,
 pbpA, mraY, murD, div1B, ftsA andftsZ genes, complete cds.] [LE:2318]
 [RE:4552] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000990_4741010_c3_956	1892	5664	846	281	650	9.8e-64

Description

sp:[LN:SUHB_BACSU] [AC:Q45499] [GN:SUHB] [OR:BACILLUS SUBTILIS]
 [DE:EXTRAGENIC SUPPRESSOR PROTEIN SUHB HOMOLOG] [SP:Q45499] [DB:swissprot]
 >pir:[LN:E69864] [AC:E69864] [PN:myo-inositol-1(or 4)-monophosphatase
 homolog yktC] [GN:yktC] [CL:suppressor protein suhB] [OR:Bacillus subtilis]
 [DB:pir2] >gp:[GI:e1185057:g2633838] [LN:BSUB0008] [AC:Z99111:AL009126]
 [GN:yktC] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus
 subtilis complete genome (section 8 of 21): from 1394791to 1603020.]
 [NT:similar to myo-inositol-1(or 4)-monophosphatase] [SP:Q45499] [LE:142056]
 [RE:142853] [DI:direct] >gp:[GI:g3282150] [LN:AF012285]
 [AC:AF012285:AF012284:U51911] [PN:unknown] [GN:yktC] [FN:unknown]
 [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis mobA-nprE
 gene region.] [NT:similar to E. coli extragenic suppressor protein]
 [LE:42544] [RE:43341] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000990_4741703_c2_894	1893	5665	2418	805	2153	5.3e-223

Description

sp:[LN:PRIA_BACSU] [AC:P94461:O34941] [GN:PRIA] [OR:BACILLUS SUBTILIS]
 [DE:PRIMOSOMAL PROTEIN N' (REPLICATION FACTOR Y)] [SP:P94461:O34941]
 [DB:swissprot] >pir:[LN:A69682] [AC:A69682] [PN:primosomal replication
 factor Y priA] [GN:priA] [CL:unassigned DEAD/H box helicases:DEAD/H box
 helicase homology] [OR:Bacillus subtilis] [DB:pir2]
 >gp:[GI:e1185162:g2633943] [LN:BSUB0009] [AC:Z99112:AL009126] [PN:primosomal
 replication factor Y (primosomal) [GN:priA] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 9 of 21):
 from 1598421to 1807200.] [NT:alternate gene name: yloJ] [SP:P94461]
 [LE:45047] [RE:47464] [DI:direct] >gp:[GI:e323502:g2337800] [LN:BSY13937]
 [AC:Y13937] [PN:putative PriA protein] [GN:yloJ] [FN:unknown] [OR:Bacillus
 subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis genomic DNA from the spoVM
 region.] [SP:P94461] [LE:6819] [RE:9236] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000990_4769512_f2_349	1894	5666	135	44		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000990_4781517_c2_888	1895	5667	129	42		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000990_4859425_f2_276	1896	5668	141	46		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000990_4875055_f1_23	1897	5669	225	74	74	0.015

Description

sp:[LN:Y27B_METJA] [AC:P81234] [GN:MJ0275.1] [OR:METHANOCOCCUS JANNASCHII]
[DE:HYPOTHETICAL PROTEIN MJ0275.1] [SP:P81234] [DB:swissprot]
>gp:[GI:g2826269] [LN:U67482] [AC:U67482:L77117] [PN:M. jannaschii predicted
coding region MJ0275.1] [GN:MJ0275.1] [OR:Methanococcus jannaschii]
[DB:genpept-bct2] [DE:Methanococcus jannaschii section 24 of 150 of the
complete genome.] [NT:Brute Force ORF; identified by GeneMark; putative]
[LE:9344] [RE:9790] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000990_4875327_f3_587	1898	5670	135	44		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000990_4875452_c3_1034	1899	5671	645	214	521	4.6e-50

Description

gp:[GI:g4982295] [LN:AE001811] [AC:AE001811:AE000512] [PN:ribulose-phosphate
3-epimerase] [GN:TM1718] [OR:Thermotoga maritima] [DB:genpept-bct2]
[DE:Thermotoga maritima section 123 of 136 of the complete genome.]
[NT:similar to GB:L77117 SP:Q58093 PID:1591395 percent] [LE:2607] [RE:3269]
[DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000990_4876542_f1_176	1900	5672	633	210	551	3.0e-53

Description

pir:[LN:D69862] [AC:D69862] [PN:formylmethionine deformylase homolog ykrB]
[GN:ykrB] [CL:polypeptide deformylase] [OR:Bacillus subtilis] [DB:pir2]
>gp:[GI:e1185046:g2633827] [LN:BSUB0008] [AC:Z99111:AL009126] [GN:ykrB]
[FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
complete genome (section 8 of 21): from 1394791to 1603020.] [NT:similar to
formylmethionine deformylase] [LE:130810] [RE:131364] [DI:complement]
>gp:[GI:g3282140] [LN:AF012285] [AC:AF012285:AF012284:U51911] [PN:unknown]
[GN:ykrB] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus
subtilis mobA-nprE gene region.] [NT:similar to polypeptide deformylase from
Mycoplasma] [LE:31298] [RE:31852] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000990_4877203_c1_793	1901	5673	936	311	661	6.7e-65

Description

pir:[LN:H69620] [AC:H69620] [PN:malonyl CoA-acyl carrier protein transacylase fabD] [GN:fabD] [CL:[acyl-carrier-protein] S-malonyltransferase: [acyl-carrier-protein] S-malonyltransferase homology] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1185181:g2633962] [LN:BSUB0009] [AC:Z99112:AL009126] [PN:malonyl CoA-acyl carrier protein transacylase] [GN:fabD] [FN:fatty acid biosynthesis] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:2.3.1.39] [DE:Bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.] [NT:alternate gene name: ylpE] [LE:64546] [RE:65499] [DI:direct] >gp:[GI:e323514:g2337819] [LN:BSY13937] [AC:Y13937] [PN:putative FabD protein] [GN:ylpE] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis genomic DNA from the spoVM region.] [LE:26318] [RE:27271] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000990_4899187_f3_569	1902	5674	1149	382	402	1.9e-37

Description

pir:[LN:B69875] [AC:B69875] [PN:conserved hypothetical protein ylbM] [GN:ylbM] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e334781:g2340009] [LN:BS16823KB] [AC:Z98682] [PN:YlbM protein] [GN:ylbM] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis genomic DNA 23.9kB fragment.] [LE:18936] [RE:20183] [DI:complement] >gp:[GI:e1185096:g2633877] [LN:BSUB0008] [AC:Z99111:AL009126] [GN:ylbM] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.] [NT:similar to hypothetical proteins] [LE:178419] [RE:179666] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000990_4970462_c2_904	1903	5675	750	249	837	1.5e-83

Description

sp:[LN:FABG_BACSU] [AC:P51831:O31733] [GN:FABG] [OR:BACILLUS SUBTILIS] [EC:1.1.1.100] [DE:ACYL CARRIER PROTEIN REDUCTASE)] [SP:P51831:O31733] [DB:swissprot] >pir:[LN:A69621] [AC:A69621:PC4176] [PN:3-oxoacyl-[acyl-carrier-protein] reductase, :3-ketoacyl-acyl carrier protein reductase fabG:srb protein] [GN:fabG:srb] [CL:ribitol dehydrogenase:short-chain alcohol dehydrogenase homology] [OR:Bacillus subtilis] [EC:1.1.1.100] [DB:pir2] >gp:[GI:e1185182:g2633963] [LN:BSUB0009] [AC:Z99112:AL009126] [PN:3-ketoacyl-acyl carrier protein reductase] [GN:fabG] [FN:fatty acid biosynthesis] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:1.1.1.100] [DE:Bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.] [NT:alternate gene name: ylpF] [SP:P51831] [LE:65492] [RE:66232] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000990_5080260_f1_43	1904	5676	141	46		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000990_5096012_f3_481	1905	5677	231	76		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000990_5117162_c2_826	1906	5678	1023	340	925	7.1e-93

Description

gp:[GI:d1039221:g4514629] [LN:AB016894] [AC:AB016894] [PN:bd-type quinol oxidase subunit II] [GN:cbdB] [OR:Bacillus stearothermophilus] [SR:Bacillus stearothermophilus (strain:K1041) DNA] [DB:genpept-bct1] [DE:Bacillus stearothermophilus genes for bd-type quinol oxidasesubunit I and subunit II, complete cds.] [NT:cytochrome bd-type quinol oxidase] [LE:1706] [RE:2734] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000990_5157963_f3_573	1907	5679	939	312	219	3.7e-22

Description

pir:[LN:E69827] [AC:E69827] [PN:glycerophosphodiester phosphodiesterase homolog yhdW] [GN:yhdW] [OR:Bacillus subtilis] [DB:pir2]
>gp:[GI:e1182963:g2633297] [LN:BSUB0006] [AC:Z99109:AL009126] [GN:yhdW] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.] [NT:similar to glycerophosphodiester phosphodiesterase] [LE:37668] [RE:38399] [DI:complement] >gp:[GI:e1191883:g2226218] [LN:BSY14082] [AC:Y14082] [PN:hypothetical protein] [GN:yhdW] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis chromosomal DNA, region 72 to 75 degrees: spoVRto sspB.] [NT:Similarity to glycerol diester phosphodiesterase] [LE:24316] [RE:25047] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000990_5162760_f3_514	1908	5680	129	42		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000990_5276712_c3_1016	1909	5681	708	235	659	1.1e-64

Description

sp:[LN:DCOP_LACLC] [AC:P50924] [GN:PYRF] [OR:LACTOCOCCUS LACTIS]
 [SR:,SUBSPCREMORIS:STREPTOCOCCUS CREMORIS] [EC:4.1.1.23] [DE:DECARBOXYLASE)]
 [SP:P50924] [DB:swissprot] >gp:[GI:e264705:g1070361] [LN:LLCPYRDB]
 [AC:X74207] [PN:OMP decarboxylase] [GN:pyrF] [OR:Lactococcus lactis]
 [DB:genpept-bct1] [DE:L.lactis pyrD and pyrF genes.] [SP:P50924] [LE:5309]
 [RE:6022] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000990_595312_c1_733	1910	5682	147	48		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000990_5974138_f1_158	1911	5683	204	67		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000990_5978453_c3_1029	1912	5684	492	163	261	1.6e-22

Description

sp:[LN:DEF_BACSU] [AC:P94462] [GN:DEF] [OR:BACILLUS SUBTILIS] [EC:3.5.1.31]
 [DE:DEFORMYLASE)] [SP:P94462] [DB:swissprot] >pir:[LN:F69613] [AC:F69613]
 [PN:polypeptide deformylase def] [GN:def] [CL:polypeptide deformylase]
 [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e290287:g1772499] [LN:BSPRIADFS]
 [AC:Y10304] [PN:polypeptide deformylase] [GN:def] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:B.subtilis priA, def, fmt, sun genes.] [SP:P94462]
 [LE:1762] [RE:2244] [DI:direct] >gp:[GI:e1185163:g2633944] [LN:BSUB0009]
 [AC:Z99112:AL009126] [PN:polypeptide deformylase] [GN:def] [OR:Bacillus
 subtilis] [DB:genpept-bct1] [EC:3.5.1.31] [DE:Bacillus subtilis complete
 genome (section 9 of 21): from 1598421to 1807200.] [NT:alternate gene name:
 yloK] [SP:P94462] [LE:47491] [RE:47973] [DI:direct]
 >gp:[GI:e323523:g2337801] [LN:BSY13937] [AC:Y13937] [PN:putative Def
 protein] [GN:yloK] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1]
 [DE:Bacillus subtilis genomic DNA from the spoVM region.] [SP:P94462]
 [LE:9263] [RE:9745] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000990_6023593_c1_730	1913	5685	288	95	296	3.2e-26

Description

pir:[LN:D69873] [AC:D69873] [PN:hypothetical protein ylaN] [GN:ylaN]
[OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1185074:g2633855] [LN:BSUB0008]
[AC:Z99111:AL009126] [GN:ylaN] [FN:unknown] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 8 of 21):
from 1394791to 1603020.] [LE:157027] [RE:157308] [DI:direct]
>gp:[GI:e1191897:g2224773] [LN:BSZ97025] [AC:Z97025] [GN:ylaN] [OR:Bacillus
subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis nprE,
yla[A,B,C,D,E,F,G,H,I,J,K,L,M,N,O] and pycAgenes.] [LE:11286] [RE:11567]
[DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000990_6072125_c1_766	1914	5686	672	223	857	1.1e-85

Description

gp:[GI:g4009493] [LN:AF068904] [AC:AF068904] [PN:YlmE] [GN:ylmE]
[OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus cell
division protein FtsZ (ftsZ) gene,partial cds; YlmD (ylmD), YlmE (ylmE),
YlmF (ylmF), YlmG (ylmG),and YlmH (ylmH) genes, complete cds; and cell
division proteinDivIVA (divIVA) gene, partial cds.] [NT:similar to Bacillus
subtilis YlmE] [LE:1246] [RE:1920] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000990_6115700_f3_647	1915	5687	1404	467	356	7.8e-64

Description

pir:[LN:H69858] [AC:H69858] [PN:cation ABC transporter (ATP-binding protei)
homolog ykoD] [GN:ykoD] [CL:ATP-binding cassette homology] [OR:Bacillus
subtilis] [DB:pir2] >gp:[GI:e1181522:g2632042] [LN:BSAJ2571] [AC:AJ002571]
[PN:YkoD] [GN:ykoD] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus
subtilis 168 56 kb DNA fragment between xlyA and ykoR.] [NT:homologous to
cobalt transport ATP binding protein] [LE:41106] [RE:42578] [DI:complement]
>gp:[GI:e1183342:g2633676] [LN:BSUB0007] [AC:Z99110:AL009126] [GN:ykoD]
[FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
complete genome (section 7 of 21): from 1194391to 1411140.] [NT:similar to
cation ABC transporter (ATP-binding) [LE:194055] [RE:195527] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000990_6131693_c1_762	1916	5688	414	137	574	1.1e-55

Description

gp:[GI:d1023421:g2463560] [LN:AB007500] [AC:AB007500:D28879]
[OR:Staphylococcus aureus] [SR:Staphylococcus aureus (strain:NCTC8325) DNA]
[DB:genpept-bct1] [DE:Staphylococcus aureus genes for penicillin-binding
protein 1, MraY,MurD, partial and complete cds.] [NT:unnamed protein
product] [LE:212] [RE:613] [DI:direct] >gp:[GI:g2149892] [LN:SAU94706]
[AC:U94706] [PN:cell division protein] [GN:y11D] [OR:Staphylococcus aureus]
[DB:genpept-bct2] [DE:Staphylococcus aureus strain ATCC 8325-4 cell
wall/cell divisiongene cluster, y11B, y11C, y11D, pbpA, mraY, murD, div1B,
ftsA andftsZ genes, complete cds.] [LE:1936] [RE:2337] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000990_6149077_c3_1033	1917	5689	891	296	708	7.0e-70

Description

pir:[LN:A69879] [AC:A69879] [PN:conserved hypothetical protein yloQ]
[GN:yloQ] [CL:conserved hypothetical protein HI1714] [OR:Bacillus subtilis]
[DB:pir2] >gp:[GI:e1185169:g2633950] [LN:BSUB0009] [AC:Z99112:AL009126]
[GN:yloQ] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus
subtilis complete genome (section 9 of 21): from 1598421to 1807200.]
[NT:similar to hypothetical proteins] [LE:54082] [RE:54978] [DI:direct]
>gp:[GI:e323525:g2337807] [LN:BSY13937] [AC:Y13937] [PN:YloQ protein]
[GN:yloQ] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus
subtilis genomic DNA from the spoVM region.] [LE:15854] [RE:16750]
[DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000990_632762_f3_671	1918	5690	222	73		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000990_642_c3_1005	1919	5691	2784	927	4356	0.0

Description

sp:[LN:SYI STAAU] [AC:P41972] [GN:ILES] [OR:STAPHYLOCOCCUS AUREUS]
[EC:6.1.1.5] [DE:(ILERS)] [SP:P41972] [DB:swissprot] >pir:[LN:S40178]
[AC:S40178] [PN:isoleucine--tRNA ligase,:isoleucyl-tRNA synthetase]
[CL:isoleucine--tRNA ligase] [OR:Staphylococcus aureus] [EC:6.1.1.5]
[DB:pir2] >gp:[GI:g437916] [LN:SAILES] [AC:X74219] [PN:isoleucyl-tRNA
synthetase] [GN:ileS] [OR:Staphylococcus aureus] [DB:genpept-bct1]
[DE:S.aureus gene for isoleucyl-tRNA synthetase.] [SP:P41972] [LE:91]
[RE:2844] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000990_6720452_c3_936	1920	5692	1356	451	1266	5.2e-129

Description

gp:[GI:d1039220:g4514628] [LN:AB016894] [AC:AB016894] [PN:bd-type quinol
oxidase subunit I] [GN:cbdA] [OR:Bacillus stearothermophilus] [SR:Bacillus
stearothermophilus (strain:K1041) DNA] [DB:genpept-bct1] [DE:Bacillus
stearothermophilus genes for bd-type quinol oxidasesubunit I and subunit II,
complete cds.] [NT:cytochrome bd-type quinol oxidase] [LE:363] [RE:1709]
[DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000990_6720655_f3_530	1921	5693	147	48	68	0.045

Description

gp:[GI:g4049913] [LN:AF063866] [AC:AF063866] [PN:ORF MSV141 hypothetical
protein] [GN:MSV141] [OR:Melanoplus sanguinipes entomopoxvirus]
[DB:genpept-vrl] [DE:Melanoplus sanguinipes entomopoxvirus, complete
genome.] [LE:121430] [RE:121630] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000990_6834687_c2_831	1922	5694	309	102	209	5.3e-17

Description

pir:[LN:C69864] [AC:C69864] [PN:hypothetical protein yktA] [GN:yktA]
[OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1185054:g2633835] [LN:BSUB0008]
[AC:Z99111:AL009126] [GN:yktA] [FN:unknown] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 8 of 21):
from 1394791to 1603020.] [LE:140551] [RE:140817] [DI:direct]
>gp:[GI:g3282148] [LN:AF012285] [AC:AF012285:AF012284:U51911] [PN:unknown]
[GN:yktA] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus
subtilis mobA-nprE gene region.] [LE:41039] [RE:41305] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000990_7225000_c3_1038	1923	5695	1026	341	898	5.2e-90

Description

pir:[LN:H69679] [AC:H69679] [PN:involved in fatty acid/phospholipid synthesis plsX] [GN:plsX] [CL:phospholipid synthesis protein] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1185180:g2633961] [LN:BSUB0009] [AC:Z99112:AL009126] [GN:plsX] [FN:involved in fatty acid/phospholipid synthesis] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.] [NT:alternate gene name: ylpD] [LE:63526] [RE:64527] [DI:direct] >gp:[GI:e323529:g2337818] [LN:BSY13937] [AC:Y13937] [PN:putative PlsX protein] [GN:ylpD] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis genomic DNA from the spoVM region.] [LE:25298] [RE:26299] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000990_7320465_c1_719	1924	5696	831	276	525	1.7e-50

Description

pir:[LN:G70179] [AC:G70179] [PN:spermidine/putrescine ABC transporter, permease protein (potC) homolog] [CL:spermidine/putrescine transport system permease protein potI] [OR:Borrelia burgdorferi] [SR:, Lyme disease spirochete] [DB:pir2] >gp:[GI:g2688564] [LN:AE001165] [AC:AE001165:AE000783] [PN:spermidine/putrescine ABC transporter, permease] [GN:BB0640] [OR:Borrelia burgdorferi] [SR:Lyme disease spirochete] [DB:genpept-bct2] [DE:Borrelia burgdorferi (section 51 of 70) of the complete genome.] [NT:similar to GB:M64519 SP:P23859 PID:147328 GB:U00096] [LE:10307] [RE:11098] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000990_867176_c3_924	1925	5697	1512	503	1090	2.3e-110

Description

pir:[LN:C70468] [AC:C70468] [PN:phosphoribosylaminoimidazolecarboxamide formyltransferase] [GN:purH] [CL:purH bifunctional enzyme] [OR:Aquifex aeolicus] [DB:pir2] >gp:[GI:g2984204] [LN:AE000765] [AC:AE000765:AE000657] [PN:phosphoribosylaminoimidazolecarboxamide] [GN:purH] [OR:Aquifex aeolicus] [DB:genpept-bct2] [DE:Aquifex aeolicus section 97 of 109 of the complete genome.] [LE:7599] [RE:9119] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000990_892141_f2_303	1926	5698	396	131	281	1.2e-24

Description

gp:[GI:e1487496:g5042304] [LN:MMU242955] [AC:AJ242955] [PN:hypothetical protein (P4(21)n)] [GN:P4(21)n] [OR:Mus musculus] [SR:house mouse] [DB:genpept-rod] [DE:Mus musculus partial mRNA for hypothetical protein (P4(21)n gene).] [NT:similar with amyh_yeast glucoamylase S1/S2] [LE:<1] [RE:1203] [DI:direct] >gp:[GI:d1042681:g5103287] [LN:AB028868] [AC:AB028868] [GN:P4(21)n] [OR:Mus musculus] [SR:Mus musculus mRNA] [DB:genpept] [DE:Mus musculus P4(21)n mRNA, partial cds.] [NT:The protein is similar with AMYH_YEAST GLUCOAMYLASE] [LE:<1] [RE:1203] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000990_892312_c3_980	1927	5699	156	51		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000990_968785_f2_361	1928	5700	939	312	1274	7.4e-130

Description

gp:[GI:g3320606] [LN:AF072726] [AC:AF072726] [PN:putative heme A synthase] [GN:ctaA] [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus putative heme A synthase (ctaA) gene,complete cds.] [NT:CtaA] [LE:139] [RE:1050] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000990_968811_c1_753	1929	5701	651	216	599	2.5e-58

Description

sp:[LN:DHSC_BACSU] [AC:P08064] [GN:SDHC] [OR:BACILLUS SUBTILIS]
 [DE:SUCCINATE DEHYDROGENASE CYTOCHROME B-558 SUBUNIT] [SP:P08064]
 [DB:swissprot] >pir:[LN:DEBSSC] [AC:A29843:I39972:E69704] [PN:succinate
 dehydrogenase, cytochrome b558:fumarate reductase C protein] [GN:sdhC:sdhA]
 [CL:succinate dehydrogenase cytochrome b558] [OR:Bacillus subtilis]
 [EC:1.3.99.1] [DB:pir1] [MP:70] >gp:[GI:g143525] [LN:BACSDHAB]
 [AC:M13470:M15107] [OR:Bacillus subtilis] [SR:B.subtilis DNA, clone pKIM4]
 [DB:genpept-bct1] [DE:B.subtilis succinate dehydrogenase complex encoding
 cytochrome b-558 subunit, complete cds, and flavoprotein subunit, 5' end.]
 [NT:succinate dehydrogenase cytochrome b-558 subunit] [LE:265] [RE:873]
 [DI:direct] >gp:[GI:e1184094:g2635310] [LN:BSUB0015] [AC:Z99118:AL009126]
 [PN:succinate dehydrogenase (cytochrome b558) [GN:sdhC] [OR:Bacillus
 subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section
 15 of 21): from 2795131to 3013540.] [SP:P08064] [LE:112102] [RE:112710]
 [DI:complement] >gp:[GI:e1165347:g1770051] [LN:BSZ75208] [AC:Z75208]
 [PN:cytochrome b558 subunit of succinate] [GN:sdhC] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [EC:1.3.99.1] [DE:B.subtilis genomic sequence 89009bp.]
 [SP:P08064] [LE:57197] [RE:57805] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000990_969052_f2_434	1930	5702	129	42		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000990_9881927_f1_75	1931	5703	180	59		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000990_990702_c1_765	1932	5704	1185	394	1809	1.5e-186

Description

sp:[LN:FTSZ_STAAU] [AC:P45498] [GN:FTSZ] [OR:STAPHYLOCOCCUS AUREUS] [DE:CELL DIVISION PROTEIN FTSZ] [SP:P45498] [DB:swissprot] >pir:[LN:S58814] [AC:S58814] [PN:cell division protein ftsZ] [CL:cell division protein ftsZ] [OR:Staphylococcus aureus] [DB:pir1] >gp:[GI:g458428] [LN:SAU06462] [AC:U06462] [PN:FtsZ] [GN:ftsZ] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:Staphylococcus aureus SA4 FtsZ (ftsZ) gene, complete cds.] [LE:27] [RE:1199] [DI:direct] >gp:[GI:g2149898] [LN:SAU94706] [AC:U94706] [PN:cell division protein] [GN:ftsZ] [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus strain ATCC 8325-4 cell wall/cell divisiongene cluster, yllB, yllC, yllD, pbpA, mraY, murD, div1B, ftsA andftsZ genes, complete cds.] [LE:10052] [RE:11224] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000990_9923437_f2_345	1933	5705	141	46		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000990_9925910_c2_813	1934	5706	597	198	430	2.0e-40

Description

sp:[LN:PUR3_BACSU] [AC:P12040] [GN:PURN] [OR:BACILLUS SUBTILIS] [EC:2.1.2.2] [DE:TRANSFORMYLASE] (5'-PHOSPHORIBOSYLGLYCINAMIDE TRANSFORMYLASE)] [SP:P12040] [DB:swissprot] >pir:[LN:XYBSGF] [AC:I29326:B69685] [PN:phosphoribosylglycinamide formyltransferase,] [GN:purN] [CL:phosphoribosylglycinamide formyltransferase: phosphoribosylglycinamide formyltransferase homology] [OR:Bacillus subtilis] [EC:2.1.2.2] [DB:pir1] [MP:18 min] >gp:[GI:g143372] [LN:BACPURF] [AC:J02732:K00047] [OR:Bacillus subtilis] [SR:B.subtilis (strain DE1 (prototroph DER. or W168)) DNA, clone pPZ] [DB:genpept-bct1] [DE:B.subtilis pur operon encoding purine biosynthesis enzymes, 12genes.] [NT:phosphoribosyl glycinamide formyltransferase] [LE:9833] [RE:10420] [DI:direct] >gp:[GI:e1182631:g2632965] [LN:BSUB0004] [AC:Z99107:AL009126] [PN:phosphoribosylglycinamide formyltransferase] [GN:purN] [FN:purine biosynthesis] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:2.1.2.2] [DE:Bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.] [SP:P12040] [LE:106815] [RE:107402] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000990_9933463_c3_933	1935	5707	1188	395	897	6.6e-90

Description

sp:[LN:YWBD_BACSU] [AC:P39587] [GN:YWBD:IPA-19D] [OR:BACILLUS SUBTILIS]
[DE:HYPOTHETICAL 44.4 KD PROTEIN IN EPR-GALK INTERGENIC REGION] [SP:P39587]
[DB:swissprot] >pir:[LN:S39674] [AC:S39674:B70051] [PN:ywbD
protein:hypothetical protein ipa-19d] [GN:ywbD] [CL:probable
methyltransferase b0967] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:g413943]
[LN:BSGENR] [AC:X73124] [GN:ipa-19d] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:B.subtilis genomic region (325 to 333).] [SP:P39587]
[LE:20551] [RE:21741] [DI:direct] >gp:[GI:e1186335:g2636371] [LN:BSUB0020]
[AC:Z99123:AL009126] [GN:ywbD] [FN:unknown] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 20 of 21):
from 3798401to 4010550.] [NT:alternate gene name: ipa-19d; similar to]
[SP:P39587] [LE:136218] [RE:137408] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000990_9954640_f3_487	1936	5708	228	75	117	3.0e-07

Description

gp:[GI:g2196686] [LN:EFU25090] [AC:U25090] [PN:pyrimidine biosynthesis
protein Ab] [GN:pyrAb] [OR:Enterococcus faecalis] [DB:genpept-bct1]
[DE:Enterococcus faecalis plasmid pKV48 pyrimidine biosynthesis proteinAb
(pyrAb) gene, partial cds.] [LE:<1] [RE:>253] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000991_10928_f1_70	1937	5709	1242	413	238	1.4e-17

Description

pir:[LN:T03492] [AC:T03492] [PN:hypothetical protein] [OR:Rhodobacter
capsulatus] [DB:pir2] [MP:1] >gp:[GI:g3128293] [LN:AF010496] [AC:AF010496]
[PN:hypothetical protein] [OR:Rhodobacter capsulatus] [DB:genpept-bct2]
[DE:Rhodobacter capsulatus strain SB1003, partial genome.] [LE:54291]
[RE:55613] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000991_10948587_c1_430	1938	5710	822	273	757	4.5e-75

Description

gp:[GI:g4160468] [LN:AF109909] [AC:AF109909] [PN:putative protein] [GN:ykoY]
[OR:Bacillus megaterium] [DB:genpept-bct2] [DE:Bacillus megaterium
polyhydroxyalkanoate gene cluster, complete sequence.] [NT:similar to toxic
anion resistance protein] [LE:277] [RE:1092] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000991_11210760_f2_261	1939	5711	162	53		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000991_11220301_c2_523	1940	5712	126	41	108	3.4e-06

Description

pir:[LN:QQSA8T] [AC:A04493] [PN:hypothetical protein B-189]
[OR:Staphylococcus aureus] [DB:pir1]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000991_1180328_c3_606	1941	5713	816	271	372	2.8e-34

Description

pir:[LN:H70003] [AC:H70003] [PN:probable prolyl aminopeptidase,
ytxM:cytosol aminopeptidase V:Pro-X aminopeptidase:proline
aminopeptidase:proline iminopeptidase] [GN:ytxM] [OR:Bacillus subtilis]
[EC:3.4.11.5] [DB:pir2] >gp:[GI:e1185954:g2635565] [LN:BSUB0016]
[AC:Z99119:AL009126] [GN:ytxM] [FN:unknown] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 16 of 21):
from 2997771to 3213410.] [NT:alternate gene name: ytfB; similar to prolyl]
[LE:151061] [RE:151885] [DI:complement] >gp:[GI:g2293147] [LN:AF008220]
[AC:AF008220] [PN:YtxM] [GN:ytxM] [OR:Bacillus subtilis] [DB:genpept-bct2]
[DE:Bacillus subtilis rrnB-dnaB genomic region.] [NT:similarity with
2-hydroxy-6-oxo-2,4-heptadienoate] [LE:28542] [RE:29366] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000991_12239817_c2_520	1942	5714	168	55		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000991_12681510_f3_365	1943	5715	825	274	702	3.0e-69

Description

pir:[LN:F69841] [AC:F69841] [PN:conserved hypothetical protein yitU]
 [GN:yitU] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e261990:g1620926]
 [LN:BS168NPRB] [AC:Z79580] [GN:putative orf] [FN:unknown] [OR:Bacillus
 subtilis] [DB:genpept-bct1] [DE:B.subtilis nprB gene.] [LE:4492] [RE:5304]
 [DI:complement] >gp:[GI:e1183116:g2633450] [LN:BSUB0006]
 [AC:Z99109:AL009126] [GN:yitU] [FN:unknown] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 6 of 21):
 from 999501 to1209940.] [NT:similar to hypothetical proteins] [LE:190463]
 [RE:191275] [DI:complement] >gp:[GI:e1173548:g2145415] [LN:BSY09476]
 [AC:Y09476] [PN:YitU] [OR:Bacillus subtilis] [DB:genpept-bct1]
 [DE:B.subtilis 54kb genomic DNA fragment.] [NT:putative ORF] [LE:47689]
 [RE:48501] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000991_12750290_c1_400	1944	5716	1122	373	1233	1.6e-125

Description

pir:[LN:B69669] [AC:B69669:S15233:D38447] [PN:oligopeptide transport
 ATP-binding protein oppD:sporulation initiation protein spo0KD]
 [GN:spo0KD:oppD] [CL:inner membrane protein malK:ATP-binding cassette
 homology] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1183166:g2633500]
 [LN:BSUB0007] [AC:Z99110:AL009126] [PN:oligopeptide ABC transporter
 (ATP-binding)] [GN:oppD] [FN:required for initiation of sporulation,]
 [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete
 genome (section 7 of 21): from 1194391to 1411140.] [NT:alternate gene name:
 spo0KD] [LE:28537] [RE:29613] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000991_13089052_f3_290	1945	5717	240	79	112	1.0e-06

Description

pir:[LN:A60998] [AC:A60998] [PN:replication protein REP] [OR:Staphylococcus
 aureus] [DB:pir2] >gp:[GI:g295834] [LN:SAPOX2000] [AC:X55798]
 [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:S.aureus plasmid poX2000.]
 [NT:ORF 154] [LE:587] [RE:1051] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000991_13829403_f1_46	1946	5718	129	42		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000991_13848387_f2_141	1947	5719	240	79	131	9.8e-09

Description

pir:[LN:S75993] [AC:S75993] [PN:hypothetical protein] [OR:Synechocystis sp.] [SR:PCC 6803, , PCC 6803] [SR:PCC 6803,] [DB:pir2]
>gp:[GI:d1011491:g1001353] [LN:SYCSLLH] [AC:D64006:AB001339]
[PN:hypothetical protein] [GN:clpP] [OR:Synechocystis sp.] [SR:Synechocystis sp. (strain:PCC6803) DNA] [DB:genpept-bct1] [DE:Synechocystis sp. PCC6803 complete genome, 25/27, 3138604-3270709.] [NT:ORF_ID:s110498] [LE:80076]
[RE:80528] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000991_1445930_f2_152	1948	5720	621	206	103	0.0023

Description

pir:[LN:A70417] [AC:A70417] [PN:hypothetical protein aq_1349] [GN:aq_1349] [OR:Aquifex aeolicus] [DB:pir2] >gp:[GI:g2983776] [LN:AE000736]
[AC:AE000736:AE000657] [PN:putative protein] [GN:aq_1349] [OR:Aquifex aeolicus] [DB:genpept-bct2] [DE:Aquifex aeolicus section 68 of 109 of the complete genome.] [LE:1950] [RE:2756] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000991_14460882_c1_443	1949	5721	1722	573	1304	4.9e-133

Description

gp:[GI:g1022726] [LN:SHU35635] [AC:U35635] [PN:unknown] [OR:Staphylococcus haemolyticus] [SR:Staphylococcus haemolyticus strain=Y176] [DB:genpept-bct1]
[DE:Staphylococcus haemolyticus IS1272 ORF1 and ORF2 genes, completedcs.] [NT:ORF1] [LE:1101] [RE:1922] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000991_14460887_f1_3	1950	5722	153	50	115	1.7e-06

Description

gp:[GI:g1022726] [LN:SHU35635] [AC:U35635] [PN:unknown] [OR:Staphylococcus haemolyticus] [SR:Staphylococcus haemolyticus strain=Y176] [DB:genpept-bct1]
[DE:Staphylococcus haemolyticus IS1272 ORF1 and ORF2 genes, completedcs.] [NT:ORF1] [LE:1101] [RE:1922] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000991_14484553_c2_467	1951	5723	1356	451	1726	9.3e-178

Description

sp:[LN:G6PA BACST] [AC:P13375] [GN:PGIA] [OR:BACILLUS STEAROTHERMOPHILUS]
[EC:5.3.1.9] [DE:ISOMERASE A] [SP:P13375] [DB:swissprot] >pir:[LN:NUBSSA]
[AC:S15936:S06196] [PN:glucose-6-phosphate isomerase, A:phosphoglucose
isomerase:phosphohexose isomerase] [CL:glucose-6-phosphate isomerase]
[OR:Bacillus stearothermophilus] [EC:5.3.1.9] [DB:pir1] >gp:[GI:g40046]
[LN:BSPGIA] [AC:X16639] [OR:Bacillus stearothermophilus] [DB:genpept-bct1]
[DE:Bacillus stearothermophilus pgIA gene for phosphoglucoisomeraseisoenzyme
A (EC 5.3.1.9).] [NT:phosphoglucose isomerase A (AA 1-449)] [SP:P13375]
[LE:95] [RE:1444] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000991_14648512_c3_585	1952	5724	126	41		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000991_14656432_c3_582	1953	5725	168	55	78	0.033

Description

gp:[GI:g3158514] [LN:CELT04D1] [AC:AF067617] [GN:T04D1.2] [OR:Caenorhabditis
elegans] [DB:genpept-inv1] [DE:Caenorhabditis elegans cosmid T04D1.]
[LE:10425:10567:11420:12480] [RE:10517:10646:11689:12789] [DI:directJoin]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000991_14884437_c1_437	1954	5726	165	54		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000991_15038450_c2_469	1955	5727	135	44		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000991_16683437_f1_5	1956	5728	1023	340	571	2.3e-55

Description

pir:[LN:A69863] [AC:A69863] [PN:conserved hypothetical protein ykrP]
[GN:ykrP] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1184942:g2633723]
[LN:BSUB0008] [AC:Z99111:AL009126] [GN:ykrP] [FN:unknown] [OR:Bacillus
subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 8
of 21): from 1394791to 1603020.] [NT:similar to hypothetical proteins]
[LE:22614] [RE:23636] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000991_16832562_f1_67	1957	5729	804	267	320	4.5e-36

Description

pir:[LN:H69843] [AC:H69843] [PN:hypothetical protein yjbH] [GN:yjbH]
[OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1183175:g2633509] [LN:BSUB0007]
[AC:Z99110:AL009126] [GN:yjbH] [FN:unknown] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 7 of 21):
from 1194391to 1411140.] [LE:38695] [RE:39522] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000991_187683_c1_417	1958	5730	228	75	256	1.3e-23

Description

sp:[LN:BIN3_STAAU] [AC:P20384] [GN:BIN3] [OR:STAPHYLOCOCCUS AUREUS]
[DE:POTENTIAL DNA-INVERTASE BIN3 (TRANSPOSON TN552)] [SP:P20384]
[DB:swissprot] >gp:[GI:g398182] [LN:SABINR3] [AC:X16298] [OR:Staphylococcus
aureus] [DB:genpept-bct1] [DE:Staphylococcus aureus plasmid pI9789 DNA with
binR and bin3 genes,derived from transposon TN552.] [NT:bin3 product]
[SP:P20384] [LE:1049] [RE:1657] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000991_195177_c2_521	1959	5731	141	46	127	2.6e-08

Description

pir:[LN:S42239] [AC:S42239] [PN:hypothetical protein 3] [OR:Staphylococcus
aureus] [DB:pir2] >gp:[GI:g501834] [LN:PNS1CG] [AC:M16217] [OR:Plasmid pNS1]
[SR:Plasmid pNS1 from Staphylococcus aureus, plasmid pTP5 DNA]
[DB:genpept-bct1] [DE:Plasmid pNS1 (from Staphylococcus aureus)
encodingtetracycline-resistance (tet), complete genome.] [NT:ORF C;
putative] [LE:1870] [RE:2409] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000991_19531626_f3_304	1960	5732	126	41		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000991_19547938_c2_498	1961	5733	372	123	224	7.4e-18

Description

sp:[LN:G6PD_LEUME] [AC:P11411] [GN:ZWF] [OR:LEUCONOSTOC MESENTEROIDES]
[EC:1.1.1.49] [DE:GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE, (G6PD)] [SP:P11411]
[DB:swissprot]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000991_19566553_c1_428	1962	5734	159	52		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000991_1960952_c2_473	1963	5735	906	301	575	8.7e-56

Description

pir:[LN:C69837] [AC:C69837] [PN:5-oxo-1,2,5-tricarboxilic-3-penten acid de
homolog yisK] [GN:yisK] [CL:2-hydroxyhepta-2,4-diene-1,7-dioate isomerase]
[OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1183077:g2633411] [LN:BSUB0006]
[AC:Z99109:AL009126] [GN:yisK] [FN:unknown] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 6 of 21):
from 999501 to1209940.] [NT:similar to 5-oxo-1,2,5-tricarboxilic-3-penten
acid] [LE:152216] [RE:153121] [DI:direct] >gp:[GI:e1173509:g2145376]
[LN:BSY09476] [AC:Y09476] [PN:YisK] [OR:Bacillus subtilis] [DB:genpept-bct1]
[DE:B.subtilis 54kb genomic DNA fragment.] [NT:putative - Homology with
oxo-tricarboxilic-pentene] [LE:9442] [RE:10347] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000991_19610442_f1_56	1964	5736	246	81	219	4.6e-18

Description

gp:[GI:d1045996:g5360820] [LN:D86934] [AC:D86934] [PN:transposase]
[OR:Staphylococcus aureus] [SR:Staphylococcus aureus (strain:N315) DNA,
clone_lib:library of N31] [DB:genpept] [DE:Staphylococcus aureus genes, mec
region, partial and complete cds.] [NT:ORF N026; putative] [LE:19527]
[RE:19751] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000991_19790902_c2_493	1965	5737	813	270	919	3.1e-92

Description

pir:[LN:F69844] [AC:F69844] [PN:conserved hypothetical protein yjbN]
 [GN:yjbN] [CL:conserved hypothetical protein HI0072] [OR:Bacillus subtilis]
 [DB:pir2] >gp:[GI:e1183181:g2633515] [LN:BSUB0007] [AC:Z99110:AL009126]
 [GN:yjbN] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus
 subtilis complete genome (section 7 of 21): from 1194391to 1411140.]
 [NT:similar to hypothetical proteins] [LE:42741] [RE:43541] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000991_20517062_c2_478	1966	5738	1002	333	961	1.1e-96

Description

pir:[LN:F69842] [AC:F69842] [PN:3-oxoacyl- acyl-carrier protein synthase
 homolog yjaX] [GN:yjaX] [CL:3-oxoacyl-[acyl-carrier-protein] synthase III]
 [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1183136:g2633470] [LN:BSUB0006]
 [AC:Z99109:AL009126] [GN:yjaX] [FN:unknown] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 6 of 21):
 from 999501 to1209940.] [NT:similar to 3-oxoacyl- acyl-carrier protein]
 [LE:208189] [RE:209127] [DI:direct] >gp:[GI:e1183153:g2633487] [LN:BSUB0007]
 [AC:Z99110:AL009126] [GN:yjaX] [FN:unknown] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 7 of 21):
 from 1194391to 1411140.] [NT:similar to 3-oxoacyl- acyl-carrier protein]
 [LE:13299] [RE:14237] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000991_20585302_f2_149	1967	5739	126	41		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000991_20739037_c1_452	1968	5740	426	141	690	5.7e-68

Description

gp:[GI:g2267243] [LN:SEU71377] [AC:U71377] [PN:putative transcriptional
 regulator AtlR] [OR:Staphylococcus epidermidis] [DB:genpept-bct1]
 [DE:Staphylococcus epidermidis autolysin AtlE and putativetranscriptional
 regulator AtlR genes, complete cds.] [LE:6867] [RE:7286] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000991_21753125_c2_481	1972	5744	1194	397	664	2.0e-79

Description

pir: [LN:S16649] [AC:S16649:S18271:E69618:I40001] [PN:dipeptide ABC transporter (permease): dciAC protein] [GN:dppC: dciAC] [CL:oligopeptide permease protein oppB] [OR:Bacillus subtilis] [DB:pir2]
 >gp: [GI:e1181495:g2632015] [LN:BSAJ2571] [AC:AJ002571] [PN:DppC] [GN:dppC] [FN:ABC-type dipeptide transport system] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis 168 56 kb DNA fragment between xlyA and ykoR.] [LE:14301] [RE:15263] [DI:direct] >gp: [GI:e1183314:g2633648] [LN:BSUB0007] [AC:Z99110:AL009126] [PN:dipeptide ABC transporter (permease)] [GN:dppC] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 7 of 21): from 1194391 to 1411140.] [NT:alternate gene name: dciAC] [LE:167250] [RE:168212] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000991_22272583_f3_291	1973	5745	123	40	86	0.0040

Description

gp: [GI:g4098413] [LN:LOU77495] [AC:U77495] [PN:putative integrase] [GN:int] [OR:Leuconostoc oenos bacteriophage 10MC] [DB:genpept-phg] [DE:Leuconostoc oenos bacteriophage 10MC putative integrase (int) gene, complete cds.] [NT:site-specific recombinase] [LE:119] [RE:1165] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000991_22456512_f3_286	1974	5746	147	48		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000991_22462787_c1_392	1975	5747	525	174	535	1.5e-51

Description

sp: [LN:LEPH_STAAU] [AC:P72364] [GN:SPSA] [OR:STAPHYLOCOCCUS AUREUS] [DE:INACTIVE SIGNAL PEPTIDASE IA] [SP:P72364] [DB:swissprot]
 >gp: [GI:g1595809] [LN:SAU65000] [AC:U65000] [PN:type-I signal peptidase SpsA] [GN:spsA] [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus type-I signal peptidase SpsA (spsA) gene, and type-I signal peptidase SpsB (spsB) gene, complete cds.] [NT:inactive signal peptidase homologue; protein lacks] [LE:40] [RE:564] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000991_22665887_c3_598	1976	5748	129	42	120	2.4e-07

Description

pir:[LN:D69838] [AC:D69838] [PN:conserved hypothetical protein yisU]
 [GN:yisU] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1183088:g2633422]
 [LN:BSUB0006] [AC:Z99109:AL009126] [GN:yisU] [FN:unknown] [OR:Bacillus
 subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 6
 of 21): from 999501 to1209940.] [NT:similar to hypothetical proteins]
 [LE:165981] [RE:166643] [DI:complement] >gp:[GI:e1173520:g2145387]
 [LN:BSY09476] [AC:Y09476] [PN:YisU] [OR:Bacillus subtilis] [DB:genpept-bct1]
 [DE:B.subtilis 54kb genomic DNA fragment.] [NT:putative] [LE:23207]
 [RE:23869] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000991_22703588_f2_137	1977	5749	954	317	803	6.0e-80

Description

sp:[LN:MENA_BACSU] [AC:P39582] [GN:MENA:IPA-6D] [OR:BACILLUS SUBTILIS]
 [EC:2.5.1.-] [DE:(DHNA-OCTAPRENYLTRANSFERASE)] [SP:P39582] [DB:swissprot]
 >pir:[LN:S39661] [AC:S39661:B70050] [PN:menaquinone biosynthesis protein
 homolog ywaB:protein ipa-6d] [GN:ywaB] [CL:quinone biosynthesis homolog
 ywaB] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:g413930] [LN:BSGENR]
 [AC:X73124] [GN:ipa-6d] [OR:Bacillus subtilis] [DB:genpept-bct1]
 [DE:B.subtilis genomic region (325 to 333).] [SP:P39582] [LE:5904] [RE:6839]
 [DI:direct] >gp:[GI:e1186348:g2636384] [LN:BSUB0020] [AC:Z99123:AL009126]
 [GN:ywaB] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus
 subtilis complete genome (section 20 of 21): from 3798401to 4010550.]
 [NT:alternate gene name: ipa-6d; similar to quinone] [SP:P39582] [LE:151120]
 [RE:152055] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000991_23438827_c3_566	1978	5750	129	42		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000991_23535910_c1_391	1979	5751	603	200	499	9.8e-48

Description

gp:[GI:g4185300] [LN:AF089862] [AC:AF089862] [PN:unknown] [OR:Staphylococcus carnosus] [DB:genpept-bct2] [DE:Staphylococcus carnosus type-I signal peptidase SipA (sipA) and type-I signal peptidase SipB (sipB) genes, complete cds; and unknown gene.] [NT:Orf1; similar to Bacillus subtilis yhjE] [LE:271] [RE:948] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000991_23593932_f2_166	1980	5752	126	41		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000991_23611563_c3_600	1981	5753	141	46		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000991_23625637_c2_526	1982	5754	183	60		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000991_23634641_c1_398	1983	5755	1248	415	1475	3.7e-151

Description

pir:[LN:G69842] [AC:G69842] [PN:3-oxoacyl-[acyl-carrier-protein] synthase,] [GN:yjaY] [CL:3-oxoacyl-[acyl-carrier-protein] synthase I: 3-oxoacyl-[acyl-carrier-protein] synthase I homology] [OR:Bacillus subtilis] [EC:2.3.1.41] [DB:pir2] >gp:[GI:e1183137:g2633471] [LN:BSUB0006] [AC:Z99109:AL009126] [GN:yjaY] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 6 of 21): from 999501 to 1209940.] [NT:similar to 3-oxoacyl-acyl-carrier protein] [LE:209150] [RE:210391] [DI:direct] >gp:[GI:e1183154:g2633488] [LN:BSUB0007] [AC:Z99110:AL009126] [GN:yjaY] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 7 of 21): from 1194391 to 1411140.] [NT:similar to 3-oxoacyl-acyl-carrier protein] [LE:14260] [RE:15501] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000991_23678800_c3_561	1984	5756	399	132	395	1.0e-36

Description

pir:[LN:H69841] [AC:H69841] [PN:conserved hypothetical protein yitW] [GN:yitW] [CL:conserved hypothetical protein MJ1129] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e261991:g1620928] [LN:BS168NPRB] [AC:Z79580] [GN:putative orf] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis nprB gene.] [LE:6256] [RE:6564] [DI:direct] >gp:[GI:e1183118:g2633452] [LN:BSUB0006] [AC:Z99109:AL009126] [GN:yitW] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.] [NT:similar to hypothetical proteins] [LE:192227] [RE:192535] [DI:direct] >gp:[GI:e1173550:g2145417] [LN:BSY09476] [AC:Y09476] [PN:YitW] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis 54kb genomic DNA fragment.] [NT:putative orf] [LE:49453] [RE:49761] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000991_2392300_f2_176	1985	5757	138	45		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000991_24022191_f2_232	1986	5758	222	73	97	3.9e-05

Description

pir:[LN:G69854] [AC:G69854] [PN:hypothetical protein yjzD] [GN:yjzD] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1183130:g2633464] [LN:BSUB0006] [AC:Z99109:AL009126] [GN:yjzD] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.] [LE:204697] [RE:204882] [DI:complement] >gp:[GI:e1183147:g2633481] [LN:BSUB0007] [AC:Z99110:AL009126] [GN:yjzD] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.] [LE:9807] [RE:9992] [DI:complement] >gp:[GI:d1023798:g2564027] [LN:D86376] [AC:D86376] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:CU741) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis ArgF and med genes, partial and complete cds.] [NT:unnamed protein product] [LE:1027] [RE:1212] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000991_24024142_c2_496	1987	5759	315	104	93	0.00010

Description

gp:[GI:g2654481] [LN:BFU89914] [AC:U89914] [PN:hypothetical 10.1 kDa protein] [OR:Bacillus firmus] [DB:genpept-bct2] [DE:Bacillus firmus hypothetical 34.0 kDa protein, hypothetical 8.9 kDa protein, hypothetical 10.1 kDa protein, hypothetical 21.0 kDa protein, putative thiosulfate sulfurtransferase, hypothetical 16.1kDa transcriptional regulator and hypothetical 18.2 kDa proteingenes, complete cds, and Na+/H+ antiporter homolog gene, partialcds.] [NT:orf4] [LE:1601] [RE:1882] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000991_24070137_c3_602	1988	5760	150	49		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000991_24105342_c1_448	1989	5761	831	276	1242	1.8e-126

Description

pir:[LN:F69656] [AC:F69656:A42715:S27512] [PN:naphthoate synthase, menB:DHNA synthase: dihydroxynaphthoate synthase: dihydroxynaphthoic acid synthetase menB:menaquinone biosynthesis enzyme/enoyl CoA hydratase homolog] [GN:menB] [CL:naphthoate synthase:enoyl-CoA hydratase homolog] [OR:Bacillus subtilis] [EC:4.1.3.36] [DB:pir2] >gp:[GI:e1185953:g2635564] [LN:BSUB0016] [AC:Z99119:AL009126] [PN:dihydroxynaphthoic acid synthetase] [GN:menB] [FN:menaquinone biosynthesis] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:4.1.3.36] [DE:Bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.] [LE:150211] [RE:151026] [DI:complement] >gp:[GI:g2293148] [LN:AF008220] [AC:AF008220] [PN:dihydroxynaphthoate synthase] [GN:menB] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis rrnB-dnaB genomic region.] [LE:29401] [RE:30216] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000991_24225010_c2_536	1990	5762	168	55		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000991_24270451_c1_432	1991	5763	135	44		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000991_24409428_c1_438	1992	5764	258	85	357	1.1e-32

Description

gp:[GI:g1731452] [LN:SAU38429] [AC:U38429] [PN:recombination protein]
[GN:pre] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:Staphylococcus
aureus chloramphenicol resistance plasmid pKH7,complete sequence.] [LE:2074]
[RE:3285] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000991_24412517_c3_581	1993	5765	393	130	213	1.2e-16

Description

sp:[LN:G6PD_BACSU] [AC:P54547] [GN:ZWF] [OR:BACILLUS SUBTILIS] [EC:1.1.1.49]
[DE:PROTEIN 11] (VEG11)] [SP:P54547] [DB:swissprot] >pir:[LN:B69964]
[AC:B69964] [PN:probable glucose-6-phosphate 1-dehydrogenase, yqjJ]
[GN:yqjJ] [CL:glucose-6-phosphate dehydrogenase] [OR:Bacillus subtilis]
[EC:1.1.1.49] [DB:pir2] >gp:[GI:d1013296:g1303961] [LN:BACJH642]
[AC:D84432:D82370] [PN:YqjJ] [OR:Bacillus subtilis] [SR:Bacillus subtilis
(strain:JH642(trpC2 PheA1)) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis
DNA, 283 Kb region containing skin element.] [LE:239025] [RE:240494]
[DI:complement] >gp:[GI:e1185654:g2634820] [LN:BSUB0013]
[AC:Z99116:AL009126] [GN:yqjJ] [FN:unknown] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 13 of 21):
from 2395261to 2613730.] [NT:similar to glucose-6-phosphate 1-dehydrogenase]
[SP:P54547] [LE:83125] [RE:84594] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000991_24415632_c1_393	1994	5766	579	192	827	1.7e-82

Description

sp:[LN:LEP_STAAU] [AC:P72365] [GN:SPSB] [OR:STAPHYLOCOCCUS AUREUS]
[EC:3.4.21.89] [DE:SIGNAL PEPTIDASE IB, (SPASE IB) (LEADER PEPTIDASE IB)]
[SP:P72365] [DB:swissprot] >gp:[GI:g1595810] [LN:SAU65000] [AC:U65000]
[PN:type-I signal peptidase SpsB] [GN:spsB] [OR:Staphylococcus aureus]
[DB:genpept-bct2] [DE:Staphylococcus aureus type-I signal peptidase SpsA
(spsA) gene, andtype-I signal peptidase SpsB (spsB) gene, complete cds.]
[NT:signal peptidase, leader peptidase, serine] [LE:580] [RE:1155]
[DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000991_24416702_f2_125	1995	5767	4008	1335	7001	0.0

Description

gp:[GI:g2267242] [LN:SEU71377] [AC:U71377] [PN:autolysin AtlE]
 [OR:Staphylococcus epidermidis] [DB:genpept-bct1] [DE:Staphylococcus
 epidermidis autolysin AtlE and putativetranscriptional regulator AtlR genes,
 complete cds.] [NT:primary attachment to a polystyrene surface] [LE:2620]
 [RE:6627] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000991_24428543_f3_297	1996	5768	174	57	72	0.017

Description

gp:[GI:g153715] [LN:STRMLIKEE] [AC:L05021] [PN:M-like protein]
 [OR:Streptococcus pyogenes] [SR:Streptococcus pyogenes DNA]
 [DB:genpept-bct1] [DE:Streptococcus pyogenes M-like protein gene, partial
 cds.] [LE:<1] [RE:>243] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000991_24475252_f3_289	1997	5769	159	52		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000991_24646886_c3_594	1998	5770	1557	518	296	2.0e-23

Description

pir:[LN:B71973] [AC:B71973] [PN:2',3'-cyclic-nucleotide
 2'-phosphodiesterase] [GN:cpdB] [CL:2',3'-cyclic-nucleotide
 2'-phosphodiesterase: 2',3'-cyclic-nucleotide 2'-phosphodiesterase
 homology:phosphoesterase core homology] [OR:Helicobacter pylori] [SR:strain
 J99, , strain J99] [SR:strain J99,] [DB:pir2] >gp:[GI:g4154615]
 [LN:AE001449] [AC:AE001449:AE001439] [PN:2',3'-CYCLIC-NUCLEOTIDE
 2'-PHOSPHODIESTERASE] [GN:cpdB] [OR:Helicobacter pylori J99]
 [DB:genpept-bct2] [DE:Helicobacter pylori, strain J99 section 10 of 132 of
 the completegenome.] [NT:similar to H. pylori 26695 gene HP0104] [LE:139]
 [RE:1884] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000991_24648412_c1_406	1999	5771	642	213	683	3.1e-67

Description

pir:[LN:E69844] [AC:E69844] [PN:GTP pyrophosphokinase homolog yjbM]
 [GN:yjbM] [CL:GTP pyrophosphokinase related protein] [OR:Bacillus subtilis]
 [DB:pir2] >gp:[GI:e1183180:g2633514] [LN:BSUB0007] [AC:Z99110:AL009126]
 [GN:yjbM] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus
 subtilis complete genome (section 7 of 21): from 1194391to 1411140.]
 [NT:similar to GTP pyrophosphokinase] [LE:42087] [RE:42722] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000991_24745437_c3_539	2000	5772	1263	420	1659	1.2e-170

Description

sp:[LN:YPCA_BACSU] [AC:P50735] [GN:YPCA] [OR:BACILLUS SUBTILIS] [EC:1.4.1.-]
 [DE:(EC 1.4.1.-)] [SP:P50735] [DB:swissprot] >pir:[LN:G69933] [AC:G69933]
 [PN:glutamate dehydrogenase homolog ypcA] [GN:ypcA] [CL:glutamate
 dehydrogenase (NAD(P)+)] [OR:Bacillus subtilis] [DB:pir2]
 >gp:[GI:e1183741:g2634714] [LN:BSUB0012] [AC:Z99115:AL009126] [GN:ypcA]
 [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
 complete genome (section 12 of 21): from 2195541to 2409220.] [NT:similar to
 glutamate dehydrogenase] [SP:P50735] [LE:205764] [RE:207044] [DI:complement]
 >gp:[GI:e1185565:g2634731] [LN:BSUB0013] [AC:Z99116:AL009126] [GN:ypcA]
 [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
 complete genome (section 13 of 21): from 2395261to 2613730.] [NT:similar to
 glutamate dehydrogenase] [SP:P50735] [LE:6044] [RE:7324] [DI:complement]
 >gp:[GI:g1146206] [LN:BACSERA] [AC:L47648] [PN:glutamate dehydrogenase]
 [GN:ypcA] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis
 phosphoglycerate dehydrogenase (serA), ypaA,ferredoxin (fer), ypbB, recS,
 ypbD, ypbE, ypbF, ypbG, ypbH,glutamate dehydrogenase (ypcA), ypdA, ypdB,
 ypdC, spore cortexlytic enzyme (sleB), ypeB, ypfA, ypfB, cytidine
 monophosphatekinase (cmk), ypfD, ypgA, yphA, yphB, yphC, NAD+
 dependentglycerol-3-phosphate dehydrogenase (glyc), yphE and yphF
 genes,complete cds.] [NT:similar to Clostridium difficile glutamate]
 [LE:9353] [RE:10633] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000991_24804677_c3_597	2001	5773	366	121	117	1.5e-06

Description

gp:[GI:g2541936] [LN:PSU27310] [AC:U27310] [PN:unknown] [OR:Pseudomonas
 syringae] [DB:genpept-bct2] [DE:Pseudomonas syringae phaseolotoxin gene
 cluster, complete sequence.] [NT:ORF6; similar to Pseudomonas syringae fatty
 acid] [LE:5079] [RE:6062] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000991_25392826_f2_175	2002	5774	1146	381	557	7.0e-54

Description

pir:[LN:G70007] [AC:G70007] [PN:conserved hypothetical protein yueF]
 [GN:yueF] [CL:Bacillus subtilis conserved hypothetical protein yueF]
 [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1184257:g2635675] [LN:BSUB0017]
 [AC:Z99120:AL009126] [GN:yueF] [FN:unknown] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 17 of 21):
 from 3197001to 3414420.] [NT:similar to hypothetical proteins] [LE:64687]
 [RE:65796] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000991_25429512_c3_593	2003	5775	1392	463	1130	1.3e-114

Description

pir:[LN:H69862] [AC:H69862] [PN:Na+-transporting ATP synthase homolog ykrM]
 [GN:ykrM] [CL:Na+-ATP synthase chain J] [OR:Bacillus subtilis] [DB:pir2]
 >gp:[GI:e1184940:g2633721] [LN:BSUB0008] [AC:Z99111:AL009126] [GN:ykrM]
 [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
 complete genome (section 8 of 21): from 1394791to 1603020.] [NT:similar to
 Na+-transporting ATP synthase] [LE:20743] [RE:22092] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000991_25430316_c2_522	2004	5776	171	56	171	5.6e-13

Description

pir:[LN:QQSA8T] [AC:A04493] [PN:hypothetical protein B-189]
 [OR:Staphylococcus aureus] [DB:pir1]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000991_26178400_c3_542	2005	5777	186	61	71	0.042

Description

sp:[LN:AOPP_HUMAN] [AC:P30044] [OR:HOMO SAPIENS] [SR:,HUMAN] [DE:71B)]
 [SP:P30044] [DB:swissprot]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000991_26212787_f3_335	2006	5778	612	203	308	1.7e-27

Description

pir:[LN:C69844] [AC:C69844] [PN:hypothetical protein yjbK] [GN:yjbK]
[OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1183178:g2633512] [LN:BSUB0007]
[AC:Z99110:AL009126] [GN:yjbK] [FN:unknown] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 7 of 21):
from 1194391to 1411140.] [LE:40993] [RE:41565] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000991_26377340_c2_488	2007	5779	999	332	208	4.6e-15

Description

gp:[GI:e257629:g1771202] [LN:LLVSPFEP] [AC:X99710] [PN:transcription
factor] [OR:Lactococcus lactis] [DB:genpept-bct1] [DE:L.lactis ORF, genes
homologous to vsf-1 and pepF2 and gene encodingprotein homologous to
methyltransferase.] [NT:weak homology with vsf-1 gene (X73635)] [LE:934]
[RE:1917] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000991_26564012_c2_477	2008	5780	2616	871	2649	1.5e-275

Description

gp:[GI:g3150046] [LN:AF016634] [AC:AF016634] [PN:ClpB chaperone homolog]
[GN:clpB] [OR:Lactococcus lactis subsp. cremoris] [DB:genpept-bct2]
[DE:Lactococcus lactis cremoris ClpB chaperone homolog (clpB)
andphosphoribosylformylglycinamide cyclo-ligase (pur5) genes, completedcds;
and phosphoribosylglycinamide formyltransferase (pur3) gene,partial cds.]
[LE:183] [RE:2786] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000991_26567557_c3_558	2009	5781	138	45		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000991_26604662_c2_495	2010	5782	630	209		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000991_26775637_c1_447	2011	5783	1389	462	599	2.5e-58

Description

sp:[LN:MENF_BACSU] [AC:P23973:P23972] [GN:MENF:ICSM] [OR:BACILLUS SUBTILIS] [EC:5.4.99.6] [DE:MENAQUINONE-SPECIFIC ISOCHORISMATE SYNTHASE,] [SP:P23973:P23972] [DB:swissprot] >pir:[LN:A69657] [AC:A69657:S27507:S27508:I39883] [PN:probable isochorismate synthase, menaquinone-specific menF] [GN:menF] [CL:isochorismate synthase] [OR:Bacillus subtilis] [EC:5.4.99.6] [DB:pir2] >gp:[GI:e1185956:g2635567] [LN:BSUB0016] [AC:Z99119:AL009126] [PN:menaquinone-specific isochorismate synthase] [GN:menF] [FN:menaquinone biosynthesis] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:5.4.99.6] [DE:Bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.] [NT:alternate gene name: icsM, entC] [SP:P23973] [LE:153612] [RE:155027] [DI:complement] >gp:[GI:g2293145] [LN:AF008220] [AC:AF008220] [PN:isochorismate synthase] [GN:menF] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis rrnB-dnaB genomic region.] [LE:25400] [RE:26815] [DI:direct] >gp:[GI:g1185288] [LN:BACMENAQOP] [AC:M74538:M74182:M74183] [PN:isochorismate synthase] [GN:menF] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain RB1) DNA] [DB:genpept-bct2] [DE:Bacillus subtilis menaquinone operon: menF, menD, menB and menEgenes, complete cds.] [NT:based on similarity to E. coli EntC, A. hydrophila] [LE:143] [RE:1558] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000991_2848308_c3_607	2012	5784	135	44		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000991_289802_f2_227	2013	5785	189	62	89	0.0019

Description

pir:[LN:F22845] [AC:F22845] [PN:hypothetical protein 6] [OR:mitochondrion Trypanosoma brucei] [DB:pir2]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000991_2922260_c3_574	2014	5786	384	127	174	2.7e-13

Description

pir:[LN:D69844] [AC:D69844] [PN:hypothetical protein yjbL] [GN:yjbL]
[OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1183179:g2633513] [LN:BSUB0007]
[AC:Z99110:AL009126] [GN:yjbL] [FN:unknown] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 7 of 21):
from 1194391to 1411140.] [LE:41690] [RE:42058] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000991_29335888_c3_562	2015	5787	135	44		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000991_29570302_f1_24	2016	5788	132	43		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000991_31281253_c3_538	2017	5789	1221	406	1513	3.5e-155

Description

sp:[LN:OAT_BACSU] [AC:P38021] [GN:ROCD] [OR:BACILLUS SUBTILIS] [EC:2.6.1.13]
[DE:AMINOTRANSFERASE]] [SP:P38021] [DB:swissprot] >pir:[LN:S55793]
[AC:S55793:S49267:B53370:H69693] [PN:ornithine--oxo-acid transaminase,
rocD:ornithine aminotransferase:ornithine--oxo-acid aminotransferase]
[GN:rocD] [CL:ornithine--oxo-acid aminotransferase] [OR:Bacillus subtilis]
[EC:2.6.1.13] [DB:pir2] >gp:[GI:d1011955:g1064807] [LN:BACGNTZA] [AC:D78193]
[PN:orthinine aminotransferase] [GN:rocD] [OR:Bacillus subtilis]
[SR:Bacillus subtilis (strain:168) DNA] [DB:genpept-bct1] [DE:Bacillus
subtilis 36kb sequence between gntZ and trnY genesencoding 34 ORFs.]
[LE:25845] [RE:27050] [DI:complement] >gp:[GI:g550311] [LN:BSROCDEF]
[AC:X81802] [PN:ornithine< aminotransferase] [GN:rocD] [OR:Bacillus
subtilis] [DB:genpept-bct1] [DE:B.subtilis rocD, rocE and rocF genes.]
[SP:P38021] [LE:241] [RE:1446] [DI:direct] >gp:[GI:e1184760:g2636581]
[LN:BSUB0021] [AC:Z99124:AL009126] [PN:ornithine aminotransferase] [GN:rocD]
[FN:arginine and ornithine utilization] [OR:Bacillus subtilis]
[DB:genpept-bct1] [EC:2.6.1.13] [DE:Bacillus subtilis complete genome
(section 21 of 21): from 3999281to 4214814.] [SP:P38021] [LE:144229]
[RE:145434] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000991_31300807_c1_436	2018	5790	156	51		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000991_31525260_c3_579	2019	5791	135	44		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000991_32062875_c1_439	2020	5792	291	96	333	3.8e-30

Description

gp:[GI:g1731452] [LN:SAU38429] [AC:U38429] [PN:recombination protein]
[GN:pre] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:Staphylococcus
aureus chloramphenicol resistance plasmid pKH7,complete sequence.] [LE:2074]
[RE:3285] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000991_32067937_f2_247	2021	5793	1365	454	1790	1.5e-184

Description

gp:[GI:g2792490] [LN:AF041467] [AC:AF041467] [PN:coenzyme A disulfide
reductase] [FN:pyridine nucleotide disulfide oxidoreductase]
[OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus
coenzyme A disulfide reductase gene, completecds.] [NT:CoADR; flavoenzyme
(FAD); single catalytic cysteine] [LE:66] [RE:1382] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000991_32132183_c1_455	2022	5794	132	43		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000991_32457312_c2_501	2023	5795	495	164	233	1.5e-19

Description

gp:[GI:e303881:g1850807] [LN:CPCPEAA] [AC:X71844] [PN:putative transposase]
[OR:Clostridium perfringens] [DB:genpept-bct1] [DE:C.perfringens uapC, cpe,
and nadC genes.] [LE:2477] [RE:2932] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000991_32635937_c1_429	2024	5796	1503	500	2239	4.1e-232

Description

gp:[GI:e1301684:g3256223] [LN:SAY14370] [AC:Y14370]
[PN:UDP-N-acetylmuramyl-tripeptide synthetase] [GN:murE] [OR:Staphylococcus
aureus] [DB:genpept-bct1] [DE:Staphylococcus aureus RF3, murE, ypfP genes.]
[LE:3244] [RE:4722] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000991_33364067_c1_431	2025	5797	1782	593	542	2.7e-52

Description

gp:[GI:g2109443] [LN:SPDNAARG] [AC:AF000658] [PN:putative serine protease]
[GN:sphtra] [OR:Streptococcus pneumoniae] [DB:genpept-bct2]
[DE:Streptococcus pneumoniae R801 tRNA-Arg gene, partial sequence,
and putative serine protease (sphtra), SPspoJ (spspoJ), initiator protein
(spdnaa) and beta subunit of DNA polymerase III (spdnan) genes, complete
cds.] [NT:SPHtra] [LE:765] [RE:1958] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000991_3371067_c2_482	2026	5798	954	317	1033	2.5e-104

Description

pir:[LN:E38447] [AC:E38447:S15234:C69669] [PN:oligopeptide transport
ATP-binding protein oppF:sporulation initiation protein spo0KE]
[GN:spo0KE:oppF] [CL:inner membrane protein malK:ATP-binding cassette
homology] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:g143608] [LN:BACSP00K]
[AC:M57689] [PN:sporulation protein] [GN:spo0KE] [OR:Bacillus subtilis]
[SR:B.subtilis (strain JH642) DNA, clones pDR20/21, pJL2/3 and pJL7]
[DB:genpept-bct1] [DE:Bacillus subtilis spo0K operon.] [LE:5152] [RE:6078]
[DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000991_33710968_f2_124	2027	5799	453	150	742	1.7e-73

Description

gp:[GI:g2267241] [LN:SEU71377] [AC:U71377] [OR:Staphylococcus epidermidis]
[DB:genpept-bct1] [DE:Staphylococcus epidermidis autolysin AtlE and
putativetranscriptional regulator AtlR genes, complete cds.] [NT:ORF3]
[LE:1957] [RE:2379] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000991_3394540_f2_138	2028	5800	312	103		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000991_34006561_f3_312	2029	5801	150	49		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000991_34062930_c1_440	2030	5802	273	90	290	1.4e-25

Description

sp:[LN:PRE3_STAAU] [AC:P03864] [OR:STAPHYLOCOCCUS AUREUS] [DE:PLASMID
RECOMBINATION ENZYME (MOBILIZATION PROTEIN)] [SP:P03864] [DB:swissprot]
>gp:[GI:g151683] [LN:PT1CG] [AC:J01764:J01765] [OR:Plasmid pT181]
[SR:Plasmid pT181 DNA from Staphylococcus aureus] [DB:genpept-bct1]
[DE:Plasmid pT181, complete genome.] [NT:Pre protein (plasmid
recombination)] [LE:2521] [RE:3762] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000991_34073552_c2_509	2031	5803	1545	514	2291	1.3e-237

Description

gp:[GI:e1301683:g3256222] [LN:SAY14370] [AC:Y14370] [PN:peptide chain
release factor 3] [GN:RF3] [OR:Staphylococcus aureus] [DB:genpept-bct1]
[DE:Staphylococcus aureus RF3, murE, ypfP genes.] [LE:1435] [RE:3000]
[DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000991_34163562_f3_322	2032	5804	486	161	329	1.0e-29

Description

pir:[LN:D69583] [AC:D69583] [PN:alcohol dehydrogenase, adhB] [GN:adhB]
[CL:alcohol dehydrogenase:long-chain alcohol dehydrogenase homology]
[OR:Bacillus subtilis] [EC:1.1.1.1] [DB:pir2] >gp:[GI:e209890:g2108273]
[LN:BS233DEG] [AC:X92868:X79978] [PN:NAD alcohol dehydrogenase] [GN:adhB]
[OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis 23.9kb fragment from
map position 233 degrees on thechromosome.] [LE:13725] [RE:14861]
[DI:complement] >gp:[GI:e1183926:g2635142] [LN:BSUB0014]
[AC:Z99117:AL009126] [PN:alcohol dehydrogenase] [GN:adhB] [OR:Bacillus
subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section
14 of 21): from 2599451to 2812870.] [LE:153270] [RE:154406] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000991_34179031_f2_122	2033	5805	135	44		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000991_34398505_f3_354	2034	5806	222	73		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000991_34407888_c3_572	2035	5807	729	242	288	1.9e-37

Description

gp:[GI:g2952027] [LN:BFU88888] [AC:U88888] [PN:MecA homolog] [GN:mecA]
[OR:Bacillus firmus] [DB:genpept-bct2] [DE:Bacillus firmus MecA homolog
(mecA) and cardiolipin synthase (cls)genes, complete cds.] [LE:349]
[RE:1002] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000991_35158177_c1_408	2036	5808	1407	468	903	1.5e-90

Description

gp:[GI:d1039121:g4514345] [LN:AB013374] [AC:AB013374] [PN:Ykok] [GN:ykok]
[OR:Bacillus halodurans] [SR:Bacillus halodurans (strain:C-125) DNA]
[DB:genpept-bct1] [DE:Bacillus halodurans C-125 mamX, yjdA, ykoK and yvfK
genes, partialand complete cds.] [LE:1793] [RE:3142] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000991_35937827_c2_505	2037	5809	510	169	343	3.3e-31

Description

pir:[LN:G69846] [AC:G69846] [PN:hypothetical protein yjcG] [GN:yjcG]
 [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1183205:g2633539] [LN:BSUB0007]
 [AC:Z99110:AL009126] [GN:yjcG] [FN:unknown] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 7 of 21):
 from 1194391to 1411140.] [LE:61943] [RE:62458] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000991_36128387_c3_621	2038	5810	165	55		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000991_36134717_c1_401	2039	5811	1647	548	889	4.6e-89

Description

pir:[LN:A53310] [AC:A53310] [PN:pheromone CAD1 binding protein
 precursor:TraC] [GN:traC] [CL:dipeptide transport protein] [OR:Enterococcus
 faecalis] [DB:pir2] >gp:[GI:g388269] [LN:AD1TRAC] [AC:L19532] [GN:traC]
 [OR:Plasmid pAD1] [SR:Plasmid pAD1 DNA] [DB:genpept-bct1] [DE:Plasmid pAD1
 (from Enterococcus faecalis strain: DS16) hemolysinbacteriocin (traC) gene,
 complete cds, traA and traB genes, 3' end.] [LE:166] [RE:1797] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000991_36229625_f3_295	2040	5812	204	67	195	1.6e-15

Description

pir:[LN:B69869] [AC:B69869] [PN:hypothetical protein ykvS] [GN:ykvS]
 [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1184971:g2633752] [LN:BSUB0008]
 [AC:Z99111:AL009126] [GN:ykvS] [FN:unknown] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 8 of 21):
 from 1394791to 1603020.] [LE:52338] [RE:52769] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000991_36611062_c3_557	2041	5813	420	139	174	2.7e-13

Description

pir:[LN:D69837] [AC:D69837] [PN:hypothetical protein yisL] [GN:yisL]
 [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1183078:g2633412] [LN:BSUB0006]
 [AC:Z99109:AL009126] [GN:yisL] [FN:unknown] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 6 of 21):
 from 999501 to1209940.] [LE:153237] [RE:153593] [DI:direct]
 >gp:[GI:e1173510:g2145377] [LN:BSY09476] [AC:Y09476] [PN:YisL] [OR:Bacillus
 subtilis] [DB:genpept-bct1] [DE:B.subtilis 54kb genomic DNA fragment.]
 [NT:putative] [LE:10463] [RE:10819] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000991_37777_c1_434	2042	5814	168	55		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000991_3954718_c1_394	2043	5815	3489	1162	1331	6.7e-136

Description

sp:[LN:ADDB_BACSU] [AC:P23477] [GN:ADDB] [OR:BACILLUS SUBTILIS]
 [DE:ATP-DEPENDENT NUCLEASE SUBUNIT B] [SP:P23477] [DB:swissprot]
 >pir:[LN:A39432] [AC:A39432:S61272:A69583] [PN:ATP-dependent
 deoxyribonuclease chain B addB:ATP-dependent exonuclease synthesis protein
 AddB] [GN:addB] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:g142439]
 [LN:BACADDAA] [AC:M63489] [PN:ATP-dependent nuclease] [GN:addA] [OR:Bacillus
 subtilis] [SR:B.subtilis DNA] [DB:genpept-bct1] [DE:Bacillus subtilis
 ATP-dependent nuclease (addA) and (addB), andopen reading frame 3, partial
 cds.] [LE:502] [RE:4002] [DI:direct] >gp:[GI:e1183064:g2633398]
 [LN:BSUB0006] [AC:Z99109:AL009126] [PN:ATP-dependent deoxyribonuclease
 (subunit B)] [GN:addB] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus
 subtilis complete genome (section 6 of 21): from 999501 to1209940.]
 [SP:P23477] [LE:136293] [RE:139793] [DI:direct] >gp:[GI:e1364880:g2226191]
 [LN:BSY14081] [AC:Y14081] [PN:ATP-dependent nuclease] [GN:addB] [OR:Bacillus
 subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis chromosomal DNA, region 92
 degrees: regionbetween comK and addAB.] [NT:TTG start; see ref [3]; In EMBL
 entry M63489 this] [LE:18588] [RE:22088] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000991_4019193_c1_418	2044	5816	783	260	749	3.2e-74

Description

pir:[LN:G69845] [AC:G69845] [PN:enoyl-[acyl-carrier-protein] reductase (NADH), yjbW] [GN:yjbW] [CL:enoyl-[acyl-carrier-protein] reductase (NADH): short-chain alcohol dehydrogenase homology] [OR:Bacillus subtilis] [EC:1.3.1.9] [DB:pir2] >gp:[GI:e1183192:g2633526] [LN:BSUB0007] [AC:Z99110:AL009126] [GN:yjbW] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.] [NT:similar to enoyl- acyl-carrier protein reductase] [LE:52836] [RE:53645] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000991_4070151_c2_472	2045	5817	447	148	165	2.4e-12

Description

gp:[GI:e1173495:g2145362] [LN:BSY09476] [AC:Y09476] [PN:AddA] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis 54kb genomic DNA fragment.] [SP:P23478] [LE:<1] [RE:702] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000991_4080443_c1_409	2046	5818	1854	617	1574	1.2e-161

Description

pir:[LN:A69845] [AC:A69845] [PN:Na+/H+ antiporter homolog yjbQ] [GN:yjbQ] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1183184:g2633518] [LN:BSUB0007] [AC:Z99110:AL009126] [GN:yjbQ] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.] [NT:similar to Na+/H+ antiporter] [LE:45437] [RE:47281] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000991_4088962_c2_508	2047	5819	279	92	76	0.0065

Description

pir:[LN:A70008] [AC:A70008] [PN:hypothetical protein yueH] [GN:yueH] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1184255:g2635673] [LN:BSUB0017] [AC:Z99120:AL009126] [GN:yueH] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.] [LE:64085] [RE:64333] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000991_4094433_f1_72	2048	5820	999	332	1184	2.5e-120

Description

sp:[LN:SYW_BACSU] [AC:P21656] [GN:TRPS] [OR:BACILLUS SUBTILIS] [EC:6.1.1.2]
[DE:(TRPRS)] [SP:P21656] [DB:swissprot] >pir:[LN:YWBS]
[AC:JT0481:A32452:E69726] [PN:tryptophan--tRNA ligase,:tryptophanyl-tRNA
synthetase] [GN:trpS] [CL:tryptophan--tRNA ligase] [OR:Bacillus subtilis]
[EC:6.1.1.2] [DB:pir1] >gp:[GI:g143786] [LN:BACTRPSA] [AC:M24068]
[OR:Bacillus subtilis] [SR:B.subtilis (strain QB928) DNA, clone pTSQ2]
[DB:genpept-bct1] [DE:B.subtilis trpS gene encoding tryptophanyl-tRNA
synthetase,complete cds.] [NT:tryptophanyl-tRNA synthetase (EC 6.1.1.2)]
[LE:171] [RE:1163] [DI:direct] >gp:[GI:e1183162:g2633496] [LN:BSUB0007]
[AC:Z99110:AL009126] [PN:tryptophanyl-tRNA synthetase] [GN:trpS]
[OR:Bacillus subtilis] [DB:genpept-bct1] [EC:6.1.1.2] [DE:Bacillus subtilis
complete genome (section 7 of 21): from 1194391to 1411140.] [SP:P21656]
[LE:23195] [RE:24187] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000991_40957_c1_407	2049	5821	858	285	513	3.2e-49

Description

sp:[LN:YJBO_BACSU] [AC:O31613] [GN:YJBO] [OR:BACILLUS SUBTILIS]
[DE:HYPOTHETICAL 31.5 KD PROTEIN IN MECA-TENA INTERGENIC REGION] [SP:O31613]
[DB:swissprot] >pir:[LN:G69844] [AC:G69844] [PN:conserved hypothetical
protein yjbo] [GN:yjbo] [CL:conserved hypothetical protein HI0176]
[OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1183182:g2633516] [LN:BSUB0007]
[AC:Z99110:AL009126] [GN:yjbo] [FN:unknown] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 7 of 21):
from 1194391to 1411140.] [NT:similar to hypothetical proteins] [SP:O31613]
[LE:43604] [RE:44455] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000991_4100393_f3_379	2050	5822	1215	404	1458	2.3e-149

Description

pir:[LN:B69589] [AC:B69589] [PN:argininosuccinate synthase argG] [GN:argG]
[CL:argininosuccinate synthase] [OR:Bacillus subtilis] [DB:pir2]
>gp:[GI:e1184194:g2635410] [LN:BSUB0015] [AC:Z99118:AL009126]
[PN:argininosuccinate synthase] [GN:argG] [FN:arginine biosynthesis]
[OR:Bacillus subtilis] [DB:genpept-bct1] [EC:6.3.4.5] [DE:Bacillus subtilis
complete genome (section 15 of 21): from 2795131to 3013540.] [LE:217075]
[RE:218286] [DI:complement] >gp:[GI:e1185818:g2635429] [LN:BSUB0016]
[AC:Z99119:AL009126] [PN:argininosuccinate synthase] [GN:argG] [FN:arginine
biosynthesis] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:6.3.4.5]
[DE:Bacillus subtilis complete genome (section 16 of 21): from 2997771to
3213410.] [LE:14435] [RE:15646] [DI:complement] >gp:[GI:g2293242]
[LN:AF008220] [AC:AF008220] [PN:arginine succinate synthase] [GN:argG]
[OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis rrnB-dnaB
genomic region.] [LE:164781] [RE:165992] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000991_4173410_c2_504	2051	5823	792	263	485	3.0e-46

Description

pir:[LN:H69846] [AC:H69846] [PN:hypothetical protein yjch] [GN:yjch]
[OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1183206:g2633540] [LN:BSUB0007]
[AC:Z99110:AL009126] [GN:yjch] [FN:unknown] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 7 of 21):
from 1194391to 1411140.] [LE:62495] [RE:63217] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000991_4181312_c2_527	2052	5824	606	201	93	0.010

Description

pir:[LN:A71455] [AC:A71455] [PN:probable acetyltransferase] [GN:PH0296]
[OR:Pyrococcus horikoshii] [DB:pir2] >gp:[GI:d1030311:g3256685]
[LN:AP0000001]
[AC:AP000001:AB009465:AB009464:AB009466:AB009467:AB009468:AB009469]
[PN:172aa long hypothetical acetyltransferase] [GN:PH0296] [OR:Pyrococcus
horikoshii] [SR:Pyrococcus horikoshii (strain:OT3) DNA] [DB:genpept-bct1]
[DE:Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt. position (1/7).]
[NT:similar to PIR:A64491 percent identity: 42.029 in] [LE:262066]
[RE:262584] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000991_4335752_f1_4	2053	5825	171	56		
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Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000991_4546890_f2_174	2054	5826	150	49		
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Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000991_4687518_c2_519	2055	5827	585	194	179	8.0e-14
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Description

sp:[LN:COMK_BACSU] [AC:P40396] [GN:COMK] [OR:BACILLUS SUBTILIS]
 [DE:COMPETENCE TRANSCRIPTION FACTOR (CTF) (COMPETENCE PROTEIN K)]
 [SP:P40396] [DB:swissprot] >pir:[LN:S43611] [AC:S43611:A69604]
 [PN:competence transcription factor (CTF) comK] [GN:comK] [OR:Bacillus
 subtilis] [DB:pir2] >gp:[GI:e1183044:g2633378] [LN:BSUB0006]
 [AC:Z99109:AL009126] [PN:competence transcription factor (CTF)] [GN:comK]
 [FN:final autoregulatory control switch prior to] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 6 of 21):
 from 999501 to1209940.] [SP:P40396] [LE:117081] [RE:117659] [DI:direct]
 >gp:[GI:g546917] [LN:S70734] [AC:S70734] [GN:comK] [OR:Bacillus subtilis]
 [SR:Bacillus subtilis E26] [DB:genpept-bct1] [DE:comK [Bacillus subtilis,
 E26, Genomic, 3 genes, 1947 nt].] [NT:This sequence comes from Fig. 3.]
 [LE:900] [RE:1478] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000991_4688750_f3_283	2056	5828	174	57		
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Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000991_4726010_c1_413	2057	5829	2304	767	1777	3.7e-183
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Description

gp:[GI:g1196907] [LN:STMDRRC] [AC:L76359] [PN:daunorubicin resistance
 protein] [GN:drnC] [OR:Streptomyces peucetius] [DB:genpept-bct1]
 [DE:Streptomyces peucetius daunorubicin resistance protein (drnC)
 gene, complete cds.] [LE:991] [RE:3285] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000991_4781275_f2_194	2058	5830	249	82		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000991_4812675_c1_412	2059	5831	321	106	273	3.1e-23

Description

sp:[LN:G6PD_BACSU] [AC:P54547] [GN:ZWF] [OR:BACILLUS SUBTILIS] [EC:1.1.1.49] [DE:PROTEIN 11] (VEG11)] [SP:P54547] [DB:swissprot] >pir:[LN:B69964] [AC:B69964] [PN:probable glucose-6-phosphate 1-dehydrogenase, yqjJ] [GN:yqjJ] [CL:glucose-6-phosphate dehydrogenase] [OR:Bacillus subtilis] [EC:1.1.1.49] [DB:pir2] >gp:[GI:d1013296:g1303961] [LN:BACJH642] [AC:D84432:D82370] [PN:YqjJ] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:JH642(trpC2 PheA1)) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis DNA, 283 Kb region containing skin element.] [LE:239025] [RE:240494] [DI:complement] >gp:[GI:e1185654:g2634820] [LN:BSUB0013] [AC:Z99116:AL009126] [GN:yqjJ] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.] [NT:similar to glucose-6-phosphate 1-dehydrogenase] [SP:P54547] [LE:83125] [RE:84594] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000991_48587_f3_381	2060	5832	1062	353	729	4.2e-72

Description

sp:[LN:GLPQ_BACSU] [AC:P37965] [GN:GLPQ] [OR:BACILLUS SUBTILIS] [EC:3.1.4.46] [DE:(GLYCEROPHOSPHODIESTER PHOSPHODIESTERASE)] [SP:P37965] [DB:swissprot] >pir:[LN:I40418] [AC:I40418:E69634:S37251] [PN:glycerophosphoryl diester phosphodiesterase glpQ] [GN:glpQ] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:d1034076:g3599635] [LN:AB006424] [AC:AB006424] [GN:ybeD] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:168) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis genomic DNA, 70 kb region between 17 and 23degree.] [LE:36004] [RE:36885] [DI:complement] >gp:[GI:g403373] [LN:BSGLPTQ] [AC:Z26522] [PN:glycerophosphoryl diester phosphodiesterase] [GN:glpQ] [FN:hydrolysis of deacylated phospholipids] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis glpT and glpQ genes for glycerol 3-phosphate permeaseand glycerophosphoryl diester phosphodiesterase.] [SP:P37965] [LE:1748] [RE:2629] [DI:direct] >gp:[GI:e1182165:g2632499] [LN:BSUB0002] [AC:Z99105:AL009126] [PN:glycerophosphoryl diester phosphodiesterase] [GN:glpQ] [FN:hydrolysis of deacylated phospholipids] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:3.1.4.46] [DE:Bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.] [NT:alternate gene name: ybeD] [SP:P37965] [LE:38353] [RE:39234] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000991_4882133_c1_435	2061	5833	150	49		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000991_4882806_c2_524	2062	5834	522	173	399	3.9e-37

Description

pir:[LN:D69838] [AC:D69838] [PN:conserved hypothetical protein yisU] [GN:yisU] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1183088:g2633422] [LN:BSUB0006] [AC:Z99109:AL009126] [GN:yisU] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.] [NT:similar to hypothetical proteins] [LE:165981] [RE:166643] [DI:complement] >gp:[GI:e1173520:g2145387] [LN:BSY09476] [AC:Y09476] [PN:YisU] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis 54kb genomic DNA fragment.] [NT:putative] [LE:23207] [RE:23869] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000991_4961000_f1_6	2063	5835	123	40		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000991_5085003_f1_118	2064	5836	1455	484	1439	2.4e-147

Description

pir:[LN:C69589] [AC:C69589] [PN:argininosuccinate lyase argH] [GN:argH] [CL:argininosuccinate lyase] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1184193:g2635409] [LN:BSUB0015] [AC:Z99118:AL009126] [PN:argininosuccinate lyase] [GN:argH] [FN:arginine biosynthesis] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:4.3.2.1] [DE:Bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.] [LE:215693] [RE:217078] [DI:complement] >gp:[GI:e1185817:g2635428] [LN:BSUB0016] [AC:Z99119:AL009126] [PN:argininosuccinate lyase] [GN:argH] [FN:arginine biosynthesis] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:4.3.2.1] [DE:Bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.] [LE:13053] [RE:14438] [DI:complement] >gp:[GI:g2293243] [LN:AF008220] [AC:AF008220] [PN:arginine succinate lyase] [GN:argH] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis rrnB-dnaB genomic region.] [LE:165989] [RE:167374] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000991_5115927_c2_528	2065	5837	1680	559	340	1.3e-59

Description

pir:[LN:S76520] [AC:S76520] [PN:hypothetical protein] [OR:Synechocystis sp.] [SR:PCC 6803, , PCC 6803] [SR:PCC 6803,] [DB:pir2]
 >gp:[GI:d1011017:g1001635] [LN:SYCSLRD] [AC:D64002:AB001339]
 [PN:2-succinyl-6-hydroxy-2,] [GN:menD] [OR:Synechocystis sp.]
 [SR:Synechocystis sp. (strain:PCC6803) DNA] [DB:genpept-bct1]
 [DE:Synechocystis sp. PCC6803 complete genome, 21/27, 2644795-2755702.]
 [NT:ORF_ID:s110603] [LE:25321] [RE:27108] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000991_5165711_f3_336	2066	5838	447	148	338	1.1e-30

Description

pir:[LN:A69844] [AC:A69844] [PN:hypothetical protein yjbI] [GN:yjbI]
 [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1183176:g2633510] [LN:BSUB0007]
 [AC:Z99110:AL009126] [GN:yjbI] [FN:unknown] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 7 of 21):
 from 1194391to 1411140.] [LE:39591] [RE:39989] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000991_5250258_c1_403	2067	5839	1839	612	1741	2.4e-179

Description

gp:[GI:d1014255:g1651216] [LN:D88209] [AC:D88209] [PN:Pz-peptidase]
 [OR:Bacillus licheniformis] [SR:Bacillus licheniformis (strain:N22) DNA]
 [DB:genpept-bct1] [DE:Bacillus licheniformis DNA for Pz-peptidase, complete
 cds.] [LE:238] [RE:2124] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000991_579441_c1_386	2068	5840	150	49		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000991_580307_f2_246	2069	5841	132	43		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000991_6057943_c2_517	2070	5842	999	332	990	9.2e-100

Description

pir:[LN:G69830] [AC:G69830] [PN:lipoate-protein ligase homolog yhfJ]
 [GN:yhfJ] [CL:lipoate-protein ligase] [OR:Bacillus subtilis] [DB:pir2]
 >gp:[GI:e1183027:g2633361] [LN:BSUB0006] [AC:Z99109:AL009126] [GN:yhfJ]
 [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
 complete genome (section 6 of 21): from 999501 to1209940.] [NT:similar to
 lipoate-protein ligase] [LE:99131] [RE:100126] [DI:direct]
 >gp:[GI:e325016:g2226243] [LN:BSY14083] [AC:Y14083] [PN:hypothetical
 protein] [GN:yhfJ] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus
 subtilis chromosomal DNA, region 76-78 degrees: betweenglyB-aprE.]
 [NT:Similarity to several lipoate-protein ligases] [LE:18990] [RE:19985]
 [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000991_6688757_f2_123	2071	5843	507	168	823	4.6e-82

Description

gp:[GI:g2267240] [LN:SEU71377] [AC:U71377] [OR:Staphylococcus epidermidis]
 [DB:genpept-bct1] [DE:Staphylococcus epidermidis autolysin AtlE and
 putativetranscriptional regulator AtlR genes, complete cds.] [NT:ORF2]
 [LE:913] [RE:1383] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000991_6921877_c1_410	2072	5844	219	72	192	2.3e-14

Description

sp:[LN:G6PD_BACSU] [AC:P54547] [GN:ZWF] [OR:BACILLUS SUBTILIS] [EC:1.1.1.49]
 [DE:PROTEIN 11) (VEG11)] [SP:P54547] [DB:swissprot] >pir:[LN:B69964]
 [AC:B69964] [PN:probable glucose-6-phosphate 1-dehydrogenase, yqjJ]
 [GN:yqjJ] [CL:glucose-6-phosphate dehydrogenase] [OR:Bacillus subtilis]
 [EC:1.1.1.49] [DB:pir2] >gp:[GI:d1013296:g1303961] [LN:BACJH642]
 [AC:D84432:D82370] [PN:YqjJ] [OR:Bacillus subtilis] [SR:Bacillus subtilis
 (strain:JH642(trpC2 PheA1)) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis
 DNA, 283 Kb region containing skin element.] [LE:239025] [RE:240494]
 [DI:complement] >gp:[GI:e1185654:g2634820] [LN:BSUB0013]
 [AC:Z99116:AL009126] [GN:yqjJ] [FN:unknown] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 13 of 21):
 from 2395261to 2613730.] [NT:similar to glucose-6-phosphate 1-dehydrogenase]
 [SP:P54547] [LE:83125] [RE:84594] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000991_7032752_f3_268	2073	5845	795	264	1335	2.5e-136

Description

gp:[GI:g2267239] [LN:SEU71377] [AC:U71377] [OR:Staphylococcus epidermidis]
[DB:genpept-bct1] [DE:Staphylococcus epidermidis autolysin AtlE and
putativetranscriptional regulator AtlR genes, complete cds.] [NT:ORF1]
[LE:<1] [RE:865] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000991_7081712_f1_27	2074	5846	234	77	84	0.00093

Description

pir:[LN:H69835] [AC:H69835] [PN:hypothetical protein yhzC] [GN:yhzC]
[OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1183043:g2633377] [LN:BSUB0006]
[AC:Z99109:AL009126] [GN:yhzC] [FN:unknown] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 6 of 21):
from 999501 to1209940.] [LE:116555] [RE:116788] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000991_7145260_f3_337	2075	5847	243	80		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000991_7228438_c2_471	2076	5848	3231	1076	1793	7.4e-185

Description

sp:[LN:ADDA_BACSU] [AC:P23478] [GN:ADDA] [OR:BACILLUS SUBTILIS]
[DE:ATP-DEPENDENT NUCLEASE SUBUNIT A] [SP:P23478] [DB:swissprot]
>pir:[LN:B39432] [AC:B39432:H69582] [PN:ATP-dependent deoxyribonuclease
chain A addA:ATP-dependent exonuclease synthesis protein AddA] [GN:addA]
[OR:Bacillus subtilis] [DB:pir2] >gp:[GI:g142440] [LN:BACADDAA] [AC:M63489]
[PN:ATP-dependent nuclease] [GN:addB] [OR:Bacillus subtilis] [SR:B.subtilis
DNA] [DB:genpept-bct1] [DE:Bacillus subtilis ATP-dependent nuclease (addA)
and (addB), andopen reading frame 3, partial cds.] [LE:3988] [RE:7687]
[DI:direct] >gp:[GI:e1183065:g2633399] [LN:BSUB0006] [AC:Z99109:AL009126]
[PN:ATP-dependent deoxyribonuclease (subunit A)] [GN:addA] [OR:Bacillus
subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 6
of 21): from 999501 to1209940.] [NT:alternate gene name: recE5] [SP:P23478]
[LE:139780] [RE:143478] [DI:direct] >gp:[GI:e1364881:g2226192] [LN:BSY14081]
[AC:Y14081] [PN:ATP-dependent nuclease] [GN:addA] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis chromosomal DNA, region 92 degrees:
regionbetween comK and addAB.] [NT:see ref [3]; In EMBL entry M63489 this
gene is] [LE:22075] [RE:25773] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000991_7241300_c2_502	2077	5849	135	44		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000991_7308375_c3_567	2078	5850	942	313	791	1.1e-78

Description

pir:[LN:H69668] [AC:H69668:S15231:B38447] [PN:oligopeptide transport system
permease protein oppB:sporulation initiation protein spo0KB] [GN:oppB:spo0KB
] [CL:oligopeptide permease protein oppB] [OR:Bacillus subtilis] [DB:pir2]
>gp:[GI:e1183164:g2633498] [LN:BSUB0007] [AC:Z99110:AL009126]
[PN:oligopeptide ABC transporter (permease)] [GN:oppB] [FN:required for
initiation of sporulation,] [OR:Bacillus subtilis] [DB:genpept-bct1]
[DE:Bacillus subtilis complete genome (section 7 of 21): from 1194391to
1411140.] [NT:alternate gene name: spo0KB] [LE:26676] [RE:27611] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000991_782816_c1_396	2079	5851	1857	618	776	3.7e-116

Description

pir:[LN:C69975] [AC:C69975] [PN:acyltransferase homolog yrhL] [GN:yrhL]
[OR:Bacillus subtilis] [DB:pir2] >gp:[GI:g1934616] [LN:BSU93874] [AC:U93874]
[PN:hypothetical protein YrhL] [GN:yrhL] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis cysteine synthase (yrhA),
cystathioninegamma-lyase (yrhB), YrhC (yrhC), YrhD (yrhD), formate
dehydrogenasechain A (yrhE), YrhF (yrhF), formate dehydrogenase (yrhG),
YrhH(yrhH), regulatory protein (yrhI), cytochrome P450 102 (yrhJ),
YrhK(yrhK), hypothetical protein YrhL (yrhL), putative anti-SigV,
factor(yrhM), RNA polymerase sigma factor SigV (sigV) and YrhO (yrhO)genes,
complete cds, and YrhP (yrhP) gene, partial cds.] [NT:similar to Haemophilus
influenzae hypothetical] [LE:13904] [RE:15808] [DI:complement]
>gp:[GI:e1183944:g2635160] [LN:BSUB0014] [AC:Z99117:AL009126] [GN:yrhL]
[FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
complete genome (section 14 of 21): from 2599451to 2812870.] [NT:similar to
acyltransferase] [LE:171138] [RE:173042] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000991_813412_c1_411	2080	5852	156	51	191	3.0e-14

Description

sp:[LN:G6PD_BACSU] [AC:P54547] [GN:ZWF] [OR:BACILLUS SUBTILIS] [EC:1.1.1.49]
[DE:PROTEIN 11] (VEG11)] [SP:P54547] [DB:swissprot] >pir:[LN:B69964]
[AC:B69964] [PN:probable glucose-6-phosphate 1-dehydrogenase, yqjJ]
[GN:yqjJ] [CL:glucose-6-phosphate dehydrogenase] [OR:Bacillus subtilis]
[EC:1.1.1.49] [DB:pir2] >gp:[GI:d1013296:g1303961] [LN:BACJH642]
[AC:D84432:D82370] [PN:YqjJ] [OR:Bacillus subtilis] [SR:Bacillus subtilis
(strain:JH642(trpC2 PheA1)) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis
DNA, 283 Kb region containing skin element.] [LE:239025] [RE:240494]
[DI:complement] >gp:[GI:e1185654:g2634820] [LN:BSUB0013]
[AC:Z99116:AL009126] [GN:yqjJ] [FN:unknown] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 13 of 21):
from 2395261to 2613730.] [NT:similar to glucose-6-phosphate 1-dehydrogenase]
[SP:P54547] [LE:83125] [RE:84594] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000991_859838_f3_357	2081	5853	384	127		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000991_978436_f2_126	2082	5854	1188	395	867	9.9e-87

Description

sp:[LN:PATA_BACSU] [AC:P16524] [GN:PATA:UAT] [OR:BACILLUS SUBTILIS]
[EC:2.6.1.-] [DE:PUTATIVE AMINOTRANSFERASE A,] [SP:P16524] [DB:swissprot]
>gp:[GI:e1181905:g2632221] [LN:BS16829KB] [AC:AJ222587] [PN:PatA protein]
[GN:patA] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
29kB DNA fragment from ykwC gene to cse15 gene.] [NT:hisC homologue]
[SP:P16524] [LE:6213] [RE:7391] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000991_985887_c3_570	2083	5855	435	144	570	2.9e-55

Description

pir:[LN:D69843] [AC:D69843] [PN:conserved hypothetical protein yjbd]
[GN:yjbd] [CL:hypothetical protein yjbd] [OR:Bacillus subtilis] [DB:pir2]
>gp:[GI:e1183170:g2633504] [LN:BSUB0007] [AC:Z99110:AL009126] [GN:yjbd]
[FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
complete genome (section 7 of 21): from 1194391to 1411140.] [NT:similar to
hypothetical proteins] [LE:32779] [RE:33174] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000991_9927077_f3_378	2084	5856	147	48		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000992_10008513_c3_117	2085	5857	2667	888	3361	0.0

Description

pir:[LN:SYBSVS] [AC:A26738] [PN:valine--tRNA ligase,:valyl-tRNA synthetase]
[GN:vals] [CL:valine--tRNA ligase] [OR:Bacillus stearothermophilus]
[EC:6.1.1.9] [DB:pir1]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000992_10720877_c1_78	2086	5858	1329	442	1343	3.6e-137

Description

pir:[LN:F69723] [AC:F69723] [PN:trigger factor (prolyl isomerase) tig]
 [GN:tig] [CL:trigger factor] [OR:Bacillus subtilis] [DB:pir2]
 >gp:[GI:e1184072:g2635288] [LN:BSUB0015] [AC:Z99118:AL009126] [PN:trigger
 factor (prolyl isomerase)] [GN:tig] [OR:Bacillus subtilis] [DB:genpept-bct1]
 [DE:Bacillus subtilis complete genome (section 15 of 21): from 2795131to
 3013540.] [NT:alternate gene name: yzzH] [SP:P80698] [LE:90286] [RE:91560]
 [DI:complement] >gp:[GI:e1165373:g1770074] [LN:BSZ75208] [AC:Z75208]
 [PN:trigger factor] [GN:tig] [OR:Bacillus subtilis] [DB:genpept-bct1]
 [DE:B.subtilis genomic sequence 89009bp.] [NT:homology to trigger factor of
 Haemophilus] [SP:P80698] [LE:78347] [RE:79621] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000992_11954500_f3_71	2087	5859	174	57		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000992_1211562_c2_94	2088	5860	1269	422	1518	1.0e-155

Description

gp:[GI:e221213:g1296452] [LN:BSCLPXGEN] [AC:X95306] [PN:ClpX protein]
 [GN:clpX] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis clpX
 gene.] [NT:ATP-dependent protease] [SP:P50866] [LE:168] [RE:1430]
 [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000992_14725300_c3_108	2089	5861	123	40		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000992_15820252_c1_81	2090	5862	141	46		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000992_16835900_c2_104	2091	5863	147	48	74	0.011

Description

gp:[GI:g1123053] [LN:CELF59A6] [AC:U41994] [GN:F59A6.2] [OR:Caenorhabditis elegans] [SR:Caenorhabditis elegans strain=Bristol N2] [DB:genpept-inv1] [DE:Caenorhabditis elegans cosmid F59A6.] [LE:19719:20072] [RE:19904:20242] [DI:directJoin]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000992_188388_c3_122	2092	5864	579	192	220	3.6e-18

Description

sp:[LN:MREC_BACSU] [AC:Q01466] [GN:MREC] [OR:BACILLUS SUBTILIS] [DE:ROD SHAPE-DETERMINING PROTEIN MREC] [SP:Q01466] [DB:swissprot] >pir:[LN:JC4595] [AC:JC4595] [PN:cell shape determinant MreC:protease secretion stimulating protein, MreC] [GN:mreC] [OR:Bacillus stearothermophilus] [DB:pir2] >pir:[LN:C45240] [AC:C45240:D45239:S27518] [PN:cell shape determinant mreC] [GN:mreC] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:g143213] [LN:BACMREMIN] [AC:M95582] [GN:mreC] [FN:cell shape determining] [OR:Bacillus subtilis]' [SR:Bacillus subtilis (strain W168) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis (mreB) gene complete cds, (mreC) gene completecds, (mreD) gene complete cds, (minC) gene complete cds, (minD)gene complete cds.] [NT:putative] [LE:1370] [RE:2242] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000992_19707767_f1_4	2093	5865	324	107		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000992_20348160_f1_1	2094	5866	222	73	71	0.022

Description

gp:[GI:g1131474] [LN:PBU42580] [AC:U42580:U17055:U32570] [GN:A130R] [OR:Paramecium bursaria Chlorella virus 1] [DB:genpept-vr1] [DE:Paramecium bursaria Chlorella virus 1, complete genome.] [LE:69061] [RE:69378] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000992_21500253_c3_109	2095	5867	177	58		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000992_21563137_c2_102	2096	5868	135	44		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000992_23444187_f3_62	2097	5869	162	53		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000992_23522567_c2_91	2098	5870	381	126	450	1.5e-42

Description

sp:[LN:RL20_BACSU] [AC:P55873] [GN:RPLT] [OR:BACILLUS SUBTILIS] [DE:50S RIBOSOMAL PROTEIN L20] [SP:P55873] [DB:swissprot] >pir:[LN:F69696] [AC:F69696] [PN:ribosomal protein L20 rplT] [GN:rplT] [CL:Escherichia coli ribosomal protein L20] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1184134:g2635350] [LN:BSUB0015] [AC:Z99118:AL009126] [PN:ribosomal protein L20] [GN:rplT] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.] [SP:P55873] [LE:156202] [RE:156561] [DI:complement] >gp:[GI:e1165301:g1770009] [LN:BSZ75208] [AC:Z75208] [PN:ribosomal protein L20] [GN:rplT] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis genomic sequence 89009bp.] [NT:homology to rplT of Bacillus stearothermophilus;] [SP:P55873] [LE:13346] [RE:13705] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000992_23531628_f2_28	2099	5871	144	47		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000992_23697141_c2_97	2100	5872	930	309	1327	1.8e-135

Description

gp:[GI:g2589181] [LN:SAU89396] [AC:U89396] [PN:porphobilinogen deaminase] [GN:hemC] [OR:Staphylococcus aureus] [DB:genpept-bct2] [EC:4.3.1.8] [DE:Staphylococcus aureus hemCDBL gene cluster: porphobilinogendeaminase (hemC), uroporphyrinogen III synthase (hemD), d-aminolevulinic acid dehydratase (hemB) and GSA-1-aminotransferase (hemL) genes, complete cds.] [LE:219] [RE:1145] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000992_24017052_c2_103	2101	5873	150	49		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000992_24240877_c3_119	2102	5874	522	173		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000992_24625161_c1_87	2103	5875	141	46	160	8.2e-12

Description

sp:[LN:RAD_C_STAAU] [AC:P31337] [GN:RAD_C] [OR:STAPHYLOCOCCUS AUREUS] [DE:DNA REPAIR PROTEIN RAD_C HOMOLOG (25 KD PROTEIN) (FRAGMENT)] [SP:P31337] [DB:swissprot] >gp:[GI:g551992] [LN:STATNIS5] [AC:K02985] [OR:Staphylococcus aureus] [SR:S.aureus (strain RN450) DNA] [DB:genpept-bct1] [DE:S.aureus (strain RN450) transposon Tn554 insertion site.] [NT:25 kD protein (putative); putative] [LE:<1] [RE:>249] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000992_24897312_c3_112	2104	5876	186	61	255	7.1e-22

Description

sp:[LN:HEM2_STAAU] [AC:P50915] [GN:HEMB] [OR:STAPHYLOCOCCUS AUREUS]
[EC:4.2.1.24] [DE:SYNTHASE) (ALAD) (ALADH)] [SP:P50915] [DB:swissprot]
>gp:[GI:g2589183] [LN:SAU89396] [AC:U89396] [PN:d-aminolevulinic acid
dehydratase] [GN:hemB] [OR:Staphylococcus aureus] [DB:genpept-bct2]
[EC:4.2.1.24] [DE:Staphylococcus aureus hemCDBL gene cluster:
porphobilinogendeaminase (hemC), uroporphyrinogen III synthase
(hemD),d-aminolevulinic acid dehydratase (hemB) and
GSA-1-aminotransferase(hemL) genes, complete cds.] [LE:1838] [RE:2809]
[DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000992_25582912_f2_23	2105	5877	123	40		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000992_25596000_c3_111	2106	5878	825	274	460	1.3e-43

Description

sp:[LN:HEMX_BACSU] [AC:P16645] [GN:HEMX] [OR:BACILLUS SUBTILIS] [DE:HEMX
PROTEIN] [SP:P16645] [DB:swissprot] >pir:[LN:B35252] [AC:B35252:C69640]
[PN:hema concentration negative effector hemX] [GN:hemX] [OR:Bacillus
subtilis] [DB:pir2] >gp:[GI:g143036] [LN:BACHEMAXC] [AC:M57676:M32130]
[GN:hemX] [OR:Bacillus subtilis] [SR:B.subtilis DNA] [DB:genpept-bct1]
[DE:Bacillus subtilis hemAXCDBL gene cluster.] [NT:unidentified gene
product] [LE:1607] [RE:2437] [DI:direct] >gp:[GI:e1184065:g2635281]
[LN:BSUB0015] [AC:Z99118:AL009126] [PN:membrane-bound protein] [GN:hemX]
[FN:negative effector of the concentration of Hema] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 15 of 21):
from 2795131to 3013540.] [SP:P16645] [LE:80898] [RE:81728] [DI:complement]
>gp:[GI:e1165382:g1770082] [LN:BSZ75208] [AC:Z75208] [PN:membrane-bound
protein] [GN:hemX] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis
genomic sequence 89009bp.] [NT:membrane bound protein dispensable for heme]
[SP:P16645] [LE:88179] [RE:89009] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000992_2866255_f3_65	2107	5879	264	87	74	0.045

Description

gp:[GI:e1250026:g2842472] [LN:SPBC20F10] [AC:AL021747] [PN:preg-like protein.] [GN:SPBC20F10.10] [OR:Schizosaccharomyces pombe] [SR:fission yeast] [DB:genpept-pln1] [DE:S.pombe chromosome II cosmid c20F10.] [NT:SPBC20F10.10, len:243, SIMILARITY:Arabidopsis] [LE:20474] [RE:21205] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000992_31510_f3_55	2108	5880	627	208	435	6.0e-41

Description

sp:[LN:3MGA_HAEIN] [AC:P44321] [GN:TAG:HI0654] [OR:HAEMOPHILUS INFLUENZAE] [EC:3.2.2.20] [DE:GLYCOSYLASE (TAG)] [SP:P44321] [DB:swissprot] >pir:[LN:G64084] [AC:G64084] [PN:3-methyladenine DNA glycosylase, I] [CL:3-methyladenine DNA glycosylase I] [OR:Haemophilus influenzae] [EC:3.2.2.-] [DB:pir2] >gp:[GI:g1573653] [LN:U32748] [AC:U32748:L42023] [PN:DNA-3-methyladenine glycosidase I (tagI)] [GN:HI0654] [OR:Haemophilus influenzae Rd] [DB:genpept-bct2] [DE:Haemophilus influenzae Rd section 63 of 163 of the complete genome.] [NT:similar to SP:P05100 GB:J02606 GB:X03845 PID:147920] [LE:6773] [RE:7330] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000992_33395050_c2_95	2109	5881	618	205	577	5.3e-56

Description

sp:[LN:YSXC_BACSU] [AC:P38424] [GN:YSXC] [OR:BACILLUS SUBTILIS] [DE:(ORFX)] [SP:P38424] [DB:swissprot] >pir:[LN:I40422] [AC:I40422:C69987:S45102] [PN:conserved hypothetical protein ysx] [GN:ysxC] [CL:Bacillus subtilis conserved hypothetical protein ysx:translation elongation factor Tu homology] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:g496558] [LN:BSLONLA] [AC:X76424] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis lon gene for protease La.] [NT:orfX] [SP:P38424] [LE:2669] [RE:3256] [DI:direct] >gp:[GI:e1184068:g2635284] [LN:BSUB0015] [AC:Z99118:AL009126] [GN:ysxC] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.] [NT:similar to hypothetical proteins] [SP:P38424] [LE:83852] [RE:84439] [DI:complement] >gp:[GI:e1165379:g1770079] [LN:BSZ75208] [AC:Z75208] [PN:hypothetical protein] [GN:ysxC] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis genomic sequence 89009bp.] [NT:unknown function; putative] [SP:P38424] [LE:85468] [RE:86055] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000992_33517_c1_82	2110	5882	1077	358	258	2.8e-21

Description

pir:[LN:E69834] [AC:E69834] [PN:hypothetical protein yhjN] [GN:yhjN]
[OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1183059:g2633393] [LN:BSUB0006]
[AC:Z99109:AL009126] [GN:yhjN] [FN:unknown] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 6 of 21):
from 999501 to1209940.] [LE:130891] [RE:132045] [DI:complement]
>gp:[GI:e324987:g2226186] [LN:BSY14081] [AC:Y14081] [PN:hypothetical
protein] [GN:yhjN] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus
subtilis chromosomal DNA, region 92 degrees: regionbetween comK and addAB.]
[NT:TTG start; Similarity to a hypothetical protein] [LE:13186] [RE:14340]
[DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000992_34642092_c1_85	2111	5883	1284	427	907	5.7e-91

Description

sp:[LN:FOLC_BACSU] [AC:Q05865] [GN:FOLC] [OR:BACILLUS SUBTILIS]
[EC:6.3.2.17] [DE:SYNTHETASE] (FPGS)] [SP:Q05865] [DB:swissprot]
>pir:[LN:B40646] [AC:B40646:B33490:D69626] [PN:folyl-polyglutamate
synthetase folC] [GN:folC] [OR:Bacillus subtilis] [DB:pir2]
>gp:[GI:g142936] [LN:BACFOLC] [AC:L04520] [PN:folyl-polyglutamate
synthetase] [GN:folC] [OR:Bacillus subtilis] [SR:Bacillus subtilis
(sub_strain PY79, strain W168) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis
valyl tRNA synthetase (vals) gene, 3' end cds;folyl-polyglutamate synthetase
(folC) gene, complete cds; comCgene, 5' end cds.] [LE:231] [RE:1523]
[DI:direct] >gp:[GI:e1184057:g2635273] [LN:BSUB0015] [AC:Z99118:AL009126]
[PN:folyl-polyglutamate synthetase] [GN:folC] [FN:folate biosynthesis]
[OR:Bacillus subtilis] [DB:genpept-bct1] [EC:6.3.2.17] [DE:Bacillus subtilis
complete genome (section 15 of 21): from 2795131to 3013540.] [SP:Q05865]
[LE:69443] [RE:70735] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000992_3914012_c2_98	2112	5884	690	229	710	4.3e-70

Description

gp:[GI:g2589182] [LN:SAU89396] [AC:U89396] [PN:uroporphyrinogen III
synthase] [GN:hemD] [OR:Staphylococcus aureus] [DB:genpept-bct2]
[EC:4.2.1.75] [DE:Staphylococcus aureus hemCDBL gene cluster:
porphobilinogendeaminase (hemC), uroporphyrinogen III synthase
(hemD),d-aminolevulinic acid dehydratase (hemB) and
GSA-1-aminotransferase(hemL) genes, complete cds.] [LE:1167] [RE:1835]
[DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000992_4080443_c3_113	2113	5885	1296	431	2041	3.9e-211

Description

sp:[LN:GSA_STAAU] [AC:O34092] [GN:HEML] [OR:STAPHYLOCOCCUS AUREUS]
[EC:5.4.3.8] [DE:(GLUTAMATE-1-SEMIALDEHYDE AMINOTRANSFERASE) (GSA-AT)]
[SP:O34092] [DB:swissprot] >gp:[GI:g2589184] [LN:SAU89396] [AC:U89396]
[PN:GSA-1-aminotransferase] [GN:hemL] [OR:Staphylococcus aureus]
[DB:genpept-bct2] [EC:5.4.3.8] [DE:Staphylococcus aureus hemCDBL gene
cluster: porphobilinogendeaminase (hemC), uroporphyrinogen III synthase
(hemD), d-aminolevulinic acid dehydratase (hemB) and
GSA-1-aminotransferase(hemL) genes, complete cds.] [LE:2857] [RE:4143]
[DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000992_439183_f1_14	2114	5886	297	98	208	6.8e-17

Description

gp:[GI:e1165375:g1770076] [LN:BSZ75208] [AC:Z75208] [PN:hypothetical
protein] [GN:ysoC] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis
genomic sequence 89009bp.] [NT:unknown function; putative] [LE:80592]
[RE:81206] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000992_4729837_c2_92	2115	5887	624	207	416	6.1e-39

Description

sp:[LN:YMAB_BACSU] [AC:P50619] [GN:YMAB] [OR:BACILLUS SUBTILIS]
[DE:HYPOTHETICAL 23.4 KD PROTEIN IN NRDF-CWLC INTERGENIC REGION] [SP:P50619]
[DB:swissprot] >pir:[LN:D69883] [AC:D69883] [PN:hypothetical protein ymaB]
[GN:ymaB] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e218063:g1154634]
[LN:BSNRDYMA] [AC:Z68500] [PN:YmaB] [GN:ymaB] [FN:unknown] [OR:Bacillus
subtilis] [DB:genpept-bct1] [DE:B.subtilis cwlc, nrde, nrdF, ymaA and ymaB
genes.] [NT:no similarities, cannot be inactivated] [SP:P50619] [LE:4450]
[RE:5070] [DI:direct] >gp:[GI:e1183399:g2634124] [LN:BSUB0010]
[AC:Z99113:AL009126] [GN:ymaB] [FN:unknown] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 10 of 21):
from 1781201to 2014980.] [LE:90169] [RE:90789] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000992_4891876_f3_45	2116	5888	141	46		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000992_500052_c3_118	2117	5889	669	222	440	1.8e-41

Description

sp:[LN:RADC_BACSU] [AC:Q02170] [GN:YSXA] [OR:BACILLUS SUBTILIS] [DE:DNA REPAIR PROTEIN RADC HOMOLOG (ORFB)] [SP:Q02170] [DB:swissprot]
>pir:[LN:B45239] [AC:B45239:B45240:I39881:A69987] [PN:DNA repair protein homolog ysxA] [GN:ysxA] [CL:DNA repair protein radc] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:g142854] [LN:BACDIVREG] [AC:M96343] [GN:orfB] [OR:Bacillus subtilis] [SR:Bacillus subtilis (sub_strain PY79, strain W168) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis orfA, orfB, mreB, mreC, mreD, minC, and minDgenes, complete coding regions.] [NT:homologous to E. coli radC gene product and to] [LE:762] [RE:1457] [DI:direct] >gp:[GI:g143162] [LN:BACMAFMREB] [AC:L08793] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain W168) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis maf gene, complete cds; orfB, complete cds; mreBgene, 5' end.] [NT:putative] [LE:1557] [RE:2252] [DI:direct] >gp:[GI:e1184053:g2635269] [LN:BSUB0015] [AC:Z99118:AL009126] [GN:ysxA] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.] [NT:similar to DNA repair protein] [SP:Q02170] [LE:65971] [RE:66666] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000992_5268775_c3_105	2118	5890	960	319	138	8.5e-07

Description

pir:[LN:H69986] [AC:H69986] [PN:hypothetical protein ysoA] [GN:ysoA] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1184073:g2635289] [LN:BSUB0015] [AC:Z99118:AL009126] [GN:ysoA] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.] [LE:91788] [RE:92720] [DI:complement] >gp:[GI:e1165372:g1770073] [LN:BSZ75208] [AC:Z75208] [PN:hypothetical protein] [GN:ysoA] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis genomic sequence 89009bp.] [NT:unknown function; putative] [LE:77187] [RE:78119] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000992_5860827_c3_110	2119	5891	1347	448	1172	4.8e-119

Description

sp:[LN:HEM1_BACSU] [AC:P16618] [GN:HEMA] [OR:BACILLUS SUBTILIS] [EC:1.2.1.-]
[DE:GLUTAMYL-TRNA REDUCTASE, (GLUTR)] [SP:P16618] [DB:swissprot]
>pir:[LN:A35252] [AC:A35252:C69639] [PN:glutamyl-tRNA reductase, hemA:hema
protein] [GN:hema] [CL:glutamyl-tRNA reductase] [OR:Bacillus subtilis]
[EC:1.2.1.-] [DB:pir2] >gp:[GI:g143035] [LN:BACHEMAXC] [AC:M57676:M32130]
[PN:NAD(P)H:glutamyl-transfer RNA reductase] [GN:hema] [OR:Bacillus
subtilis] [SR:B.subtilis DNA] [DB:genpept-bct1] [DE:Bacillus subtilis
hemAXCDBL gene cluster.] [NT:The product of this hemA gene is not an]
[LE:232] [RE:1599] [DI:direct] >gp:[GI:e1184066:g2635282] [LN:BSUB0015]
[AC:Z99118:AL009126] [PN:glutamyl-tRNA reductase] [GN:hema] [FN:porphyrin
biosynthesis] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:1.2.1.-]
[DE:Bacillus subtilis complete genome (section 15 of 21): from 2795131to
3013540.] [SP:P16618] [LE:81736] [RE:83103] [DI:complement]
>gp:[GI:e1165381:g1770081] [LN:BSZ75208] [AC:Z75208]
[PN:NAD(P)H:glutamyl-transfer RNA reductase] [GN:hema] [OR:Bacillus
subtilis] [DB:genpept-bct1] [EC:2.3.1.37] [DE:B.subtilis genomic sequence
89009bp.] [NT:NAD(P)H:glutamyl-t-RNA reductase of the C-5 pathway]
[SP:P16618] [LE:86804] [RE:88171] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000992_6845382_f2_26	2120	5892	219	72	72	0.034

Description

gp:[GI:e1358367:g3979946] [LN:CEY18D10A] [AC:AL034393] [GN:Y18D10A.14]
[OR:Caenorhabditis elegans] [DB:genpept-inv1] [DE:Caenorhabditis elegans
cosmid Y18D10A, complete sequence.] [LE:113813:114013:114203]
[RE:113961:114112:114448] [DI:directJoin]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000992_7050319_c2_90	2121	5893	237	78	226	8.4e-19

Description

sp:[LN:RL35_BACSU] [AC:P55874] [GN:RPMI] [OR:BACILLUS SUBTILIS] [DE:50S
RIBOSOMAL PROTEIN L35] [SP:P55874] [DB:swissprot]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000992_7283437_c1_89	2122	5894	162	54		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000992_806510_c1_86	2123	5895	714	237	189	7.0e-15

Description

sp:[LN:LEP3_BACSU] [AC:P15378] [GN:COMC] [OR:BACILLUS SUBTILIS]
[EC:3.4.99.-] [DE:(LATE COMPETENCE PROTEIN COMC)] [SP:P15378] [DB:swissprot]
>pir:[LN:A33490] [AC:A33490:E40646:F40646:B69602] [PN:type IV prepilin
peptidase,:genetic transformation late competence protein ComC] [GN:comC]
[CL:type IV prepilin peptidase] [OR:Bacillus subtilis] [EC:3.4.99.-]
[DB:pir2] >gp:[GI:g142704] [LN:BACCOMC] [AC:M30805] [PN:late competence
protein] [GN:comC] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain
IS75) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis late competence protein
(comC) gene, completecds.] [LE:819] [RE:1565] [DI:direct]
>gp:[GI:e1184056:g2635272] [LN:BSUB0015] [AC:Z99118:AL009126]
[PN:DNA-binding protein] [GN:comC] [FN:required for the processing and
translocation] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus
subtilis complete genome (section 15 of 21): from 2795131to 3013540.]
[SP:P15378] [LE:68557] [RE:69303] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000992_820253_f1_15	2124	5896	297	98	206	1.1e-16

Description

gp:[GI:e1165375:g1770076] [LN:BSZ75208] [AC:Z75208] [PN:hypothetical
protein] [GN:ysoC] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis
genomic sequence 89009bp.] [NT:unknown function; putative] [LE:80592]
[RE:81206] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000992_978562_c1_79	2125	5897	861	286	1261	1.8e-128

Description

sp:[LN:HEM2_STAAU] [AC:P50915] [GN:HEMB] [OR:STAPHYLOCOCCUS AUREUS]
[EC:4.2.1.24] [DE:SYNTHASE) (ALAD) (ALADH)] [SP:P50915] [DB:swissprot]
>gp:[GI:g2589183] [LN:SAU89396] [AC:U89396] [PN:d-aminolevulinic acid
dehydratase] [GN:hemB] [OR:Staphylococcus aureus] [DB:genpept-bct2]
[EC:4.2.1.24] [DE:Staphylococcus aureus hemCDBL gene cluster:
porphobilinogendeaminase (hemC), uroporphyrinogen III synthase
(hemD),d-aminolevulinic acid dehydratase (hemB) and
GSA-1-aminotransferase(hemL) genes, complete cds.] [LE:1838] [RE:2809]
[DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000993_10266875_c2_761	2126	5898	156	51		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000993_10463_c2_803	2127	5899	504	167	315	3.1e-28

Description

sp: [LN:YTXG_BACSU] [AC:P40779] [GN:YTXG] [OR:BACILLUS SUBTILIS]
 [DE:HYPOTHETICAL 15.7 KD PROTEIN IN MURC-AOA INTERGENIC REGION (ORF1)]
 [SP:P40779] [DB:swissprot] >pir: [LN:D70003] [AC:D70003:S71001] [PN:general
 stress protein homolog ytxG] [GN:ytxG] [OR:Bacillus subtilis] [DB:pir2]
 >gp: [GI:g556015] [LN:BACUNAM] [AC:L31845] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:Bacillus subtilis UDP-N-acetylmuramate-alanine ligase
 gene, partialcds, and 3 ORF's.] [NT:ORF1] [LE:1211] [RE:1642] [DI:direct]
 >gp: [GI:e1185851:g2635462] [LN:BSUB0016] [AC:Z99119:AL009126] [GN:ytxG]
 [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
 complete genome (section 16 of 21): from 2997771to 3213410.] [NT:alternate
 gene name: csb40; similar to general] [SP:P40779] [LE:48897] [RE:49328]
 [DI:complement] >gp: [GI:g2293217] [LN:AF008220] [AC:AF008220] [PN:YtxG]
 [GN:ytxG] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis
 rrnB-dnaB genomic region.] [LE:131098] [RE:131529] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000993_10548383_f1_3	2128	5900	237	78		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000993_10564375_f3_510	2129	5901	123	40		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000993_1056693_c2_793	2130	5902	1101	366	774	7.1e-77

Description

pir:[LN:B69998] [AC:B69998] [PN:endo-1,4-beta-glucanase homolog ytoP]
 [GN:ytoP] [CL:thermophilic aminopeptidase I alpha chain] [OR:Bacillus
 subtilis] [DB:pir2] >gp:[GI:e1185859:g2635470] [LN:BSUB0016]
 [AC:Z99119:AL009126] [GN:ytoP] [FN:unknown] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 16 of 21):
 from 2997771to 3213410.] [NT:similar to endo-1,4-beta-glucanase] [LE:56559]
 [RE:57632] [DI:complement] >gp:[GI:g2293210] [LN:AF008220] [AC:AF008220]
 [PN:YtoP] [GN:ytoP] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus
 subtilis rrnB-dnaB genomic region.] [NT:similar to hypothetical protein f356
 from E. coli] [LE:122794] [RE:123867] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000993_10588877_f1_52	2131	5903	138	45		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000993_10667002_f1_111	2132	5904	165	54		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000993_109430_f3_485	2133	5905	144	47		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000993_10969427_f3_448	2134	5906	156	51		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000993_112525_f3_546	2135	5907	141	46		
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Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000993_116337_f2_251	2136	5908	627	208	199	6.1e-16
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Description

gp:[GI:g3043872] [LN:LLU95837] [AC:U95837] [PN:transmembrane protein Tmp3]
[OR:Lactococcus lactis] [DB:genpept-bct2] [DE:Lactococcus lactis
transmembrane protein Tmp3 gene, partial cds.] [NT:PBP1A homolog; identified
as a fusion to a signal] [LE:<1] [RE:588] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000993_11881325_f3_568	2137	5909	147	48		
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Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000993_1203827_c3_893	2138	5910	639	212	475	3.4e-45
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Description

sp:[LN:RISA_ACTPL] [AC:P50854] [GN:RIBE:RIBB] [OR:ACTINOBACILLUS
PLEUROPNEUMONIAE] [SR:,HAEMOPHILUS PLEUROPNEUMONIAE] [EC:2.5.1.9]
[DE:RIBOFLAVIN SYNTHASE ALPHA CHAIN,] [SP:P50854] [DB:swissprot]
>gp:[GI:g1173517] [LN:APU27202] [AC:U27202] [PN:riboflavin synthase alpha
subunit] [GN:ribB] [OR:Actinobacillus pleuropneumoniae] [DB:genpept-bct1]
[DE:Actinobacillus pleuropneumoniae riboflavin biosynthesis
operon,riboflavin-specific deaminase (ribG), riboflavin synthase
alphasubunit (ribB), bifunctional GTP
cyclohydraseII/3,4-dihydroxy-2-butanone-4-phosphate synthase (ribA),
andriboflavin synthase beta subunit (ribH) genes, complete cds.]
[NT:lumazine synthase; similar to Bacillus subtilis] [LE:1685] [RE:2332]
[DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000993_1209417_c3_959	2139	5911	1704	567	797	2.6e-79

Description

sp:[LN:PHOR_BACSU] [AC:P23545] [GN:PHOR] [OR:BACILLUS SUBTILIS] [EC:2.7.3.-]
[DE:ALKALINE PHOSPHATASE SYNTHESIS SENSOR PROTEIN PHOR,] [SP:P23545]
[DB:swissprot] >pir:[LN:A27650] [AC:A27650:G69676] [PN:phosphate response
regulator histidine kinase phoR] [GN:phoR] [OR:Bacillus subtilis] [DB:pir2]
>gp:[GI:g143331] [LN:BACPHORP] [AC:M23549] [PN:alkaline phosphatase
regulatory protein] [GN:phoR] [OR:Bacillus subtilis] [SR:Bacillus subtilis
DNA] [DB:genpept-bct1] [DE:Bacillus subtilis alkaline phosphatase regulatory
protein (phoPgene, 3' end and phoR gene, complete cds).] [LE:85] [RE:1824]
[DI:direct] >gp:[GI:e1184159:g2635375] [LN:BSUB0015] [AC:Z99118:AL009126]
[PN:two-component sensor histidine kinase] [GN:phoR] [FN:involved in
phosphate regulation] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus
subtilis complete genome (section 15 of 21): from 2795131to 3013540.]
[SP:P23545] [LE:180011] [RE:181750] [DI:complement] >gp:[GI:g2293271]
[LN:AF008220] [AC:AF008220] [PN:signal transduction protein kinase]
[GN:phoR] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis
rrnB-dnaB genomic region.] [LE:201317] [RE:203056] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000993_125880_f2_361	2140	5912	309	102		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000993_1284381_c1_652	2141	5913	741	246	297	2.5e-26

Description

sp:[LN:TAL_METJA] [AC:Q58370] [GN:TAL:MJ0960] [OR:METHANOCOCCUS JANNASCHII]
[EC:2.2.1.-] [DE:TRANSALDOLASE-LIKE PROTEIN,] [SP:Q58370] [DB:swissprot]
>pir:[LN:H64419] [AC:H64419] [PN:transaldolase,] [CL:Bacillus subtilis 23K
phosphoprotein orfU] [OR:Methanococcus jannaschii] [EC:2.2.1.2] [DB:pir2]
[MP:REV892437-891784] >gp:[GI:g1591624] [LN:U67539] [AC:U67539:L77117]
[PN:transaldolase] [GN:MJ0960] [OR:Methanococcus jannaschii]
[DB:genpept-bct2] [DE:Methanococcus jannaschii section 81 of 150 of the
complete genome.] [NT:similar to SP:P19669 PID:853766 GB:AL009126 percent]
[LE:7990] [RE:8643] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000993_12894378_f2_347	2142	5914	177	58		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000993_13001537_f3_444	2143	5915	249	82		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000993_13089052_f3_538	2144	5916	141	46		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000993_1352042_c2_777	2145	5917	180	59		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000993_13678452_c1_628	2146	5918	1263	420	438	2.9e-41

Description

sp:[LN:ECSB_BACSU] [AC:P55340] [GN:ECSB:PRST] [OR:BACILLUS SUBTILIS]
 [DE:PROTEIN ECSB] [SP:P55340] [DB:swissprot] >pir:[LN:G69619] [AC:G69619]
 [PN:ABC transporter (membrane protein) ecsB] [GN:ecsB] [OR:Bacillus
 subtilis] [DB:pir2] >gp:[GI:e183450:g1177254] [LN:BSECSABCG] [AC:X87807]
 [PN:hypothetical EcsB protein] [GN:ecsB] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:B.subtilis ecsA, ecsB, and ecsC genes.] [SP:P55340]
 [LE:984] [RE:2210] [DI:direct] >gp:[GI:e1183007:g2633341] [LN:BSUB0006]
 [AC:Z99109:AL009126] [PN:ABC transporter (membrane protein)] [GN:ecsB]
 [FN:regulates both components of the protein] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 6 of 21):
 from 999501 to1209940.] [NT:alternate gene name: prsT, yhaC] [SP:P55340]
 [LE:78149] [RE:79375] [DI:direct] >gp:[GI:e324951:g2226114] [LN:BSY14077]
 [AC:Y14077] [PN:Hypothetical protein] [GN:yhaC] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:Bacillus subitlis 10.6 Kb chromosomal DNA: glyB-prsA
 region.] [NT:Identified as ecsB. Hypothetical integral membrane] [SP:P55340]
 [LE:1538] [RE:2764] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000993_13722338_c3_943	2147	5919	507	168	505	2.3e-48

Description

pir:[LN:F69992] [AC:F69992] [PN:thiol peroxidase homolog ytgI] [GN:ytgI]
[CL:thiol peroxidase] [OR:Bacillus subtilis] [DB:pir2]
>gp:[GI:e1185822:g2635433] [LN:BSUB0016] [AC:Z99119:AL009126] [GN:ytgI]
[FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
complete genome (section 16 of 21): from 2997771to 3213410.] [NT:similar to
thiol peroxidase] [LE:18998] [RE:19501] [DI:complement] >gp:[GI:g2293238]
[LN:AF008220] [AC:AF008220] [PN:YtgI] [GN:ytgI] [OR:Bacillus subtilis]
[DB:genpept-bct2] [DE:Bacillus subtilis rrnB-dnaB genomic region.]
[NT:similarity to tagD protein from V.cholerae] [LE:160926] [RE:161429]
[DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000993_13723318_c3_945	2148	5920	1149	382	1230	3.4e-125

Description

pir:[LN:JE0388] [AC:JE0388] [PN:alanine dehydrogenase,] [OR:Enterobacter
aerogenes] [EC:1.4.1.1] [DB:pir3] >gp:[GI:d1041279:g4803749] [LN:AB013821]
[AC:AB013821] [PN:alanine dehydrogenase] [GN:aladh] [OR:Enterobacter
aerogenes] [SR:Enterobacter aerogenes DNA] [DB:genpept-bct1] [EC:1.4.1.1]
[DE:Enterobacter aerogenes aladh gene for alanine dehydrogenase,complete
cds.] [LE:174] [RE:1307] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000993_13787912_c3_891	2149	5921	1524	507	118	1.7e-05

Description

pir:[LN:D64924] [AC:D64924] [PN:hypothetical protein b1668] [OR:Escherichia
coli] [DB:pir2] >gp:[GI:g1549279] [LN:ECU68703] [AC:U68703] [OR:Escherichia
coli] [DB:genpept-bct1] [DE:Escherichia coli K-12 MG1655 genome, ribC-pykF
region.] [NT:hypothetical protein] [LE:4535] [RE:6139] [DI:direct]
>gp:[GI:g1787957] [LN:AE000262] [AC:AE000262:U00096] [PN:orf, hypothetical
protein] [GN:b1668] [FN:orf; Unknown] [OR:Escherichia coli]
[DB:genpept-bct2] [DE:Escherichia coli K-12 MG1655 section 152 of 400 of the
completegenome.] [NT:o534; This 534 aa ORF is 38 pct identical (6 gaps)]
[LE:872] [RE:2476] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000993_13852187_f1_136	2150	5922	186	61	113	4.5e-06

Description

pir:[LN:S77632] [AC:S77632:S52761] [PN:probable integrase] [GN:int]
[OR:Staphylococcus aureus phage phi-13] [DB:pir2] >gp:[GI:g758229]
[LN:PHI13INT] [AC:X82312] [PN:integrase] [GN:int] [FN:integration of phi-13
in S.aureus genome] [OR:Bacteriophage phi-13] [DB:genpept-phg]
[DE:Bacteriophage phi-13 integrase gene.] [LE:461] [RE:1498] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000993_13939027_f3_560	2151	5923	186	61		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000993_14251933_f2_239	2152	5924	663	220	818	1.5e-81

Description

pir:[LN:A37146] [AC:A37146:A44901:S11354:C69699:I39962] [PN:ribosomal
protein S4:ribosomal protein BS4 (rpsD)] [GN:rpsD] [CL:Escherichia coli
ribosomal protein S4] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:g143467]
[LN:BACRPSD] [AC:M59358:M34718] [PN:ribosomal protein S4] [GN:rpsD]
[OR:Bacillus subtilis] [SR:B.subtilis (strain 168, isolate BR151) DNA]
[DB:genpept-bct1] [DE:B.subtilis ribosomal protein S4 gene, complete cds and
tyrosyl tRNAsynthetase (tyrS) gene, 3' end.] [LE:756] [RE:1358] [DI:direct]
>gp:[GI:e1185839:g2635450] [LN:BSUB0016] [AC:Z99119:AL009126] [PN:ribosomal
protein S4 (BS4)] [GN:rpsD] [OR:Bacillus subtilis] [DB:genpept-bct1]
[DE:Bacillus subtilis complete genome (section 16 of 21): from 2997771to
3213410.] [SP:P21466] [LE:37035] [RE:37637] [DI:direct] >gp:[GI:g2293319]
[LN:AF008220] [AC:AF008220] [PN:ribosomal protein S4] [GN:rpsD] [OR:Bacillus
subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis rrnB-dnaB genomic region.]
[LE:142790] [RE:143392] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000993_14460877_c3_963	2153	5925	138	45	131	2.8e-08

Description

gp:[GI:g1022726] [LN:SHU35635] [AC:U35635] [PN:unknown] [OR:Staphylococcus
haemolyticus] [SR:Staphylococcus haemolyticus strain=Y176] [DB:genpept-bct1]
[DE:Staphylococcus haemolyticus IS1272 ORF1 and ORF2 genes, completecds.]
[NT:ORF1] [LE:1101] [RE:1922] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000993_14460882_c1_649	2154	5926	177	58	227	6.6e-19

Description

gp:[GI:g1022726] [LN:SHU35635] [AC:U35635] [PN:unknown] [OR:Staphylococcus haemolyticus] [SR:Staphylococcus haemolyticus strain=Y176] [DB:genpept-bct1] [DE:Staphylococcus haemolyticus IS1272 ORF1 and ORF2 genes, completedcds.] [NT:ORF1] [LE:1101] [RE:1922] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000993_14460932_c1_612	2155	5927	177	58	211	3.3e-17

Description

gp:[GI:g1022726] [LN:SHU35635] [AC:U35635] [PN:unknown] [OR:Staphylococcus haemolyticus] [SR:Staphylococcus haemolyticus strain=Y176] [DB:genpept-bct1] [DE:Staphylococcus haemolyticus IS1272 ORF1 and ORF2 genes, completedcds.] [NT:ORF1] [LE:1101] [RE:1922] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000993_14460932_f2_226	2156	5928	168	55	196	1.3e-15

Description

gp:[GI:g1022726] [LN:SHU35635] [AC:U35635] [PN:unknown] [OR:Staphylococcus haemolyticus] [SR:Staphylococcus haemolyticus strain=Y176] [DB:genpept-bct1] [DE:Staphylococcus haemolyticus IS1272 ORF1 and ORF2 genes, completedcds.] [NT:ORF1] [LE:1101] [RE:1922] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000993_14656327_c2_751	2157	5929	624	207	799	1.6e-79

Description

gp:[GI:g1916729] [LN:AF134905] [AC:AF134905:U76550] [PN:CadD] [GN:cadD] [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus plasmid pRW001 CadD (cadD) gene, completedcds.] [NT:confers low level cadmium resistance] [LE:2328] [RE:2957] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000993_14658152_f3_589	2158	5930	156	51		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000993_14742937_c2_774	2159	5931	231	76		
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Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000993_14877316_f1_64	2160	5932	483	160	407	5.5e-38
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Description

sp:[LN:YEHR_ECOLI] [AC:P76270:O07976:O07978] [GN:YEHR] [OR:ESCHERICHIA COLI]
 [DE:HYPOTHETICAL 20.3 KD PROTEIN IN PRC-PPHA INTERGENIC REGION]
 [SP:P76270:O07976:O07978] [DB:swissprot] >pir:[LN:H64944] [AC:H64944]
 [PN:probable membrane protein b1832] [CL:hypothetical protein YKL069w]
 [OR:Escherichia coli] [DB:pir2] >gp:[GI:d1016364:g1736473] [LN:D90826]
 [AC:D90826:AB001340] [GN:YKL069W, YKL340] [OR:Escherichia coli]
 [SR:Escherichia coli (strain:K12) DNA, clone_lib:Kohara lambda minise]
 [DB:genpept-bct1] [DE:E.coli genomic DNA, Kohara clone #335(40.9-41.3
 min.)] [NT:ORF_ID:o335#13; similar to [SwissProt Accession] [LE:16795]
 [RE:17346] [DI:complement] >gp:[GI:d1016369:g1736479] [LN:D90827]
 [AC:D90827:AB001340] [GN:YKL069W, YKL340] [OR:Escherichia coli]
 [SR:Escherichia coli (strain:K12) DNA, clone_lib:Kohara lambda minise]
 [DB:genpept-bct1] [DE:E.coli genomic DNA, Kohara clone #336(41.2-41.6
 min.)] [NT:ORF_ID:o335#13; similar to [SwissProt Accession] [LE:2748]
 [RE:3299] [DI:complement] >gp:[GI:g1788136] [LN:AE000277]
 [AC:AE000277:U00096] [PN:orf, hypothetical protein] [GN:b1832] [FN:orf;
 Unknown] [OR:Escherichia coli] [DB:genpept-bct2] [DE:Escherichia coli K-12
 MG1655 section 167 of 400 of the completegenome.] [NT:f183; residues 72-127
 are 57 pct identical to] [LE:7076] [RE:7627] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000993_14882928_c3_923	2161	5933	1098	365	1279	2.2e-130
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Description

gp:[GI:e220317:g1177684] [LN:SXCCPA] [AC:X95439] [PN:chorismate mutase]
 [GN:aroA] [OR:Staphylococcus xylosus] [DB:genpept-bct1] [EC:5.4.99.5]
 [DE:S.xylosus aroA, ccpA, acuC and acuA genes.] [LE:<1] [RE:807] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000993_15650303_c3_882	2162	5934	207	68		
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Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000993_163151_c3_886	2163	5935	1248	415	1800	1.3e-185

Description

sp:[LN:METK_STAAU] [AC:P50307] [GN:METK] [OR:STAPHYLOCOCCUS AUREUS]
[EC:2.5.1.6] [DE:ADENOSYLTRANSFERASE) (ADOMET SYNTHETASE)] [SP:P50307]
[DB:swissprot] >gp:[GI:g1020317] [LN:SAU36379] [AC:U36379]
[PN:S-adenosylmethionine synthetase] [FN:catalyses the synthesis of SAM]
[OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:Staphylococcus aureus
S-adenosylmethionine synthetase gene,complete cds.] [NT:SAM synthetase]
[LE:212] [RE:1405] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000993_16533442_c2_738	2164	5936	522	173	546	1.0e-52

Description

gp:[GI:g1381681] [LN:BSU58864] [AC:U58864] [PN:CspR] [GN:cspR] [OR:Bacillus
subtilis] [SR:Bacillus subtilis strain=JH642] [DB:genpept-bct1] [DE:Bacillus
subtilis methylase homolog (cspR) gene, complete cds.] [NT:methylase
homolog] [LE:573] [RE:1046] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000993_16586012_f2_308	2165	5937	588	195	456	3.5e-43

Description

pir:[LN:E69999] [AC:E69999] [PN:hypothetical protein ytgB] [GN:ytqB]
[OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1185922:g2635533] [LN:BSUB0016]
[AC:Z99119:AL009126] [GN:ytqB] [FN:unknown] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 16 of 21):
from 2997771to 3213410.] [LE:122275] [RE:122859] [DI:direct]
>gp:[GI:g2293301] [LN:AF008220] [AC:AF008220] [PN:YtgB] [GN:ytqB]
[OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis rrnB-dnaB
genomic region.] [LE:57568] [RE:58152] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000993_165908_f2_353	2166	5938	507	168	182	3.8e-14

Description

sp:[LN:YHGC_BACSU] [AC:P38049] [GN:YHGC] [OR:BACILLUS SUBTILIS]
 [DE:HYPOTHETICAL 18.8 KD PROTEIN IN ECSC-PBPF INTERGENIC REGION] [SP:P38049]
 [DB:swissprot] >pir:[LN:B40614] [AC:B40614:F69832] [PN:conserved
 hypothetical protein yhgC:hypothetical protein X (pbpF 5' region)] [GN:yhgC]
 [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:g304160] [LN:BACBPBF] [AC:L10630]
 [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain W168) DNA]
 [DB:genpept-bct1]. [DE:Bacillus subtilis penicillin-binding protein (pbpF)
 gene, 5' end.] [NT:product unknown] [LE:247] [RE:747] [DI:complement]
 >gp:[GI:e1183012:g2633346] [LN:BSUB0006] [AC:Z99109:AL009126] [GN:yhgC]
 [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
 complete genome (section 6 of 21): from 999501 to1209940.] [NT:alternate
 gene name: yixC; similar to hypothetical] [SP:P38049] [LE:83202] [RE:83702]
 [DI:complement] >gp:[GI:e325006:g2226228] [LN:BSY14083] [AC:Y14083]
 [PN:Hypothetical protein] [GN:yixC] [OR:Bacillus subtilis] [DB:genpept-bct1]
 [DE:Bacillus subtilis chromosomal DNA, region 76-78 degrees:
 betweenglyB-aprE.] [NT:See Swiss Prot P38049; YIXC_BACSU] [SP:P38049]
 [LE:3061] [RE:3561] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000993_16835053_c2_758	2167	5939	168	55		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000993_16994043_c3_933	2168	5940	1128	375	81	0.0062

Description

pir:[LN:E69106] [AC:E69106] [PN:hypothetical protein MTH1793] [GN:MTH1793]
 [OR:Methanobacterium thermoautotrophicum] [DB:pir2] >gp:[GI:g2622925]
 [LN:AE000934] [AC:AE000934:AE000666] [PN:unknown] [GN:MTH1793]
 [OR:Methanobacterium thermoautotrophicum] [DB:genpept-bct2]
 [DE:Methanobacterium thermoautotrophicum from bases 1640298 to
 1655421(section 140 of 148) of the complete genome.] [NT:Function Code:14.00
 - Unknown, ; similar to,] [LE:89] [RE:790] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000993_189437_f1_34	2169	5941	144	47		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000993_191713_c3_904	2170	5942	11091	3696	1884	6.9e-195

Description

gp:[GI:e286140:g4775551] [LN:SACTORF13] [AC:Y09928] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:S.aureus CTORF1365, partial.] [NT:CTORF1365] [LE:<1] [RE:>3982] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000993_19565876_c3_915	2171	5943	201	66		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000993_1960937_c3_964	2172	5944	177	58	228	5.1e-19

Description

gp:[GI:g1022726] [LN:SHU35635] [AC:U35635] [PN:unknown] [OR:Staphylococcus haemolyticus] [SR:Staphylococcus haemolyticus strain=Y176] [DB:genpept-bct1] [DE:Staphylococcus haemolyticus IS1272 ORF1 and ORF2 genes, completecds.] [NT:ORF1] [LE:1101] [RE:1922] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000993_19742842_c2_769	2173	5945	849	282	776	4.4e-77

Description

pir:[LN:C70040] [AC:C70040] [PN:plant-metabolite dehydrogenase homolog yvgN] [GN:yvgN] [CL:aldehyde reductase] [OR:Bacillus subtilis] [DB:pir2]
>gp:[GI:e1249784:g2832788] [LN:BS43KBDNA] [AC:AJ223978] [PN:putative reductase protein, YvgN] [GN:yvgN] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis 42.7kB DNA fragment from yvsa to yvqa.] [LE:646] [RE:1476] [DI:direct] >gp:[GI:e1186028:g2635853] [LN:BSUB0018] [AC:Z99121:AL009126] [GN:yvgN] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.] [NT:alternate gene name: yvsB; similar to] [LE:26261] [RE:27091] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000993_19770437_c2_830	2174	5946	1332	443	1018	9.9e-103

Description

pir:[LN:A69998] [AC:A69998] [PN:hypothetical protein ytoI] [GN:ytoI]
 [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1184176:g2635392] [LN:BSUB0015]
 [AC:Z99118:AL009126] [GN:ytoI] [FN:unknown] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 15 of 21):
 from 2795131to 3013540.] [LE:201244] [RE:202563] [DI:complement]
 >gp:[GI:g2293258] [LN:AF008220] [AC:AF008220] [PN:YtoI] [GN:ytoI]
 [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis rrnB-dnaB
 genomic region.] [NT:similarity with hypothetical protein 3 from]
 [LE:180504] [RE:181823] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000993_1991325_f3_469	2175	5947	219	72		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000993_19922162_c3_857	2176	5948	1161	386	527	1.1e-50

Description

gp:[GI:g3688818] [LN:AF084104] [AC:AF084104] [PN:hypothetical protein]
 [OR:Bacillus firmus] [DB:genpept-bct2] [DE:Bacillus firmus AcsA (acsA) gene,
 partial cds; SspA (sspA),hypothetical protein, maltose transportor
 ATP-binding protein(malK), leucine-rich protein transcriptional regulator
 (lrpR),hypothetical proteins, ABC transporter ATP-binding protein
 (natC),NatA (natA), NatB (natB), and hypothetical protein genes,
 completecds; and SpoIIIJ (spoIIIJ) gene, partial cds.] [NT:Orf10; similar to
 hypothetical protein YheB from] [LE:5845] [RE:6957] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000993_1992943_f3_561	2177	5949	747	248	104	2.3e-05

Description

gp:[GI:g160225] [LN:PFACSPI] [AC:M18821] [PN:circumsporozoite protein]
 [GN:CSP] [OR:Plasmodium yoelii] [SR:Plasmodium yoelii (strain 17X NL) DNA]
 [DB:genpept-inv1] [DE:Plasmodium yoelii circumsporozoite protein (CSP) gene,
 5' end.] [NT:precursor] [LE:1] [RE:>420] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000993_20365892_c1_731	2178	5950	150	49		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000993_2051502_f2_250	2179	5951	159	52		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000993_20706557_c3_860	2180	5952	1254	417	592	1.4e-57

Description

pir:[LN:A69819] [AC:A69819] [PN:probable phosphoesterase, yhaO] [GN:yhaO]
[CL:unassigned probable phosphoesterases: phosphoesterase core homology]
[OR:Bacillus subtilis] [EC:3.1.-.-] [DB:pir2] >gp:[GI:e1182993:g2633327]
[LN:BSUB0006] [AC:Z99109:AL009126] [GN:yhaO] [FN:unknown] [OR:Bacillus
subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 6
of 21): from 999501 to1209940.] [NT:similar to hypothetical proteins]
[LE:64822] [RE:66048] [DI:direct] >gp:[GI:e324934:g2226129] [LN:BSY14078]
[AC:Y14078] [PN:Hypothetical protein] [GN:yhaO] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis 8.7 Kb chromosomal DNA: downstream
glyB-prsAregion.] [NT:similarity to exonuclease sbcD from Escherichia]
[LE:4292] [RE:5518] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000993_20834812_f2_339	2181	5953	306	101	86	0.0039

Description

pir:[LN:S77632] [AC:S77632:S52761] [PN:probable integrase] [GN:int]
[OR:Staphylococcus aureus phage phi-13] [DB:pir2] >gp:[GI:g758229]
[LN:PHI13INT] [AC:X82312] [PN:integrase] [GN:int] [FN:integration of phi-13
in S.aureus genome] [OR:Bacteriophage phi-13] [DB:genpept-phg]
[DE:Bacteriophage phi-13 integrase gene.] [LE:461] [RE:1498] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000993_20901713_c3_939	2182	5954	1707	568	613	8.2e-60

Description

pir:[LN:G70002] [AC:G70002] [PN:hypothetical protein ytwP] [GN:ytwP]
 [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1185834:g2635445] [LN:BSUB0016]
 [AC:Z99119:AL009126] [GN:ytwP] [FN:unknown] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 16 of 21):
 from 2997771to 3213410.] [LE:31035] [RE:32723] [DI:complement]
 >gp:[GI:g2293228] [LN:AF008220] [AC:AF008220] [PN:YtwP] [GN:ytwP]
 [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis rrnB-dnaB
 genomic region.] [NT:similarity to fcrA protein precursor from] [LE:147704]
 [RE:149392] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000993_20947781_f2_348	2183	5955	126	41		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000993_2115812_f2_222	2184	5956	1113	370	843	3.5e-84

Description

pir:[LN:G69869] [AC:G69869] [PN:Xaa-Pro dipeptidase homolog ykvY] [GN:ykvY]
 [CL:X-Pro aminopeptidase] [OR:Bacillus subtilis] [DB:pir2]
 >gp:[GI:e1184976:g2633757] [LN:BSUB0008] [AC:Z99111:AL009126] [GN:ykvY]
 [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
 complete genome (section 8 of 21): from 1394791to 1603020.] [NT:similar to
 Xaa-Pro dipeptidase] [LE:58367] [RE:59458] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000993_2117077_f3_536	2185	5957	366	121	195	1.6e-15

Description

pir:[LN:A70341] [AC:A70341] [PN:conserved hypothetical protein aq_449]
 [GN:aq_449] [CL:hypothetical protein MJ1523] [OR:Aquifex aeolicus]
 [DB:pir2] >gp:[GI:g2983116] [LN:AE000690] [AC:AE000690:AE000657]
 [PN:hypothetical protein] [GN:aq_449] [OR:Aquifex aeolicus]
 [DB:genpept-bct2] [DE:Aquifex aeolicus section 22 of 109 of the complete
 genome.] [LE:10789] [RE:11163] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000993_2126250_f2_305	2186	5958	210	69		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000993_21491462_c1_722	2187	5959	1161	386	1188	9.6e-121

Description

sp:[LN:CISZ_BACSU] [AC:P39120:O34435] [GN:CITZ:CITA2] [OR:BACILLUS SUBTILIS] [EC:4.1.3.7] [DE:CITRATE SYNTHASE II,] [SP:P39120:O34435] [DB:swissprot] >pir:[LN:G69600] [AC:G69600:I40381] [PN:citrate synthase II,] [GN:citZ] [CL:citrate (si)-synthase] [OR:Bacillus subtilis] [EC:4.1.3.-] [DB:pir2] >gp:[GI:el184163:g2635379] [LN:BSUB0015] [AC:Z99118:AL009126] [PN:citrate synthase II] [GN:citZ] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:4.1.3.7] [DE:Bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.] [NT:alternate gene name: cita2] [SP:P39120] [LE:185094] [RE:186212] [DI:complement] >gp:[GI:g2293267] [LN:AF008220] [AC:AF008220] [PN:citrate synthase subunit II] [GN:citZ] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis rrnB-dnaB genomic region.] [LE:196855] [RE:197973] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000993_21520887_c2_781	2188	5960	135	44		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000993_21522010_f2_331	2189	5961	1725	574	2393	2.0e-248

Description

sp:[LN:PPCK_STAAU] [AC:P51065] [GN:PCKA] [OR:STAPHYLOCOCCUS AUREUS] [EC:4.1.1.49] [DE:PHOSPHOENOLPYRUVATE CARBOXYKINASE [ATP],] [SP:P51065] [DB:swissprot] >gp:[GI:g1255262] [LN:SAU51133] [AC:U51133] [PN:phosphoenolpyruvate carboxykinase] [GN:pcka] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:Staphylococcus aureus phosphoenolpyruvate carboxykinase (pcka)gene, complete cds.] [LE:160] [RE:1752] [DI:direct] >gp:[GI:g860732] [LN:STAPEPCK] [AC:L42943] [PN:phosphoenolpyruvate carboxykinase] [GN:pcka] [OR:Staphylococcus aureus] [DB:genpept-bct1] [EC:4.1.1.32] [DE:Staphylococcus aureus (clone KIN50) phosphoenolpyruvatecarboxykinase (pcka) gene, complete cds.] [NT:PEPCK; homologue] [LE:409] [RE:2001] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000993_21523400_f2_356	2190	5962	162	53		
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Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000993_21645967_f3_575	2191	5963	993	330	368	7.5e-34
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Description

sp:[LN:PRSA_BACSU] [AC:P24327] [GN:PRSA] [OR:BACILLUS SUBTILIS] [DE:PROTEIN EXPORT PROTEIN PRSA PRECURSOR] [SP:P24327] [DB:swissprot] >pir:[LN:S15269] [AC:S15269:I40003:H69682] [PN:post-translocation molecular chaperone prsA:33K lipoprotein prsA] [GN:prsA] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:g39782] [LN:BS33KDA] [AC:X57271:S67658] [PN:33kDa lipoprotein] [GN:prsA] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis prsA gene for a 33kDa lipoprotein.] [SP:P24327] [LE:63] [RE:941] [DI:direct] >gp:[GI:e1182997:g2633331] [LN:BSUB0006] [AC:Z99109:AL009126] [PN:molecular chaperonin] [GN:prsA] [FN:essential for the stability of secreted] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.] [SP:P24327] [LE:70340] [RE:71218] [DI:complement] >gp:[GI:e325181:g2226124] [LN:BSY14077] [AC:Y14077] [PN:33kDa lipoprotein] [GN:prsA] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis 10.6 Kb chromosomal DNA: glyB-prsA region.] [NT:See Swiss Prot P24327] [SP:P24327] [LE:9695] [RE:10573] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000993_2189718_f3_412	2192	5964	1371	456	1309	1.4e-133
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Description

sp:[LN:CYCA_ECOLI] [AC:P39312] [GN:CYCA:DAGA] [OR:ESCHERICHIA COLI] [DE:D-SERINE/D-ALANINE/GLYCINE TRANSPORTER] [SP:P39312] [DB:swissprot] >pir:[LN:S56433] [AC:S56433:C65232] [PN:d-serine/d-alanine/glycine transporter] [GN:cycA] [CL:arginine permease] [OR:Escherichia coli] [DB:pir2] >gp:[GI:g537049] [LN:ECOUW93] [AC:U14003] [OR:Escherichia coli] [DB:genpept-bct1] [DE:Escherichia coli K-12 chromosomal region from 92.8 to 00.1 minutes.] [NT:ORF_o470] [LE:120696] [RE:122108] [DI:direct] >gp:[GI:g1790653] [LN:AE000492] [AC:AE000492:U00096] [PN:transport of D-alanine, D-serine, and glycine] [GN:cycA] [FN:transport; Transport of small molecules: Amino] [OR:Escherichia coli] [DB:genpept-bct2] [DE:Escherichia coli K-12 MG1655 section 382 of 400 of the completegenome.] [NT:o470; 100 pct identical amino acid sequence and] [LE:2436] [RE:3848] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000993_22078331_f3_564	2193	5965	252	83		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000993_22164757_f2_244	2194	5966	132	43		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000993_22271932_c1_651	2195	5967	132	43		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000993_22277327_c3_968	2196	5968	1371	456	496	2.0e-47

Description

sp:[LN:DNAB_BACSU] [AC:P07908] [GN:DNAB] [OR:BACILLUS SUBTILIS]
 [DE:REPLICATION INITIATION AND MEMBRANE ATTACHMENT PROTEIN] [SP:P07908]
 [DB:swissprot] >pir:[LN:B26580] [AC:B26580:A24720:A69617] [PN:chromosome
 replication initiation / membrane attachment protein dnaB:dnaB protein]
 [GN:dnaB] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:g142863] [LN:BACDNAB]
 [AC:M15183] [PN:replication initiation protein] [GN:dnaB] [OR:Bacillus
 subtilis] [SR:Bacillus subtilis (sub_strain PY79, strain W168) DNA]
 [DB:genpept-bct1] [DE:B.subtilis dnaB gene, encoding the replication
 initiation andmembrane attachment protein, complete cds, clone pdnaB12.]
 [NT:The part of the protein encoded by 634-693 binds to] [LE:397] [RE:1815]
 [DI:direct] >gp:[GI:e1184148:g2635364] [LN:BSUB0015] [AC:Z99118:AL009126]
 [PN:membrane attachment protein] [GN:dnaB] [FN:initiation of chromosome
 replication (DNA) [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus
 subtilis complete genome (section 15 of 21): from 2795131to 3013540.]
 [LE:168092] [RE:169510] [DI:complement] >gp:[GI:e1165285:g1769995]
 [LN:BSZ75208] [AC:Z75208] [PN:replication initiation protein] [GN:dnaB]
 [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis genomic sequence
 89009bp.] [NT:the part of the protein encoded by 634-693 binds to]
 [SP:P07908] [LE:397] [RE:1815] [DI:direct] >gp:[GI:g2293280] [LN:AF008220]
 [AC:AF008220] [PN:DnaB] [GN:dnaB] [OR:Bacillus subtilis] [DB:genpept-bct2]
 [DE:Bacillus subtilis rrnB-dnaB genomic region.] [LE:213557] [RE:214975]
 [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000993_22391432_f3_562	2197	5969	525	174	288	2.3e-25

Description

pir:[LN:S77632] [AC:S77632:S52761] [PN:probable integrase] [GN:int]
 [OR:Staphylococcus aureus phage phi-13] [DB:pir2] >gp:[GI:g758229]
 [LN:PHI13INT] [AC:X82312] [PN:integrase] [GN:int] [FN:integration of phi-13
 in S.aureus genome] [OR:Bacteriophage phi-13] [DB:genpept-phg]
 [DE:Bacteriophage phi-13 integrase gene.] [LE:461] [RE:1498] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000993_22459692_f1_125	2198	5970	201	66		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000993_22664125_c2_832	2199	5971	165	54		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000993_23438837_f3_600	2200	5972	132	43		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000993_23468812_f1_141	2201	5973	129	42		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000993_23485443_c1_709	2202	5974	1239	412	931	1.6e-93

Description

sp:[LN:THII_BACSU] [AC:O34595] [GN:THII] [OR:BACILLUS SUBTILIS] [DE:PROBABLE THIAMIN BIOSYNTHESIS PROTEIN THII] [SP:O34595] [DB:swissprot]
 >pir:[LN:E69988] [AC:E69988] [PN:conserved hypothetical protein ytbJ]
 [GN:ytbJ] [CL:Mycoplasma genitalium hypothetical protein MG372]
 [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1185831:g2635442] [LN:BSUB0016]
 [AC:Z99119:AL009126] [GN:ytbJ] [FN:unknown] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 16 of 21):
 from 2997771to 3213410.] [NT:similar to hypothetical proteins] [SP:O34595]
 [LE:27183] [RE:28259] [DI:complement] >gp:[GI:g2293230] [LN:AF008220]
 [AC:AF008220] [PN:YtbJ] [GN:ytbJ] [OR:Bacillus subtilis] [DB:genpept-bct2]
 [DE:Bacillus subtilis rrnB-dnaB genomic region.] [NT:similar to hypothetical
 protein MG372 from M.] [LE:152168] [RE:153244] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000993_23489090_c2_835	2203	5975	1038	345	1033	2.5e-104

Description

sp:[LN:K6PF_BACSU] [AC:O34529] [GN:PFKA:PFK] [OR:BACILLUS SUBTILIS]
 [EC:2.7.1.11] [DE:(PHOSPHOHEXOKINASE)] [SP:O34529] [DB:swissprot]
 >pir:[LN:A69675] [AC:A69675] [PN:6-phosphofructokinase pfk] [GN:pfk]
 [CL:6-phosphofructokinase:6-phosphofructokinase 1 homology] [OR:Bacillus
 subtilis] [DB:pir2] >gp:[GI:e1184168:g2635384] [LN:BSUB0015]
 [AC:Z99118:AL009126] [PN:6-phosphofructokinase] [GN:pfk] [FN:glycolysis]
 [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:2.7.1.11] [DE:Bacillus subtilis
 complete genome (section 15 of 21): from 2795131to 3013540.] [SP:O34529]
 [LE:190531] [RE:191490] [DI:complement] >gp:[GI:g2293264] [LN:AF008220]
 [AC:AF008220] [PN:6-phosphofructokinase] [GN:pfk] [OR:Bacillus subtilis]
 [DB:genpept-bct2] [DE:Bacillus subtilis rrnB-dnaB genomic region.]
 [LE:191577] [RE:192536] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000993_23555302_f2_233	2204	5976	387	128	91	0.00083

Description

gp:[GI:e1363147:g4127385] [LN:APR011678] [AC:AJ011678] [PN:immunodominant
 protein] [OR:Apple proliferation phytoplasma] [DB:genpept-bct1] [DE:Apple
 proliferation phytoplasma immunodominant protein gene, strainAT.] [LE:885]
 [RE:1382] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000993_23601713_c3_894	2205	5977	1194	397	1108	2.9e-112

Description

sp:[LN:GCH2_BACAM] [AC:P51695] [GN:RIBA] [OR:BACILLUS AMYLOLIQUEFACIENS]
[EC:3.5.4.25] [DE:PHOSPHATE SYNTHASE (DHBP SYNTHASE)] [SP:P51695]
[DB:swissprot] >gp:[GI:e223994:g1212775] [LN:BARIBGENS] [AC:X95955]
[PN:3,4-dihydroxy-2-butanone 4-phosphate synthase] [GN:riba] [OR:Bacillus
amyloliquefaciens] [DB:genpept-bct1] [DE:B.amyloliquefaciens ribB, ribG,
ribA, ribH & ribT genes.] [NT:GTP cyclohydrolase II] [SP:P51695] [LE:2411]
[RE:3607] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000993_23603375_f2_219	2206	5978	417	138	139	1.4e-09

Description

sp:[LN:Y577_METJA] [AC:Q57997] [GN:MJ0577] [OR:METHANOCOCCUS JANNASCHII]
[DE:PROTEIN MJ0577] [SP:Q57997] [DB:swissprot] >pir:[LN:A64372] [AC:A64372]
[PN:hypothetical protein homolog MJ0577] [CL:Escherichia coli ybdQ protein]
[OR:Methanococcus jannaschii] [DB:pir2] [MP:FOR512975-513463]
>gp:[GI:g1591284] [LN:U67506] [AC:U67506:L77117] [PN:conserved hypothetical
protein] [GN:MJ0577] [OR:Methanococcus jannaschii] [DB:genpept-bct2]
[DE:Methanococcus jannaschii section 48 of 150 of the complete genome.]
[NT:similar to SP:P42297 PID:603780 PID:849027] [LE:8204] [RE:8692]
[DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000993_2362587_f2_321	2207	5979	150	49		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000993_23651567_c3_961	2208	5980	888	295	387	5.2e-41

Description

gp:[GI:d1025814:g2897751] [LN:AB008520] [AC:AB008520] [GN:mutM] [OR:Thermus
thermophilus] [SR:Thermus thermophilus (strain:HB8) DNA] [DB:genpept-bct1]
[DE:Thermus thermophilus MutM gene, complete cds.] [LE:297] [RE:1100]
[DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000993_23694052_f2_359	2209	5981	603	200	82	0.0040

Description

pir:[LN:E69818] [AC:E69818] [PN:hypothetical protein yhaK] [GN:yhaK]
 [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1182998:g2633332] [LN:BSUB0006]
 [AC:Z99109:AL009126] [GN:yhaK] [FN:unknown] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 6 of 21):
 from 999501 to1209940.] [LE:72018] [RE:72272] [DI:complement]
 >gp:[GI:e324957:g2226123] [LN:BSY14077] [AC:Y14077] [PN:Hypothetical
 protein] [GN:yhaK] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus
 subtilis 10.6 Kb chromosomal DNA: glyB-prsA region.] [LE:8641] [RE:8895]
 [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000993_23710885_f2_167	2210	5982	147	48	76	0.027

Description

pir:[LN:S72289] [AC:S72289] [PN:ribosomal protein L2] [GN:rpl2]
 [OR:plastid Plasmodium falciparum] [DB:pir2] >gp:[GI:e220178:g1171595]
 [LN:PFCOMPIRB] [AC:X95276] [GN:rpl2] [OR:Plasmodium falciparum] [SR:malaria
 parasite P. falciparum] [DB:genpept-inv1] [DE:P.falciparum complete gene map
 of plastid-like DNA (IR-B).] [LE:2799] [RE:3536] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000993_2380342_c2_741	2211	5983	636	211	463	6.4e-44

Description

pir:[LN:F69824] [AC:F69824] [PN:two-component response regulator [YhcY]
 homolog yhcZ] [GN:yhcZ] [CL:regulatory protein comA:response regulator
 homology] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1182922:g2633256]
 [LN:BSUB0005] [AC:Z99108:AL009126] [GN:yhcZ] [FN:unknown] [OR:Bacillus
 subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 5
 of 21): from 802821 to1011250.] [NT:similar to two-component response
 regulator [YhcY]] [LE:206441] [RE:207085] [DI:direct]
 >gp:[GI:e1182934:g2633268] [LN:BSUB0006] [AC:Z99109:AL009126] [GN:yhcZ]
 [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
 complete genome (section 6 of 21): from 999501 to1209940.] [NT:similar to
 two-component response regulator [YhcY]] [LE:9761] [RE:10405] [DI:direct]
 >gp:[GI:e324945:g2226141] [LN:BSY14079] [AC:Y14079] [PN:hypothetical
 protein] [GN:yhcZ] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus
 subtilis chromosomal DNA, region 75 degrees: glpPFKDoperon and downstream.]
 [NT:similarity to the transcriptional regulator degU] [LE:9409] [RE:10053]
 [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000993_2383253_c1_635	2212	5984	198	65		
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Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000993_23984787_c3_924	2213	5985	1011	336	1404	1.2e-143
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Description

sp:[LN:CCPA_STAXY] [AC:Q56194] [GN:CCPA] [OR:STAPHYLOCOCCUS XYLOSUS]
 [DE:PROBABLE CATABOLITE CONTROL PROTEIN A] [SP:Q56194] [DB:swissprot]
 >gp:[GI:e220318:g1177685] [LN:SXCCPA] [AC:X95439] [GN:ccpA]
 [OR:Staphylococcus xylosus] [DB:genpept-bct1] [DE:S.xylosus aroA, ccpA, acuC
 and acuA genes.] [SP:Q56194] [LE:1305] [RE:2294] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000993_24017890_c2_843	2214	5986	1428	476	1242	1.8e-126
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Description

sp:[LN:LYSP_ECOLI] [AC:P25737] [GN:LYSP:CADR] [OR:ESCHERICHIA COLI]
 [DE:LYSINE-SPECIFIC PERMEASE] [SP:P25737] [DB:swissprot]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000993_24020250_c1_654	2215	5987	882	293	551	6.5e-52
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Description

gp:[GI:e1295630:g3184134] [LN:SSAASPROT] [AC:AJ000007] [PN:AAS surface
 protein] [GN:aas] [OR:Staphylococcus saprophyticus] [DB:genpept-bct1]
 [DE:Staphylococcus saprophyticus aas gene.] [LE:203] [RE:4594] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000993_24025463_c1_620	2216	5988	2952	983	1357	1.2e-138
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Description

gp:[GI:g710421] [LN:SAU21636] [AC:U21636] [PN:unknown] [OR:Staphylococcus
 aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus cmp-binding-factor 1
 (cbf1) and ORF X genes,complete cds.] [NT:ORF X] [LE:52] [RE:1158]
 [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000993_24226543_c1_704	2217	5989	783	260	365	1.6e-33

Description

pir:[LN:E69827] [AC:E69827] [PN:glycerophosphodiester phosphodiesterase homolog yhdW] [GN:yhdW] [OR:Bacillus subtilis] [DB:pir2]
 >gp:[GI:e1182963:g2633297] [LN:BSUB0006] [AC:Z99109:AL009126] [GN:yhdW] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.] [NT:similar to glycerophosphodiester phosphodiesterase] [LE:37668] [RE:38399] [DI:complement] >gp:[GI:e1191883:g2226218] [LN:BSY14082] [AC:Y14082] [PN:hypothetical protein] [GN:yhdW] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis chromosomal DNA, region 72 to 75 degrees: spoVRto sspB.] [NT:Similarity to glycerol diester phosphodiesterase] [LE:24316] [RE:25047] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000993_2426312_f1_103	2218	5990	135	44		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000993_24272568_c2_782	2219	5991	147	48		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000993_2428950_c3_844	2220	5992	444	147	227	6.6e-19

Description

gp:[GI:g1022725] [LN:SHU35635] [AC:U35635] [PN:unknown] [OR:Staphylococcus haemolyticus] [SR:Staphylococcus haemolyticus strain=Y176] [DB:genpept-bct1] [DE:Staphylococcus haemolyticus IS1272 ORF1 and ORF2 genes, completecds.] [NT:ORF2] [LE:394] [RE:1083] [DI:complement] >gp:[GI:g295162] [LN:STAMECRA] [AC:L14017] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus (strain COL) DNA] [DB:genpept-bct1] [DE:Staphylococcus aureus methicillin-resistance protein (mecR) geneand unknown ORF, complete cds.] [NT:unknown ORF1; putative] [LE:1492] [RE:2181] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000993_24296925_f3_534	2221	5993	552	183	127	6.2e-08

Description

gp:[GI:e184374:g2104803] [LN:CBDNAPTCG] [AC:X87972] [GN:P-21]
[OR:Clostridium botulinum] [DB:genpept-bct1] [DE:C.botulinum progenitor
toxin complex genes.] [LE:2337] [RE:2882] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000993_24307677_c2_772	2222	5994	144	47		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000993_24334563_c2_789	2223	5995	453	150	109	1.5e-05

Description

gp:[GI:e1492342:g5262792] [LN:ATT13K14] [AC:AL080282] [PN:putative protein]
[GN:T13K14.180] [OR:Arabidopsis thaliana] [SR:thale cress] [DB:genpept]
[DE:Arabidopsis thaliana DNA chromosome 4, BAC clone T13K14 (ESSAproject).]
[NT:similarity to desiccation-related protein,] [LE:67362:67832]
[RE:67502:68491] [DI:directJoin]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000993_24337750_c3_913	2224	5996	852	283	1238	4.8e-126

Description

sp:[LN:DAAA_STAHA] [AC:P54694] [GN:DAT] [OR:STAPHYLOCOCCUS HAEMOLYTICUS]
[EC:2.6.1.21] [DE:TRANSAMINASE]] [SP:P54694] [DB:swissprot] >gp:[GI:g517475]
[LN:SHU12238] [AC:U12238] [PN:D-amino acid transaminase] [GN:dat]
[OR:Staphylococcus haemolyticus] [DB:genpept-bct1] [DE:Staphylococcus
haemolyticus Y176 D-amino acid transaminase (dat)gene, complete cds.]
[LE:216] [RE:1064] [DI:direct].

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000993_24407577_c1_724	2225	5997	738	245	833	4.0e-83

Description

sp:[LN:PHOP_BACSU] [AC:P13792] [GN:PHOP] [OR:BACILLUS SUBTILIS] [DE:PHOP]
[SP:P13792] [DB:swissprot] >gp:[GI:g40056] [LN:BSPHOPDNA] [AC:X67676]
[GN:phoP] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis phoP
gene.] [SP:P13792] [LE:199] [RE:921] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000993_24407765_c1_710	2226	5998	795	264	413	1.3e-38

Description

sp:[LN:YCB9_PSEDE] [AC:P29942] [OR:PSEUDOMONAS DENITRIFICANS]
 [DE:HYPOTHETICAL 27.4 KD PROTEIN IN COBO 3'REGION (ORF9)] [SP:P29942]
 [DB:swissprot] >pir:[LN:I38164] [AC:I38164] [PN:hypothetical protein 9]
 [OR:Pseudomonas sp.] [DB:pir2] >gp:[GI:g551929] [LN:PSECOBGEN] [AC:M62866]
 [OR:Pseudomonas denitrificans] [SR:Pseudomonas denitrificans (strain SC510)
 DNA] [DB:genpept-bct1] [DE:P.denitrificans cobN, cobO, cobP, cobQ, cobW, and
 ORF6-9 genes,complete cds.] [NT:ORF9] [LE:12364] [RE:13149] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000993_24409803_c1_633	2227	5999	123	40	81	0.019

Description

pir:[LN:S75730] [AC:S75730:S50064] [PN:8-amino-7-oxononanoate
 synthase,:7-keto-8-aminopelargonic acid synthetase:protein
 slr0917:7-keto-8-aminopelargonic acid synthetase:protein slr0917] [GN:bioF]
 [CL:5-aminolevulinate synthase] [OR:Synechocystis sp.] [SR:PCC 6803, , PCC
 6803] [SR:PCC 6803,] [EC:2.3.1.47] [DB:pir2] >gp:[GI:d1011116:g1673311]
 [LN:SYCSLLE] [AC:D64003:AB001339] [PN:7-keto-8-aminopelargonic acid
 synthetase] [GN:bioF] [OR:Synechocystis sp.] [SR:Synechocystis sp.
 (strain:PCC6803) DNA] [DB:genpept-bct1] [DE:Synechocystis sp. PCC6803
 complete genome, 22/27, 2755703-2868766.] [NT:ORF_ID:slr0917] [LE:35986]
 [RE:37299] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000993_24417252_c3_902	2228	6000	1248	415	1038	7.5e-105

Description

pir:[LN:F70001] [AC:F70001] [PN:multidrug resistance protein homolog yttB]
 [GN:yttB] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1185908:g2635519]
 [LN:BSUB0016] [AC:Z99119:AL009126] [GN:yttB] [FN:unknown] [OR:Bacillus
 subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section
 16 of 21): from 2997771to 3213410.] [NT:similar to multidrug resistance
 protein] [LE:108543] [RE:109736] [DI:complement] >gp:[GI:g2293179]
 [LN:AF008220] [AC:AF008220] [PN:YttB] [GN:yttB] [OR:Bacillus subtilis]
 [DB:genpept-bct2] [DE:Bacillus subtilis rrnB-dnaB genomic region.]
 [NT:similarity to tetracycline resistance protein from] [LE:70691]
 [RE:71884] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000993_24428760_f3_509	2229	6001	129	42		
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Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000993_24475377_f3_537	2230	6002	159	52		
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Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000993_24490702_c1_616	2231	6003	405	134	74	0.011
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Description

sp:[LN:Y70A_METJA] [AC:P81311] [GN:MJ0703.1] [OR:METHANOCOCCUS JANNASCHII]
 [DE:HYPOTHETICAL PROTEIN MJ0703.1] [SP:P81311] [DB:swissprot]
 >gp:[GI:g2826311] [LN:U67517] [AC:U67517:L77117] [PN:M. jannaschii predicted
 coding region MJ0703.1] [GN:MJ0703.1] [OR:Methanococcus jannaschii]
 [DB:genpept-bct2] [DE:Methanococcus jannaschii section 59 of 150 of the
 complete genome.] [NT:Brute Force ORF; identified by GeneMark; putative]
 [LE:94] [RE:402] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000993_24492130_f1_70	2232	6004	123	40		
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Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000993_24508552_c3_971	2233	6005	1953	650	2471	1.1e-256

Description

sp:[LN:SYT1_BACSU] [AC:P18255:P06570] [GN:THRS:THRSV] [OR:BACILLUS SUBTILIS] [EC:6.1.1.3] [DE:(THRRS)] [SP:P18255:P06570] [DB:swissprot] >pir:[LN:YSBST1] [AC:B37770:E24720:B69723] [PN:threonine--tRNA ligase,, major (thrS):threonyl-tRNA synthetase] [GN:thrS:thrSv] [CL:threonine--tRNA ligase] [OR:Bacillus subtilis] [EC:6.1.1.3] [DB:pir1] [MP:250 (degrees)] >gp:[GI:g143766] [LN:BACTRNASB] [AC:M36594] [OR:Bacillus subtilis] [SR:B.subtilis (strain 168) vegetative form DNA] [DB:genpept-bct1] [DE:B.subtilis threonyl-tRNA synthetase (thrSv) gene, complete cds.] [NT:(thrSv) (EC 6.1.1.3)] [LE:365] [RE:2296] [DI:direct] >gp:[GI:e1184144:g2635360] [LN:BSUB0015] [AC:Z99118:AL009126] [PN:threonyl-tRNA synthetase] [GN:thrS] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:6.1.1.3] [DE:Bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.] [SP:P18255] [LE:163202] [RE:165133] [DI:complement] >gp:[GI:e1165290:g1769999] [LN:BSZ75208] [AC:Z75208] [PN:threonyl-tRNA-synthetase] [GN:thrS] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:6.1.1.3] [DE:B.subtilis genomic sequence 89009bp.] [NT:thrS (111-180); Major threonyl-tRNA synthetase] [SP:P18255] [LE:4774] [RE:6705] [DI:direct] >gp:[GI:g2293284] [LN:AF008220] [AC:AF008220] [PN:threonine tRNA synthetase] [GN:thrS] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis rrnB-dnaB genomic region.] [LE:217934] [RE:219865] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000993_24609676_c2_773	2234	6006	471	156	72	0.030

Description

sp:[LN:NULM_DASNO] [AC:O21333] [GN:MTND4L:ND4L:NADH4L] [OR:DASYPUS NOVMCINCTUS] [SR:,NINE-BANDED ARMADILLO] [EC:1.6.5.3] [DE:NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4L,] [SP:O21333] [DB:swissprot] >gp:[GI:e311022:g2252509] [LN:MTDNCOMGN] [AC:Y11832] [GN:NADH4L] [OR:Mitochondrion Dasypus novemcinctus] [SR:nine-banded armadillo] [DB:genpept-mam] [DE:D.novemcinctus complete mitochondrial genome.] [SP:O21333] [LE:9903] [RE:10199] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000993_24662915_c3_960	2235	6007	2718	905	2572	2.1e-267

Description

sp:[LN:DPO1_BACSU] [AC:O34996] [GN:POLA] [OR:BACILLUS SUBTILIS] [EC:2.7.7.7] [DE:DNA POLYMERASE I, (POL I)] [SP:O34996] [DB:swissprot] >pir:[LN:E69680] [AC:E69680] [PN:DNA polymerase I polA] [GN:polA] [CL:DNA-directed DNA polymerase I] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1184158:g2635374] [LN:BSUB0015] [AC:Z99118:AL009126] [PN:DNA polymerase I] [GN:polA] [FN:replication and DNA repair] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:2.7.7.7] [DE:Bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.] [SP:O34996] [LE:177125] [RE:179767] [DI:complement] >gp:[GI:g2293272] [LN:AF008220] [AC:AF008220] [PN:DNA-polymerase I] [GN:polA] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis rrnB-dnaB genomic region.] [LE:203300] [RE:205942] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000993_24692338_c3_895	2236	6008	474	157	540	4.5e-52

Description

sp:[LN:RISB_BACAM] [AC:Q44681] [GN:RIBH] [OR:BACILLUS AMYLOLIQUEFACIENS] [EC:2.5.1.9] [DE:(LUMAZINE SYNTHASE) (RIBOFLAVIN SYNTHASE BETA CHAIN)] [SP:Q44681] [DB:swissprot] >gp:[GI:e223995:g1212776] [LN:BARIBGENS] [AC:X95955] [PN:lumazine synthase (b-subunit)] [GN:ribH] [OR:Bacillus amyloliquefaciens] [DB:genpept-bct1] [DE:B.amyloliquefaciens ribB, ribG, ribA, ribH & ribT genes.] [SP:Q44681] [LE:3639] [RE:4103] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000993_24720291_f2_322	2237	6009	498	165		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000993_24726077_c3_965	2238	6010	1026	341	1088	3.8e-110

Description

sp:[LN:G3P2_BACSU] [AC:O34425] [GN:GAPB] [OR:BACILLUS SUBTILIS]
[EC:1.2.1.12] [DE:GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE 2, (GAPDH)]
[SP:O34425] [DB:swissprot] >pir:[LN:G69628] [AC:G69628]
[PN:glyceraldehyde-3-phosphate dehydrogenase, gapB] [GN:gapB]
[CL:glyceraldehyde-3-phosphate dehydrogenase] [OR:Bacillus subtilis]
[EC:1.2.1.12] [DB:pir2] >gp:[GI:e1184151:g2635367] [LN:BSUB0015]
[AC:Z99118:AL009126] [PN:glyceraldehyde-3-phosphate dehydrogenase] [GN:gapB]
[FN:glycolysis] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:1.2.1.12]
[DE:Bacillus subtilis complete genome (section 15 of 21): from 2795131to
3013540.] [SP:O34425] [LE:170976] [RE:171998] [DI:complement]
>gp:[GI:g2293277] [LN:AF008220] [AC:AF008220]
[PN:glyceraldehyde-3-P-dehydrogenase] [GN:gapB] [OR:Bacillus subtilis]
[DB:genpept-bct2] [DE:Bacillus subtilis rrnB-dnaB genomic region.]
[LE:211069] [RE:212091] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000993_24740701_c3_903	2239	6011	2508	835	3293	0.0

Description

sp:[LN:SYL_BACSU] [AC:P36430:O34465] [GN:LEUS] [OR:BACILLUS SUBTILIS]
[EC:6.1.1.4] [DE:LEUCYL-TRNA SYNTHETASE, (LEUCINE--TRNA LIGASE) (LEURS)]
[SP:P36430:O34465] [DB:swissprot] >pir:[LN:D69650] [AC:D69650:A41882]
[PN:leucine--trna ligase, :leucyl-trna synthetase] [GN:leuS]
[CL:leucine--trna ligase] [OR:Bacillus subtilis] [EC:6.1.1.4] [DB:pir2]
>gp:[GI:e1185905:g2635516] [LN:BSUB0016] [AC:Z99119:AL009126]
[PN:leucyl-trna synthetase] [GN:leuS] [OR:Bacillus subtilis]
[DB:genpept-bct1] [EC:6.1.1.4] [DE:Bacillus subtilis complete genome
(section 16 of 21): from 2997771to 3213410.] [SP:P36430] [LE:103940]
[RE:106354] [DI:complement] >gp:[GI:g2293181] [LN:AF008220] [AC:AF008220]
[PN:leucine trna synthetase] [GN:leuS] [OR:Bacillus subtilis]
[DB:genpept-bct2] [DE:Bacillus subtilis rrnB-dnaB genomic region.]
[LE:74073] [RE:76487] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000993_24744077_c2_739	2240	6012	183	60	74	0.011

Description

pir:[LN:B60608] [AC:B60608] [PN:myosin heavy chain] [CL:myosin heavy
chain:myosin motor domain homology] [OR:Schistosoma mansoni] [DB:pir2]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000993_24797177_c1_689	2241	6013	3534	1177	1450	1.7e-148

Description

pir:[LN:C69999] [AC:C69999] [PN:DNA translocase stage III sporulation prot homolog ytpT] [GN:ytpT] [OR:Bacillus subtilis] [DB:pir2]
>gp:[GI:e1185853:g2635464] [LN:BSUB0016] [AC:Z99119:AL009126] [GN:ytpT] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.] [NT:similar to DNA translocase stage III sporulation] [LE:51038] [RE:53146] [DI:complement]
>gp:[GI:g2293215] [LN:AF008220] [AC:AF008220] [PN:YtpT] [GN:ytpT] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis rrnB-dnaB genomic region.] [NT:strong similarity to FtsK of E. coli and SpoIIIE of] [LE:127280] [RE:129388] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000993_24853437_c1_661	2242	6014	831	276	423	1.1e-39

Description

pir:[LN:D69998] [AC:D69998] [PN:lysophospholipase homolog ytpA] [GN:ytpA] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1185924:g2635535] [LN:BSUB0016] [AC:Z99119:AL009126] [GN:ytpA] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.] [NT:similar to lysophospholipase] [LE:123973] [RE:124752] [DI:complement] >gp:[GI:g2293167] [LN:AF008220] [AC:AF008220] [PN:probable lysophospholipase] [GN:ytpA] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis rrnB-dnaB genomic region.] [LE:55675] [RE:56454] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000993_2538252_c2_752	2243	6015	981	326	988	1.5e-99

Description

sp:[LN:HEMZ_BACSU] [AC:P32396] [GN:HEMH:HEMF] [OR:BACILLUS SUBTILIS]
[EC:4.99.1.1] [DE:SYNTHETASE]] [SP:P32396] [DB:swissprot] >pir:[LN:C47045]
[AC:C47045:H69639] [PN:ferrochelata^{se}, hemH] [GN:hemH] [OR:Bacillus
subtilis] [EC:4.99.1.1] [DB:pir2] >gp:[GI:g143044] [LN:BACHEMEHY]
[AC:M97208] [PN:ferrochelata^{se}] [GN:hemH] [FN:iron is inserted into
protoporphyrin IX giving] [OR:Bacillus subtilis] [SR:Bacillus subtilis
(strain W168) DNA] [DB:genpept-bct1] [EC:4.99.1.1] [DE:Bacillus subtilis
penicillin binding protein 1A (ponA) gene;uroporphyrinogen decarboxylase
(hemE) gene; ferrochelata^{se} (hemH)gene complete cds, (hemY) gene, complete
cds; ORFA, complete cds;ORFB 5' end.] [LE:3038] [RE:3970] [DI:direct]
>gp:[GI:e1183015:g2633349] [LN:BSUB0006] [AC:Z99109:AL009126]
[PN:ferrochelata^{se}] [GN:hemH] [FN:incorporation of iron into protoporphyrin
IX] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:4.99.1.1] [DE:Bacillus
subtilis complete genome (section 6 of 21): from 999501 to1209940.]
[NT:alternate gene name: hemF] [SP:P32396] [LE:87223] [RE:88155] [DI:direct]
>gp:[GI:e1191886:g2226231] [LN:BSY14083] [AC:Y14083] [PN:Ferrochelata^{se} (EC
4.99.1.1); incorporation of] [GN:hemH] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis chromosomal DNA, region 76-78
degrees: betweenglyB-aprE.] [NT:see Swiss Prot P32396; HEMZ_BACSU.]
[SP:P32396] [LE:7082] [RE:8014] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000993_25398425_c2_824	2244	6016	1167	388	731	2.6e-72

Description

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pir:[LN:F69666] [AC:F69666 ] [PN:Nifs protein homolog nifZ] [GN:nifZ ]
[CL:nitrogen fixation protein nifs] [OR:Bacillus subtilis] [DB:pir2]
>gp:[GI:e1185832:g2635443] [LN:BSUB0016] [AC:Z99119:AL009126] [PN:Nifs
protein homolog] [GN:nifZ] [FN:unknown] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 16 of 21):
from 2997771to 3213410.] [LE:28263] [RE:29408] [DI:complement]
>gp:[GI:g2293229] [LN:AF008220] [AC:AF008220] [PN:Nifs2] [GN:nifs2]
[OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis rrnB-dnaB
genomic region.] [NT:similar to R.sphaeroides nitrogenase stabilizer]
[LE:151019] [RE:152164] [DI:direct]

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000993_25476375_c2_813	2245	6017	135	44		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000993_2548537_c1_703	2246	6018	222	73		
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000993_25586632_c2_759	2247	6019	135	44		
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000993_25665878_c1_683	2248	6020	1665	554	1014	2.6e-102
<u>Description</u>						

pir:[LN:G69992] [AC:G69992] [PN:spore cortex protein homolog ytgP] [GN:ytgP]
] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1185878:g2635489] [LN:BSUB0016]
 [AC:Z99119:AL009126] [GN:ytgP] [FN:unknown] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 16 of 21):
 from 2997771to 3213410.] [NT:similar to spore cortex protein] [LE:74841]
 [RE:76475] [DI:complement] >gp:[GI:g2293198] [LN:AF008220] [AC:AF008220]
 [PN:YtgP] [GN:ytgP] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus
 subtilis rrnB-dnaB genomic region.] [NT:similar to SpoVB protein from B.
 subtilis] [LE:103951] [RE:105585] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000993_25667217_c3_962	2249	6021	627	208	405	9.0e-38
<u>Description</u>						

sp:[LN:YTAG_BACSU] [AC:O34932] [GN:YTAG] [OR:BACILLUS SUBTILIS]
 [DE:HYPOTHETICAL 22.0 KD PROTEIN IN GAPB-MUTM INTERGENIC REGION] [SP:O34932]
 [DB:swissprot] >pir:[LN:A69988] [AC:A69988] [PN:conserved hypothetical
 protein ytaG] [GN:ytaG] [CL:conserved hypothetical protein YDR196c]
 [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1184155:g2635371] [LN:BSUB0015]
 [AC:Z99118:AL009126] [GN:ytaG] [FN:unknown] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 15 of 21):
 from 2795131to 3013540.] [NT:similar to hypothetical proteins] [SP:O34932]
 [LE:174866] [RE:175459] [DI:complement] >gp:[GI:g2293275] [LN:AF008220]
 [AC:AF008220] [PN:YtaG] [GN:ytaG] [OR:Bacillus subtilis] [DB:genpept-bct2]
 [DE:Bacillus subtilis rrnB-dnaB genomic region.] [NT:similar to hypothetical
 protein HI0890 from H.] [LE:207608] [RE:208201] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000993_25972087_c3_846	2250	6022	147	48		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000993_26175952_f3_532	2251	6023	258	85		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000993_26181551_c2_834	2252	6024	948	315	1016	1.6e-102

Description

sp:[LN:ACCA_BACSU] [AC:O34847] [GN:ACCA] [OR:BACILLUS SUBTILIS] [EC:6.4.1.2] [DE:(EC 6.4.1.2)] [SP:O34847] [DB:swissprot] >pir:[LN:G69580] [AC:G69580] [PN:acetyl-CoA carboxylase,, carboxyltransferase alpha chain] [GN:acca] [CL:acetyl-CoA carboxylase, carboxyltransferase alpha chain] [OR:Bacillus subtilis] [EC:6.4.1.2] [DB:pir2] >gp:[GI:e1184169:g2635385] [LN:BSUB0015] [AC:Z99118:AL009126] [PN:acetyl CoA carboxylase (alpha subunit)] [GN:acca] [FN:long-chain fatty acid biosynthesis] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.] [SP:O34847] [LE:191674] [RE:192651] [DI:complement] >gp:[GI:g2293263] [LN:AF008220] [AC:AF008220] [PN:acetyl-CoA carboxylase subunit] [GN:acca] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis rrnB-dnaB genomic region.] [LE:190416] [RE:191393] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000993_26188891_f1_29	2253	6025	210	69	75	0.012

Description

pir:[LN:S58751] [AC:S58751] [PN:NADH dehydrogenase (ubiquinone), chain 3] [CL:NADH dehydrogenase (ubiquinone) chain 3] [OR:mitochondrion Hansenula wingei] [EC:1.6.5.3] [DB:pir2]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000993_26259686_f3_450	2254	6026	1242	413	801	9.8e-80

Description

pir:[LN:A69643] [AC:A69643] [PN:serine proteinase Do, heat-shock protein htrA] [GN:htrA] [CL:proteinase hhoB] [OR:Bacillus subtilis] [DB:pir2]
>gp:[GI:e1181491:g2632011] [LN:BSAJ2571] [AC:AJ002571] [PN:YkdA] [GN:ykdA] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis 168 56 kb DNA fragment between xlyA and ykoR.] [NT:putative serine protease, heat-shock inducible;] [LE:10063] [RE:11412] [DI:complement] >gp:[GI:e1183310:g2633644] [LN:BSUB0007] [AC:Z99110:AL009126] [PN:serine protease Do (heat-shock protein)] [GN:htrA] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.] [NT:alternate gene name: ykdA] [LE:163012] [RE:164361] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000993_26567062_c1_642	2255	6027	792	263	428	3.3e-40

Description

pir:[LN:A69996] [AC:A69996] [PN:hypothetical protein ytmA] [GN:ytmA] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1185931:g2635542] [LN:BSUB0016] [AC:Z99119:AL009126] [GN:ytmA] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.] [LE:132757] [RE:133530] [DI:complement] >gp:[GI:g2293162] [LN:AF008220] [AC:AF008220] [PN:putative peptidase] [GN:ytmA] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis rrnB-dnaB genomic region.] [LE:46897] [RE:47670] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000993_26596062_f3_484	2256	6028	1284	427	1198	8.3e-122

Description

gp:[GI:g2293312] [LN:AF008220] [AC:AF008220] [PN:YtFP] [GN:ytFP] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis rrnB-dnaB genomic region.] [NT:similarity to hypothetical protein f400 from E.] [LE:102487] [RE:103704] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000993_2741536_c2_805	2257	6029	162	53		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000993_2757633_c2_765	2258	6030	1494	497	1275	1.9e-164

Description

sp:[LN:MENE_STAAU] [AC:Q53634] [GN:MENE] [OR:STAPHYLOCOCCUS AUREUS]
[EC:6.2.1.26] [DE:(O-SUCCINYLBENZOATE-COA SYNTHASE)] [SP:Q53634]
[DB:swissprot] >gp:[GI:g1255259] [LN:SAU51132] [AC:U51132]
[PN:o-succinylbenzoic acid (OSB) CoA ligase] [GN:mene] [FN:converts OSB to
OSB-CoA in menaquinone] [OR:Staphylococcus aureus] [DB:genpept-bct1]
[DE:Staphylococcus aureus o-succinylbenzoic acid CoA ligase (mene), and
o-succinylbenzoic acid synthetase (menc) genes, complete cds.] [LE:491]
[RE:1969] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000993_2869676_f2_338	2259	6031	123	40		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000993_2923202_c1_699	2260	6032	1473	490	1202	3.1e-122

Description

gp:[GI:g1732197] [LN:VFU65014] [AC:U65014] [PN:PTS permease for
N-acetylglucosamine and] [GN:nagE] [OR:Vibrio furnissii] [DB:genpept-bct2]
[DE:Vibrio furnissii PTS permease for N-acetylglucosamine and glucose(nagE)
gene, complete cds.] [NT:PTS enzyme IINag] [LE:115] [RE:1605] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000993_29562552_f3_555	2261	6033	276	91	281	1.2e-24

Description

pir:[LN:H69993] [AC:H69993] [PN:hypothetical protein ytjA] [GN:ytjA]
[CL:conserved hypothetical protein HI1000] [OR:Bacillus subtilis] [DB:pir2]
>gp:[GI:e1185941:g2635552] [LN:BSUB0016] [AC:Z99119:AL009126] [GN:ytjA]
[FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
complete genome (section 16 of 21): from 2997771to 3213410.] [LE:139407]
[RE:139634] [DI:direct] >gp:[GI:g2293294] [LN:AF008220] [AC:AF008220]
[PN:YtjA] [GN:ytjA] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus
subtilis rrnB-dnaB genomic region.] [NT:similar to hypothetical 9.3 kD
protein from P.] [LE:40793] [RE:41020] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000993_30079651_f1_66	2262	6034	1620	539	1135	4.0e-115

Description

sp:[LN:SERA_BACSU] [AC:P35136:O32011] [GN:SERA] [OR:BACILLUS SUBTILIS] [EC:1.1.1.95] [DE:D-3-PHOSPHOGLYCERATE DEHYDROGENASE, (PGDH)] [SP:P35136:O32011] [DB:swissprot] >pir:[LN:C69705] [AC:C69705:S45534] [PN:phosphoglycerate dehydrogenase, serA] [GN:serA] [CL:Bacillus phosphoglycerate dehydrogenase] [OR:Bacillus subtilis] [EC:1.1.1.95] [DB:pir2] >gp:[GI:e1185576:g2634742] [LN:BSUB0013] [AC:Z99116:AL009126] [PN:phosphoglycerate dehydrogenase] [GN:serA] [FN:serine biosynthesis] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:1.1.1.95] [DE:Bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.] [SP:P35136] [LE:15060] [RE:16637] [DI:direct] >gp:[GI:g1146196] [LN:BACSERA] [AC:L47648] [PN:phosphoglycerate dehydrogenase] [GN:serA] [FN:serine biosynthesis] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis phosphoglycerate dehydrogenase (serA), ypaA,ferredoxin (fer), ypbB, recS, ypbD, ypbE, ypbF, ypbG, ypbH,glutamate dehydrogenase (ypcA), ypdA, ypdB, ypdC, spore cortexlytic enzyme (sleB), ypeB, ypfA, ypfB, cytidine monophosphatekinase (cmk), ypfD, ypgA, yphA, yphB, yphC, NAD+ dependentglycerol-3-phosphate dehydrogenase (glyc), yphE and yphF genes,complete cds.] [LE:40] [RE:1617] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000993_30084402_f3_446	2263	6035	1188	395	716	1.0e-70

Description

sp:[LN:DHSS_SYNPI] [AC:P14776] [OR:SYNECHOCOCCUS SP] [SR:PCC 6716,] [EC:1.12.-.-] [DE:SUBUNIT)] [SP:P14776] [DB:swissprot] >pir:[LN:HQYCSS] [AC:S06919] [PN:soluble hydrogenase, small chain] [CL:serine--pyruvate aminotransferase] [OR:Synechococcus sp.] [EC:1.12.-.-] [DB:pir1] >gp:[GI:g48054] [LN:SYNSOLHY] [AC:X16658] [OR:Synechococcus sp.] [SR:Synechococcus sp] [DB:genpept-bct1] [DE:Synechococcus DNA for the small subunit of soluble hydrogenase.] [NT:small subunit of soluble hydrogenase (AA 1-384)] [SP:P14776] [LE:226] [RE:1380] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000993_30114637_c3_847	2264	6036	1167	388	1177	1.4e-119

Description

pir:[LN:E69820] [AC:E69820] [PN:conserved hypothetical protein yhbA] [GN:yhbA] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1182880:g2633214] [LN:BSUB0005] [AC:Z99108:AL009126] [GN:yhbA] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.] [NT:alternate gene name: ygaP; similar to hypothetical] [LE:164477] [RE:165784] [DI:direct] >gp:[GI:e308636:g1903044] [LN:BSZ93102] [AC:Z93102] [PN:hypothetical 48.5 kd protein] [GN:ygaP] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis yga[L,M,N,O,P,Q,R,S,T], yzdB and yze[A,C] genes.] [LE:6803] [RE:8110] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000993_30274187_f3_522	2265	6037	969	322	1317	2.0e-134

Description

pir:[LN:D69999] [AC:D69999] [PN:conserved hypothetical protein ytqA] [GN:ytqA] [CL:Methanococcus jannaschii conserved hypothetical protein MJ0486] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1185921:g2635532] [LN:BSUB0016] [AC:Z99119:AL009126] [GN:ytqA] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.] [NT:similar to hypothetical proteins] [LE:121310] [RE:122278] [DI:direct] >gp:[GI:g2293302] [LN:AF008220] [AC:AF008220] [PN:YtqA] [GN:ytqA] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis rrnB-dnaB genomic region.] [NT:similarity to biotine synthase from B.sphaericus] [LE:58149] [RE:59117] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000993_30508255_c3_912	2266	6038	1416	471	1011	5.5e-102

Description

pir:[LN:S43914] [AC:S43914] [PN:hypothetical protein 1] [CL:peptidase V] [OR:Bacillus stearothermophilus] [DB:pir2] >gp:[GI:g436965] [LN:BACMALA] [AC:L13418] [OR:Bacillus stearothermophilus] [SR:Bacillus stearothermophilus (library: ATCC 7953) DNA] [DB:genpept-bct1] [DE:Bacillus stearothermophilus maltose permease (malA) gene, completecds.] [LE:24] [RE:1376] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000993_31256568_c2_817	2267	6039	201	66	114	6.2e-07

Description

pir:[LN:F71011] [AC:F71011] [PN:hypothetical protein PH1388] [GN:PH1388]
 [OR:Pyrococcus horikoshii] [DB:pir2] >gp:[GI:d1031437:g3257811]
 [LN:AP000006]
 [AC:AP000006:AB005215:AB009510:AB009511:AB009512:AB009513:AB009514]
 [PN:119aa long hypothetical protein] [GN:PH1388] [OR:Pyrococcus horikoshii]
 [SR:Pyrococcus horikoshii (strain:OT3) DNA, clone:Pyrococcus horikoshi]
 [DB:genpept-bct1] [DE:Pyrococcus horikoshii OT3 genomic DNA, 1166001-1485000
 nt. position(6/7).] [LE:86760] [RE:87119] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000993_3140917_c3_954	2268	6040	189	62		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000993_31539156_c3_874	2269	6041	204	67		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000993_3158502_c2_792	2270	6042	225	74	122	2.7e-07

Description

pir:[LN:A69997] [AC:A69997] [PN:hypothetical protein ytmP] [GN:ytmP]
 [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1185865:g2635476] [LN:BSUB0016]
 [AC:Z99119:AL009126] [GN:ytmP] [FN:unknown] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 16 of 21):
 from 2997771to 3213410.] [LE:61986] [RE:62795] [DI:complement]
 >gp:[GI:g2293206] [LN:AF008220] [AC:AF008220] [PN:YtmP] [GN:ytmP]
 [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis rrnB-dnaB
 genomic region.] [LE:117631] [RE:118440] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000993_33209677_c2_831	2271	6043	972	323	764	8.2e-76

Description

pir:[LN:F69999] [AC:F69999] [PN:conserved hypothetical protein ytqI] [GN:ytqI] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1184174:g2635390] [LN:BSUB0015] [AC:Z99118:AL009126] [GN:ytqI] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.] [NT:similar to hypothetical proteins] [LE:199851] [RE:200792] [DI:complement] >gp:[GI:g2293259] [LN:AF008220] [AC:AF008220] [PN:YtqI] [GN:ytqI] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis rrnB-dnaB genomic region.] [NT:similarity to MGPA protein from M.genitalium] [LE:182275] [RE:183216] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000993_33287515_f1_122	2272	6044	330	109	89	0.0022

Description

gp:[GI:g4091929] [LN:AF069752] [AC:AF069752] [PN:C5,6 desaturase] [GN:ERG3] [OR:Candida albicans] [DB:genpept-pln2] [DE:Candida albicans C5,6 desaturase (ERG3) gene, complete cds.] [LE:387] [RE:1547] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000993_33292165_f1_155	2273	6045	156	51		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000993_33317002_f1_114	2274	6046	123	40		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000993_33360312_f1_74	2275	6047	420	139	295	1.6e-25

Description

gp:[GI:e1284114:g2982646] [LN:SPAJ2293] [AC:AJ002293] [PN:penicillin-binding protein 1b] [GN:pbp1b] [OR:Streptococcus pneumoniae] [DB:genpept-bct1] [DE:Streptococcus pneumoniae pbp1b gene, partial, beta-lactamresistant.] [LE:<1] [RE:>1600] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000993_33647577_c2_740	2276	6048	1386	461	1586	6.4e-163

Description

gp:[GI:e1249821:g2832825] [LN:BS43KBDNA] [AC:AJ223978] [PN:fumarase protein, CitG] [GN:citG] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis 42.7kB DNA fragment from yvsA to yvqA.] [LE:37816] [RE:39204] [DI:direct] >gp:[GI:e1184383:g2635801] [LN:BSUB0017] [AC:Z99120:AL009126] [PN:fumarate hydratase] [GN:citG] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:4.2.1.2] [DE:Bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.] [LE:191083] [RE:192471] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000993_33650137_c2_794	2277	6049	207	68	177	1.3e-13

Description

pir:[LN:A69999] [AC:A69999] [PN:phenylalanyl-tRNA synthetase (beta subunit) homolog ytpR] [GN:ytpR] [CL:Mycoplasma genitalium hypothetical protein MG449] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1185855:g2635466] [LN:BSUB0016] [AC:Z99119:AL009126] [GN:ytpR] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.] [NT:similar to phenylalanyl-tRNA synthetase (beta)] [LE:54055] [RE:54660] [DI:complement] >gp:[GI:g2293213] [LN:AF008220] [AC:AF008220] [PN:YtpR] [GN:ytpR] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis rrnB-dnaB genomic region.] [NT:similarity to phenylalanine tRNA ligase of E. coli] [LE:125766] [RE:126371] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000993_3365887_c2_791	2278	6050	630	209	501	6.0e-48

Description

pir:[LN:A69997] [AC:A69997] [PN:hypothetical protein ytmP] [GN:ytmP] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1185865:g2635476] [LN:BSUB0016] [AC:Z99119:AL009126] [GN:ytmP] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.] [LE:61986] [RE:62795] [DI:complement] >gp:[GI:g2293206] [LN:AF008220] [AC:AF008220] [PN:YtmP] [GN:ytmP] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis rrnB-dnaB genomic region.] [LE:117631] [RE:118440] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000993_33792687_c1_629	2279	6051	129	42		
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Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000993_33831512_f2_373	2280	6052	234	77	82	0.0093
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Description

gp:[GI:e1346461:g3876981] [LN:CEF40D4] [AC:Z81536] [GN:F40D4.10]
[OR:Caenorhabditis elegans] [DB:genpept-inv1] [DE:Caenorhabditis elegans
cosmid F40D4, complete sequence.] [LE:20486:20882:21041:21585]
[RE:20830:20997:21200:21746] [DI:directJoin]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000993_33985077_c1_720	2281	6053	1230	409	1529	7.0e-157
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Description

pir:[LN:C70001] [AC:C70001] [PN:malate dehydrogenase homolog ytsJ] [GN:ytsJ]
[CL:malate dehydrogenase (oxaloacetate-decarboxylating)] [OR:Bacillus
subtilis] [DB:pir2] >gp:[GI:e1184171:g2635387] [LN:BSUB0015]
[AC:Z99118:AL009126] [GN:ytsJ] [FN:unknown] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 15 of 21):
from 2795131to 3013540.] [NT:similar to malate dehydrogenase] [LE:193843]
[RE:195075] [DI:complement] >gp:[GI:g2293261] [LN:AF008220] [AC:AF008220]
[PN:YtsJ] [GN:ytsJ] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus
subtilis rrnB-dnaB genomic region.] [NT:similarity to malate dehydrogenase
(NADP+) from] [LE:187992] [RE:189224] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000993_34177127_c1_721	2282	6054	1806	601	1853	3.3e-191
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Description

sp:[LN:KPYK_BACLI] [AC:P51181] [GN:PYK] [OR:BACILLUS LICHENIFORMIS]
[EC:2.7.1.40] [DE:PYRUVATE KINASE, (PK)] [SP:P51181] [DB:swissprot]
>pir:[LN:JC4220] [AC:JC4220] [PN:pyruvate kinase,:ATP:pyruvate
2-O-phosphotransferase] [CL:pyruvate kinase] [OR:Bacillus licheniformis]
[EC:2.7.1.40] [DB:pir2] >gp:[GI:d1007299:g1041099] [LN:BACPYK2] [AC:D31955]
[PN:Pyruvate Kinase] [OR:Bacillus licheniformis] [SR:Bacillus licheniformis
DNA] [DB:genpept-bct1] [DE:Bacillus licheniformis gene for pyruvate kinase,
complete cds.] [LE:132] [RE:1889] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000993_34178128_c3_888	2283	6055	216	71		
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Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000993_34181551_c2_841	2284	6056	924	307	618	2.4e-60
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Description

sp:[LN:DNAI_BACSU] [AC:P06567] [GN:DNAI] [OR:BACILLUS SUBTILIS]
 [DE:PRIMOSOMAL PROTEIN DNAI] [SP:P06567] [DB:swissprot] >pir:[LN:IQBS44]
 [AC:B24720:C26580:F69617] [PN:primosome component (helicase loader)
 dnaI:dnaA protein homolog, 44K:hypothetical protein Y (dnaB 3' region)]
 [GN:dnaI] [CL:44K dnaA protein homolog] [OR:Bacillus subtilis] [DB:pir1]
 >gp:[GI:g39881] [LN:BSDNAB] [AC:X04963] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:Bacillus subtilis dnaB gene for initiation of
 chromosomal replication.] [NT:ORF 311 (AA 1-311)] [SP:P06567] [LE:1843]
 [RE:2778] [DI:direct] >gp:[GI:e1184147:g2635363] [LN:BSUB0015]
 [AC:Z99118:AL009126] [PN:helicase loader] [GN:dnaI] [FN:DNA synthesis]
 [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete
 genome (section 15 of 21): from 2795131to 3013540.] [NT:alternate gene name:
 ytxA, dnaY] [SP:P06567] [LE:167129] [RE:168064] [DI:complement]
 >gp:[GI:e1165286:g1769996] [LN:BSZ75208] [AC:Z75208] [PN:replication
 protein] [GN:dnaI] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis
 genomic sequence 89009bp.] [NT:DNA synthesis; putative primosome component]
 [SP:P06567] [LE:1843] [RE:2778] [DI:direct] >gp:[GI:g2293281] [LN:AF008220]
 [AC:AF008220] [PN:DnaI] [GN:dnaI] [OR:Bacillus subtilis] [DB:genpept-bct2]
 [DE:Bacillus subtilis rrnB-dnaB genomic region.] [LE:215003] [RE:215938]
 [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000993_34199077_c3_883	2285	6057	1017	338	864	2.1e-86
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Description

gp:[GI:g1255260] [LN:SAU51132] [AC:U51132] [PN:o-succinylbenzoic acid (OSB)
 synthetase] [GN:menc] [FN:converts SHCHC to OSB in menaquinone]
 [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:Staphylococcus aureus
 o-succinylbenzoic acid CoA ligase (mene),and o-succinylbenzoic acid
 synthetase (menc) genes, complete cds.] [LE:1974] [RE:2975] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000993_34272752_c3_862	2286	6058	963	320	1413	1.4e-144

Description

gp:[GI:g710422] [LN:SAU21636] [AC:U21636] [PN:cmp-binding-factor 1]
[GN:cbf1] [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus
aureus cmp-binding-factor 1 (cbf1) and ORF X genes,complete cds.] [LE:1155]
[RE:2096] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000993_34415925_c3_914	2287	6059	654	217	540	4.5e-52

Description

pir:[LN:B69997] [AC:B69997] [PN:conserved hypothetical protein ytmQ]
[GN:ytmQ] [CL:hypothetical protein HI0340] [OR:Bacillus subtilis] [DB:pir2]
>gp:[GI:e1185863:g2635474] [LN:BSUB0016] [AC:Z99119:AL009126] [GN:ytmQ]
[FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
complete genome (section 16 of 21): from 2997771to 3213410.] [NT:similar to
hypothetical proteins] [LE:60859] [RE:61500] [DI:complement]
>gp:[GI:g2293207] [LN:AF008220] [AC:AF008220] [PN:YtmQ] [GN:ytmQ]
[OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis rrnB-dnaB
genomic region.] [NT:similar to hypothetical protein HI0340 from H.]
[LE:118926] [RE:119567] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000993_34429838_c3_884	2288	6060	483	160	261	1.6e-22

Description

pir:[LN:E69994] [AC:E69994] [PN:hypothetical protein ytkD] [GN:ytkD]
[OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1185936:g2635547] [LN:BSUB0016]
[AC:Z99119:AL009126] [GN:ytkD] [FN:unknown] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 16 of 21):
from 2997771to 3213410.] [LE:136293] [RE:136769] [DI:complement]
>gp:[GI:g2293161] [LN:AF008220] [AC:AF008220] [PN:YtkD] [GN:ytkD]
[OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis rrnB-dnaB
genomic region.] [LE:43658] [RE:44134] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000993_34610925_f3_445	2289	6061	462	153	274	6.9e-24

Description

pir:[LN:F69883] [AC:F69883] [PN:conserved hypothetical protein ymaD]
 [GN:ymaD] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1183387:g2634112]
 [LN:BSUB0010] [AC:Z99113:AL009126] [GN:ymaD] [FN:unknown] [OR:Bacillus
 subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section
 10 of 21): from 1781201to 2014980.] [NT:similar to hypothetical proteins]
 [LE:82267] [RE:82719] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000993_34617017_c3_869	2290	6062	759	252	773	9.1e-77

Description

sp:[LN:ECSA_BACSU] [AC:P55339] [GN:ECSA:PRST] [OR:BACILLUS SUBTILIS]
 [DE:ABC-TYPE TRANSPORTER ATP-BINDING PROTEIN ECSA] [SP:P55339]
 [DB:swissprot] >pir:[LN:F69619] [AC:F69619] [PN:ABC transporter
 (ATP-binding protein) ecsA] [GN:ecsA] [CL:ATP-binding cassette homology]
 [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e183449:g1177253] [LN:BSECSABCG]
 [AC:X87807] [PN:putative ATP-binding protein of ABC-type] [GN:ecsA]
 [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis ecsA, ecsB, and ecsC
 genes.] [SP:P55339] [LE:248] [RE:991] [DI:direct] >gp:[GI:e1183006:g2633340]
 [LN:BSUB0006] [AC:Z99109:AL009126] [PN:ABC transporter (ATP-binding
 protein)] [GN:ecsA] [FN:regulates both components of the protein]
 [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete
 genome (section 6 of 21): from 999501 to1209940.] [NT:alternate gene name:
 prsT, ecs-26, yhaD] [SP:P55339] [LE:77413] [RE:78156] [DI:direct]
 >gp:[GI:e324952:g2226115] [LN:BSY14077] [AC:Y14077] [PN:Hypothetical
 protein] [GN:yhaD] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus
 subitlis 10.6 Kb chromosomal DNA: glyB-prsA region.] [NT:Identified as ecsA.
 Similar to many ATP binding ABC] [SP:P55339] [LE:2757] [RE:3500]
 [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000993_35360932_c3_944	2291	6063	1278	425	1493	4.6e-153

Description

sp:[LN:ACKA_BACSU] [AC:P37877] [GN:ACKA] [OR:BACILLUS SUBTILIS] [EC:2.7.2.1] [DE:ACETATE KINASE, (ACETOKINASE)] [SP:P37877] [DB:swissprot]
 >pir:[LN:B49935] [AC:B49935:C69581] [PN:acetate kinase, ackA] [GN:ackA] [CL:acetate kinase] [OR:Bacillus subtilis] [EC:2.7.2.1] [DB:pir2]
 >gp:[GI:e1185820:g2635431] [LN:BSUB0016] [AC:Z99119:AL009126] [PN:acetate kinase] [GN:ackA] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:2.7.2.1] [DE:Bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.] [SP:P37877] [LE:16413] [RE:17600] [DI:complement]
 >gp:[GI:g2293240] [LN:AF008220] [AC:AF008220] [PN:acetate kinase] [GN:ackA] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis rrnB-dnaB genomic region.] [LE:162827] [RE:164014] [DI:direct] >gp:[GI:g405134] [LN:BACACKA] [AC:L17320] [PN:acetate kinase] [GN:ackA] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain W168) DNA] [DB:genpept-bct2] [DE:Bacillus subtilis acetate kinase (ackA) gene, complete cds.] [LE:698] [RE:1885] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000993_36152191_c3_863	2292	6064	126	41		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000993_36541078_c1_647	2293	6065	171	56		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000993_3906642_c1_632	2294	6066	600	199	244	1.0e-20

Description

pir:[LN:H69778] [AC:H69778] [PN:hypothetical protein ydeN] [GN:ydeN] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:d1020114:g1881334] [LN:AB001488] [AC:AB001488] [GN:ydeN] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:168) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.] [NT:FUNCTION UNKNOWN.] [LE:106671] [RE:107243] [DI:complement] >gp:[GI:e1182492:g2632826] [LN:BSUB0003] [AC:Z99106:AL009126] [GN:ydeN] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.] [LE:170416] [RE:170988] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000993_3944015_c1_608	2295	6067	540	179	331	6.2e-30

Description

pir:[LN:S68867] [AC:S68867:S54422] [PN:probable transport protein arpJ:ABC transporter arpJ] [OR:Listeria monocytogenes] [DB:pir2]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000993_4073892_c1_631	2296	6068	1458	485	1083	1.3e-109

Description

sp:[LN:PPOX_BACSU] [AC:P32397] [GN:HEMY:HEMG] [OR:BACILLUS SUBTILIS] [EC:1.3.3.4] [DE:PROTOPORPHYRINOGEN OXIDASE, (PPO)] [SP:P32397] [DB:swissprot] >pir:[LN:D47045] [AC:D47045:D69640] [PN:coproporphyrinogen III oxidase / protoporphyrinogen IX oxidase hemY] [GN:hemY] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:g143045] [LN:BACHEMEHY] [AC:M97208] [GN:hemY] [FN:involved in a late step of protoheme IX] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain W168) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis penicillin binding protein 1A (ponA) gene;uroporphyrinogen decarboxylase (hemE) gene; ferrochelatase (hemH)gene complete cds, (hemY) gene, complete cds; ORFA, complete cds;ORFB 5' end.] [LE:3985] [RE:5397] [DI:direct] >gp:[GI:e1183016:g2633350] [LN:BSUB0006] [AC:Z99109:AL009126] [PN:protoporphyrinogen IX and coproporphyrinogen III] [GN:hemY] [FN:late steps of protoheme IX synthesis (porphyrin) [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:1.3.3.4] [DE:Bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.] [NT:alternate gene name: hemG] [SP:P32397] [LE:88170] [RE:89582] [DI:direct] >gp:[GI:e325009:g2226232] [LN:BSY14083] [AC:Y14083] [PN:Protoporphyrinogen IX oxidase] [GN:hemY] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis chromosomal DNA, region 76-78 degrees: betweenglyB-aprE.] [NT:see Swiss Prot P32397; HEMG_BACSU.] [SP:P32397] [LE:8029] [RE:9441] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000993_4110882_f3_473	2297	6069	351	116	90	0.00022

Description

pir:[LN:D70004] [AC:D70004] [PN:hypothetical protein ytzB] [GN:ytzB] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1185860:g2635471] [LN:BSUB0016] [AC:Z99119:AL009126] [GN:ytzB] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.] [LE:57791] [RE:58108] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000993_4173427_c2_742	2298	6070	474	157	82	0.0020

Description

pir:[LN:A64334] [AC:A64334] [PN:hypothetical protein MJ0272]
 [OR:Methanococcus jannaschii] [DB:pir2] [MP:FOR257413-257652]
 >gp:[GI:g1590997] [LN:U67482] [AC:U67482:L77117] [PN:repressor protein,
 putative (yorfE)] [GN:MJ0272] [OR:Methanococcus jannaschii]
 [DB:genpept-bct2] [DE:Methanococcus jannaschii section 24 of 150 of the
 complete genome.] [NT:similar to GP:1536960 percent identity: 40.32;]
 [LE:5633] [RE:5872] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000993_4183428_c3_921	2299	6071	1329	442	1966	3.5e-203

Description

sp:[LN:MURC_STAAU] [AC:O31211] [GN:MURC] [OR:STAPHYLOCOCCUS AUREUS]
 [EC:6.3.2.8] [DE:ACETYLMURANOYL-L-ALANINE SYNTHETASE)] [SP:O31211]
 [DB:swissprot] >gp:[GI:g2642659] [LN:AF034076] [AC:AF034076]
 [PN:UDP-N-acetylmuramoyl-L-alanine synthetase] [GN:murC] [FN:cell wall
 biosynthesis] [OR:Staphylococcus aureus] [DB:genpept-bct2]
 [DE:Staphylococcus aureus UDP-N-acetylmuramoyl-L-alanine synthetase(murC)
 gene, complete cds.] [NT:MurC; UDP-N-acetylmuramate-alanine ligase] [LE:1]
 [RE:1314] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000993_4296950_c2_764	2300	6072	198	65		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000993_4299175_c1_637	2301	6073	240	79	102	0.00012

Description

pir:[LN:T00158] [AC:T00158] [PN:amidase,] [OR:Staphylococcus aureus phage
 phi PVL] [EC:3.5.-.-] [DB:pir3] >gp:[GI:d1032859:g3341932] [LN:AB009866]
 [AC:AB009866] [PN:amidase (peptidoglycan hydrolase)] [OR:bacteriophage phi
 PVL] [SR:bacteriophage phi PVL (specific_host:Staphylococcus aureus ATC]
 [DB:genpept-phg] [DE:Bacteriophage phi PVL proviral DNA, complete sequence.]
 [NT:orf 25] [LE:20199] [RE:21653] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000993_4345967_f2_357	2302	6074	441	146	368	7.5e-34

Description

sp:[LN:HIT_BACSU] [AC:O07513] [GN:HIT] [OR:BACILLUS SUBTILIS] [DE:HIT PROTEIN] [SP:O07513] [DB:swissprot] >pir:[LN:A69642] [AC:A69642] [PN:cell-cycle regulation histidine triad (HIT) protein] [GN:hit] [CL:protein kinase C inhibitor:histidine triad homology] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1183005:g2633339] [LN:BSUB0006] [AC:Z99109:AL009126] [PN:Hit-like protein] [GN:hit] [FN:cell-cycle regulation (inhibition of cell) [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.] [NT:alternate gene name: yhaE] [SP:O07513] [LE:76488] [RE:76925] [DI:complement] >gp:[GI:e325178:g2226116] [LN:BSY14077] [AC:Y14077] [PN:Hypothetical protein] [GN:yhaE] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis 10.6 Kb chromosomal DNA: glyB-prsA region.] [NT:Similarity to the Hit family of proteins] [SP:O07513] [LE:3988] [RE:4425] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000993_4453537_c3_937	2303	6075	159	52		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000993_4459380_c1_712	2304	6076	207	68		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000993_4502308_c2_812	2305	6077	636	211	502	4.7e-48

Description

pir:[LN:E69826] [AC:E69826] [PN:1-acylglycerol-3-phosphate O-acyltransfera homolog yhdO] [GN:yhdO] [OR:Bacillus subtilis] [DB:pir2]
 >gp:[GI:e1182955:g2633289] [LN:BSUB0006] [AC:Z99109:AL009126] [GN:yhdO] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.] [NT:similar to 1-acylglycerol-3-phosphate] [LE:31375] [RE:31974] [DI:direct]
 >gp:[GI:e325031:g2226210] [LN:BSY14082] [AC:Y14082] [PN:hypothetical protein] [GN:yhdO] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis chromosomal DNA, region 72 to 75 degrees: spoVRto sspB.] [NT:Similarity to a hypothetical protein from] [LE:18023] [RE:18622] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000993_4511283_c3_859	2306	6078	153	50		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000993_4568761_c1_630	2307	6079	1116	371	1257	4.7e-128

Description

sp:[LN:DCUP_BACSU] [AC:P32395] [GN:HEME] [OR:BACILLUS SUBTILIS] [EC:4.1.1.37] [DE:UROPORPHYRINOGEN DECARBOXYLASE, (UPD)] [SP:P32395] [DB:swissprot] >pir:[LN:B47045] [AC:B47045:G69639] [PN:uroporphyrinogen decarboxylase, hemE:uroporphyrinogen III decarboxylase hemE] [GN:heme] [CL:uroporphyrinogen decarboxylase] [OR:Bacillus subtilis] [EC:4.1.1.37] [DB:pir2] >gp:[GI:g143043] [LN:BACHEMEHY] [AC:M97208] [PN:uroporphyrinogen decarboxylase] [GN:heme] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain W168) DNA] [DB:genpept-bct1] [EC:4.1.1.37] [DE:Bacillus subtilis penicillin binding protein 1A (ponA) gene;uroporphyrinogen decarboxylase (hemE) gene; ferrochelatase (hemH)gene complete cds, (hemY) gene, complete cds; ORFA, complete cds;ORFB 5' end.] [LE:1905] [RE:2966] [DI:direct]
 >gp:[GI:e1183014:g2633348] [LN:BSUB0006] [AC:Z99109:AL009126] [PN:uroporphyrinogen III decarboxylase] [GN:heme] [FN:porphyrin biosynthesis] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:4.1.1.37] [DE:Bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.] [SP:P32395] [LE:86090] [RE:87151] [DI:direct]
 >gp:[GI:e325194:g2226230] [LN:BSY14083] [AC:Y14083] [PN:Uroporphyrinogen III decarboxylase] [GN:heme] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:4.1.1.37] [DE:Bacillus subtilis chromosomal DNA, region 76-78 degrees: betweenglyB-aprE.] [NT:see Swiss Prot P32395; DCUP_BACSU.] [SP:P32395] [LE:5949] [RE:7010] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000993_4579675_f3_569	2308	6080	129	42		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000993_4693800_f2_225	2309	6081	570	189	191	4.3e-15

Description

pir:[LN:A69220] [AC:A69220] [PN:conserved hypothetical protein MTH898]
 [GN:MTH898] [CL:Escherichia coli ybdQ protein] [OR:Methanobacterium
 thermoautotrophicum] [DB:pir2] >gp:[GI:g2621993] [LN:AE000865]
 [AC:AE000865:AE000666] [PN:conserved protein] [GN:MTH898]
 [OR:Methanobacterium thermoautotrophicum] [DB:genpept-bct1]
 [DE:Methanobacterium thermoautotrophicum from bases 808939 to 820180(section
 71 of 148) of the complete genome.] [NT:Function Code:14.01 - Unknown,
 Conserved protein;] [LE:6700] [RE:7149] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000993_4697318_c3_919	2310	6082	867	288	671	5.8e-66

Description

pir:[LN:H69998] [AC:H69998] [PN:hypothetical protein ytpQ] [GN:ytpQ]
 [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1185856:g2635467] [LN:BSUB0016]
 [AC:Z99119:AL009126] [GN:ytpQ] [FN:unknown] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 16 of 21):
 from 2997771to 3213410.] [LE:54676] [RE:55485] [DI:complement]
 >gp:[GI:g2293212] [LN:AF008220] [AC:AF008220] [PN:YtpQ] [GN:ytpQ]
 [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis rrnB-dnaB
 genomic region.] [LE:124941] [RE:125750] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000993_472538_c1_707	2311	6083	144	47		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000993_4776702_c1_669	2312	6084	312	103	164	3.1e-12

Description

sp:[LN:YRKF_BACSU] [AC:P54433] [GN:YRKF] [OR:BACILLUS SUBTILIS]
[DE:HYPOTHETICAL 20.7 KD PROTEIN IN BLTR-SPOIIIIC INTERGENIC REGION]
[SP:P54433] [DB:swissprot] >pir:[LN:D69976] [AC:D69976] [PN:conserved
hypothetical protein yrkF] [GN:yrkF] [OR:Bacillus subtilis] [DB:pir2]
>gp:[GI:d1013040:g1303705] [LN:BACJH642] [AC:D84432:D82370] [PN:YrkF]
[OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:JH642(trpC2 PheA1))
DNA] [DB:genpept-bct1] [DE:Bacillus subtilis DNA, 283 Kb region containing
skin element.] [LE:6477] [RE:7034] [DI:direct] >gp:[GI:e1183882:g2635098]
[LN:BSUB0014] [AC:Z99117:AL009126] [GN:yrkF] [FN:unknown] [OR:Bacillus
subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section
14 of 21): from 2599451to 2812870.] [NT:similar to hypothetical proteins
from B. subtilis] [SP:P54433] [LE:112396] [RE:112953] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000993_4876300_c2_806	2313	6085	1695	564	1845	2.3e-190

Description

sp:[LN:FTHS_STRMU] [AC:Q59925:Q59926] [GN:FHS] [OR:STREPTOCOCCUS MUTANS]
[EC:6.3.4.3] [DE:SYNTHETASE) (FHS) (FTHFS)] [SP:Q59925:Q59926]
[DB:swissprot] >gp:[GI:g1103865] [LN:SMU39612] [AC:U39612]
[PN:formyl-tetrahydrofolate synthetase] [GN:fhs] [FN:enzyme involved in the
formation of] [OR:Streptococcus mutans] [DB:genpept-bct1] [EC:6.3.4.3]
[DE:Streptococcus mutans formyl-tetrahydrofolate synthetase (fhs)
gene,complete cds.] [NT:formyl-tetrahydrofolate ligase; ATP-dependant]
[LE:115] [RE:1785] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000993_4876718_c1_617	2314	6086	1143	380	810	1.1e-80

Description

pir:[LN:E69824] [AC:E69824] [PN:two-component sensor histidine kinase homolog yhcY] [GN:yhcY] [OR:Bacillus subtilis] [DB:pir2]
 >gp:[GI:e1182921:g2633255] [LN:BSUB0005] [AC:Z99108:AL009126] [GN:yhcY] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.] [NT:similar to two-component sensor histidine kinase] [LE:205305] [RE:206444] [DI:direct]
 >gp:[GI:e1182933:g2633267] [LN:BSUB0006] [AC:Z99109:AL009126] [GN:yhcY] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.] [NT:similar to two-component sensor histidine kinase] [LE:8625] [RE:9764] [DI:direct]
 >gp:[GI:e1191876:g2226140] [LN:BSY14079] [AC:Y14079] [PN:hypothetical protein] [GN:yhcY] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis chromosomal DNA, region 75 degrees: glpPFDoperon and downstream.] [NT:similarity to the sensory transduction kinase degS] [LE:8273] [RE:9412] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000993_4882963_f3_591	2315	6087	834	277	457	2.8e-43

Description

sp:[LN:YHCT BACSU] [AC:P54604] [GN:YHCT] [OR:BACILLUS SUBTILIS] [DE:HYPOTHETICAL 33.7 KD PROTEIN IN CSPB-GLPP INTERGENIC REGION] [SP:P54604] [DB:swissprot] >pir:[LN:H69823] [AC:H69823] [PN:conserved hypothetical protein yhcT] [GN:yhcT] [CL:conserved hypothetical protein HI0176] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e233879:g1239996] [LN:BS75DGREG] [AC:X96983] [PN:hypothetical protein] [GN:yhcT] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis chromosomal DNA (region 75 degrees: cspB upstream ofglpPFD operon).] [NT:Similarity to DRAP deaminase from Saccharomyces] [SP:P54604] [LE:16504] [RE:17412] [DI:complement]
 >gp:[GI:e1182910:g2633244] [LN:BSUB0005] [AC:Z99108:AL009126] [GN:yhcT] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.] [NT:similar to hypothetical proteins] [SP:P54604] [LE:192310] [RE:193218] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000993_4938877_c2_778	2316	6088	147	48		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000993_5081252_f2_327	2317	6089	360	119	199	6.1e-16

Description

pir:[LN:A70341] [AC:A70341] [PN:conserved hypothetical protein aq_449]
 [GN:aq_449] [CL:hypothetical protein MJ1523] [OR:Aquifex aeolicus]
 [DB:pir2] >gp:[GI:g2983116] [LN:AE000690] [AC:AE000690:AE000657]
 [PN:hypothetical protein] [GN:aq_449] [OR:Aquifex aeolicus]
 [DB:genpept-bct2] [DE:Aquifex aeolicus section 22 of 109 of the complete
 genome.] [LE:10789] [RE:11163] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000993_5132078_c3_845	2318	6090	729	242	752	1.5e-74

Description

pir:[LN:H69334] [AC:H69334] [PN:glutamine transport protein glnQ] [GN:glnQ]
] [CL:inner membrane protein malK:ATP-binding cassette homology]
 [OR:Archaeoglobus fulgidus] [DB:pir2] >gp:[GI:g2649950] [LN:AE001058]
 [AC:AE001058:AE000782] [PN:glutamine ABC transporter, ATP-binding protein]
 [GN:AF0680] [OR:Archaeoglobus fulgidus] [DB:genpept-bct2] [DE:Archaeoglobus
 fulgidus section 49 of 172 of the complete genome.] [NT:similar to GB:M61017
 SP:P27675 PID:142988 percent] [LE:10147] [RE:10875] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000993_5135265_c3_967	2319	6091	504	167	438	2.9e-41

Description

gp:[GI:g4982284] [LN:AE001810] [AC:AE001810:AE000512] [PN:conserved
 hypothetical protein] [GN:TM1707] [OR:Thermotoga maritima] [DB:genpept-bct2]
 [DE:Thermotoga maritima section 122 of 136 of the complete genome.]
 [NT:similar to GB:M15183 PID:468267 PID:2293279] [LE:13832] [RE:14302]
 [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000993_5273425_c2_735	2320	6092	1053	350	473	5.6e-45

Description

gp:[GI:g4981111] [LN:AE001734] [AC:AE001734:AE000512] [PN:amino acid ABC
 transporter, permease protein] [GN:TM0592] [OR:Thermotoga maritima]
 [DB:genpept-bct2] [DE:Thermotoga maritima section 46 of 136 of the complete
 genome.] [NT:similar to GB:AE000782 percent identity: 72.86;] [LE:3214]
 [RE:3864] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000993_5355250_c1_696	2321	6093	1284	427	1343	3.6e-137

Description

sp:[LN:SYB_BACST] [AC:P00952] [GN:TYRS] [OR:BACILLUS STEAROTHERMOPHILUS] [EC:6.1.1.1] [DE:TYROSYL-TRNA SYNTHETASE, (TYROSINE--TRNA LIGASE) (TYRRS)] [SP:P00952] [DB:swissprot] >pir:[LN:SYBSYF] [AC:A01179:I40506] [PN:tyrosine--trna ligase,:tyrosyl-trna synthetase] [CL:tyrosine--trna ligase] [OR:Bacillus stearothermophilus] [EC:6.1.1.1] [DB:pir1]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000993_551907_f3_559	2322	6094	708	235	183	3.0e-14

Description

gp:[GI:g2897104] [LN:AF020798] [AC:AF020798] [PN:putative host cell surface-exposed lipoprotein] [OR:Streptococcus thermophilus bacteriophage TP-J34] [DB:genpept-phg] [DE:Streptococcus thermophilus bacteriophage lysogeny module, integrasehomolog (int), putative host cell surface-exposed lipoprotein,putative metallo-proteinase, repressor, Cro-like regulatoryprotein, and P1-antirepressor homolog genes, complete cds.] [NT:orf142] [LE:3941] [RE:4369] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000993_572186_c1_692	2323	6095	1284	427	190	2.4e-11

Description

pir:[LN:I51116] [AC:I51116] [PN:NF-180] [OR:Petromyzon marinus] [SR:, sea lamprey] [DB:pir2] >gp:[GI:g632549] [LN:PMU19361] [AC:U19361] [PN:NF-180] [OR:Petromyzon marinus] [SR:sea lamprey] [DB:genpept-vrt] [DE:Petromyzon marinus neurofilament subunit NF-180 mRNA, complete cds.] [NT:180 kDa neurofilament subunit] [LE:122] [RE:3454] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000993_581382_f2_281	2324	6096	183	60	46	0.040

Description

sp:[LN:PA2A_PSETE] [AC:P23026] [OR:PSEUDONAJA TEXTILIS] [SR:,EASTERN BROWN SNAKE] [EC:3.1.1.4] [DE:PHOSPHOLIPASE A2 HOMOLOG, TEXTILOTOXIN A CHAIN,] [SP:P23026] [DB:swissprot] >pir:[LN:S29651] [AC:S29651] [PN:textilotoxin chain A] [CL:phospholipase A2] [OR:Pseudonaja textilis] [SR:, eastern brown snake] [DB:pir2]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000993_5882753_c3_956	2325	6097	273	90		
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Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000993_5911592_c3_887	2326	6098	924	307	89	0.0048
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Description

gp:[GI:e1347496:g3877859] [LN:CEF58G6] [AC:Z68217] [GN:F58G6.1]
[OR:Caenorhabditis elegans] [DB:genpept-inv1] [DE:Caenorhabditis elegans
cosmid F58G6, complete sequence.] [NT:Similarity to Chicken amphiphysin (PIR
Acc. No.)] [LE:4939:5597:5746] [RE:5253:5662:5844] [DI:complementJoin]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000993_6070392_c3_911	2327	6099	708	235	458	2.2e-43
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Description

gp:[GI:g4980760] [LN:AE001708] [AC:AE001708:AE000512] [PN:16S
pseudouridylate synthase] [GN:TM0264] [OR:Thermotoga maritima]
[DB:genpept-bct2] [DE:Thermotoga maritima section 20 of 136 of the complete
genome.] [NT:similar to SP:P33918 PID:405907 GB:U00096] [LE:17059]
[RE:17778] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000993_6100150_c3_881	2328	6100	189	62		
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Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000993_6125262_c2_840	2329	6101	192	63	71	0.022
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Description

pir:[LN:S72295] [AC:S72295] [PN:ribosomal protein S8] [GN:rps8]
[OR:plastid Plasmodium falciparum] [DB:pir2] >gp:[GI:e220199:g1171601]
[LN:PFCOMPIRB] [AC:X95276] [GN:rps8] [OR:Plasmodium falciparum] [SR:malaria
parasite P. falciparum] [DB:genpept-inv1] [DE:P.falciparum complete gene map
of plastid-like DNA (IR-B).] [LE:5492] [RE:5878] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000993_6317_c1_687	2330	6102	411	136	267	3.8e-23

Description

pir:[LN:G69998] [AC:G69998] [PN:thioredoxin H1 homolog ytpP] [GN:ytpP] [CL:thioredoxin:thioredoxin homology] [OR:Bacillus subtilis] [DB:pir2]
>gp:[GI:e1185857:g2635468] [LN:BSUB0016] [AC:Z99119:AL009126] [GN:ytpP] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.] [NT:similar to thioredoxin H1] [LE:55500] [RE:55823] [DI:complement] >gp:[GI:g2293211] [LN:AF008220] [AC:AF008220] [PN:putative thioredoxin] [GN:ytpP] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis rrnB-dnaB genomic region.] [LE:124603] [RE:124926] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000993_6689717_c3_849	2331	6103	615	204	72	0.0043

Description

gp:[GI:g4105715] [LN:AF050754] [AC:AF050754] [PN:glucose 6-phosphate isomerase] [GN:GPI1] [OR:Giardia intestinalis] [DB:genpept-inv2] [EC:5.3.1.10] [DE:Giardia intestinalis glucose 6-phosphate isomerase (GPI1) gene,complete cds.] [NT:aminating isomerase] [LE:432] [RE:1232] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000993_6828305_f3_438	2332	6104	132	43		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000993_6906300_c2_826	2333	6105	1014	337	519	7.5e-50

Description

sp:[LN:YTXK_BACSU] [AC:P37876] [GN:YTXK] [OR:BACILLUS SUBTILIS] [DE:HYPOTHETICAL 37.4 KD PROTEIN IN ACKA-SSPA INTERGENIC REGION] [SP:P37876] [DB:swissprot] >pir:[LN:G70003] [AC:G70003:A49935] [PN:hypothetical protein ytxK:hypothetical protein (ackA 5' region)] [GN:ytxK] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1185821:g2635432] [LN:BSUB0016] [AC:Z99119:AL009126] [GN:ytxK] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.] [NT:alternate gene name: ythI] [SP:P37876] [LE:17948] [RE:18937] [DI:complement] >gp:[GI:g2293239] [LN:AF008220] [AC:AF008220] [PN:YtxK] [GN:ytxK] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis rrnB-dnaB genomic region.] [NT:similarity to modification metilase AccI] [LE:161490] [RE:162479] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000993_6929651_c3_858	2334	6106	366	121	289	1.8e-25

Description

pir:[LN:A69828] [AC:A69828] [PN:hypothetical protein yheA] [GN:yheA]
[OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1182981:g2633315] [LN:BSUB0006]
[AC:Z99109:AL009126] [GN:yheA] [FN:unknown] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 6 of 21):
from 999501 to1209940.] [LE:54726] [RE:55079] [DI:direct]
>gp:[GI:e324964:g2226157] [LN:BSY14080] [AC:Y14080] [PN:hypothetical
protein] [GN:yheA] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus
subtilis chromosomal DNA, region 75 degrees: sspB upstreamof glyB.]
[LE:6651] [RE:7004] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000993_7066588_c1_719	2335	6107	3204	1067	1849	5.1e-212

Description

sp:[LN:DP3A_BACSU] [AC:O34623] [GN:DNAE] [OR:BACILLUS SUBTILIS] [EC:2.7.7.7]
[DE:DNA POLYMERASE III, ALPHA CHAIN,] [SP:O34623] [DB:swissprot]
>pir:[LN:D69617] [AC:D69617] [PN:DNA polymerase III (alpha subunit) dnaE]
[GN:dnaE] [CL:DNA-directed DNA polymerase III alpha chain] [OR:Bacillus
subtilis] [DB:pir2] >gp:[GI:e1184172:g2635388] [LN:BSUB0015]
[AC:Z99118:AL009126] [PN:DNA polymerase III (alpha subunit)] [GN:dnaE]
[OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete
genome (section 15 of 21): from 2795131to 3013540.] [SP:O34623] [LE:195212]
[RE:198559] [DI:complement] >gp:[GI:g2293260] [LN:AF008220] [AC:AF008220]
[PN:DNA-polymerase III alpha-chain] [GN:dnaE] [OR:Bacillus subtilis]
[DB:genpept-bct2] [DE:Bacillus subtilis rrnB-dnaB genomic region.]
[LE:184508] [RE:187855] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000993_7244012_c1_723	2336	6108	1287	428	1768	3.3e-182

Description

gp:[GI:e320380:g2168132] [LN:BIISOCIT] [AC:Y13358] [PN:isocitrate
dehydrogenase] [OR:Bacillus israeli] [DB:genpept-bct1] [DE:Bacillus israeli
isocitrate dehydrogenase gene.] [LE:242] [RE:1519] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000993_785952_c1_688	2337	6109	459	152	380	4.0e-35

Description

pir:[LN:A69999] [AC:A69999] [PN:phenylalanyl-tRNA synthetase (beta subunit) homolog ytpR] [GN:ytpR] [CL:Mycoplasma genitalium hypothetical protein MG449] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1185855:g2635466] [LN:BSUB0016] [AC:Z99119:AL009126] [GN:ytpR] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.] [NT:similar to phenylalanyl-tRNA synthetase (beta) [LE:54055] [RE:54660] [DI:complement] >gp:[GI:g2293213] [LN:AF008220] [AC:AF008220] [PN:YtpR] [GN:ytpR] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis rrnB-dnaB genomic region.] [NT:similarity to phenylalanine tRNA ligase of E. coli] [LE:125766] [RE:126371] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000993_803393_c3_947	2338	6110	732	243	536	1.2e-51

Description

pir:[LN:H69407] [AC:H69407] [PN:conserved hypothetical protein AF1265] [CL:conserved hypothetical protein MJ1163] [OR:Archaeoglobus fulgidus] [DB:pir2] >gp:[GI:g2649315] [LN:AE001017] [AC:AE001017:AE000782] [PN:conserved hypothetical protein] [GN:AF1265] [OR:Archaeoglobus fulgidus] [DB:genpept-bct2] [DE:Archaeoglobus fulgidus section 90 of 172 of the complete genome.] [NT:similar to GB:L77117 PID:1591789 percent identity:] [LE:9248] [RE:9943] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000993_817555_f2_358	2339	6111	447	148		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000993_824086_c3_952	2340	6112	882	293	859	7.0e-86

Description

pir:[LN:G70001] [AC:G70001] [PN:acetyl-CoA carboxylase homolog yttI]
 [GN:yttI] [CL:acetyl-CoA carboxylase, carboxyltransferase beta chain]
 [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1184170:g2635386] [LN:BSUB0015]
 [AC:Z99118:AL009126] [GN:yttI] [FN:unknown] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 15 of 21):
 from 2795131to 3013540.] [NT:similar to acetyl-CoA carboxylase] [LE:192636]
 [RE:193424] [DI:complement] >gp:[GI:g2293262] [LN:AF008220] [AC:AF008220]
 [PN:acetyl-CoA carboxylase subunit] [GN:yttI] [OR:Bacillus subtilis]
 [DB:genpept-bct2] [DE:Bacillus subtilis rrnB-dnaB genomic region.]
 [LE:189643] [RE:190431] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000993_82562_f3_523	2341	6113	1110	369	680	6.5e-67

Description

pir:[LN:H69758] [AC:H69758] [PN:proline oxidase homolog ycgM] [GN:ycgM]
 [CL:proline dehydrogenase homolog yusM] [OR:Bacillus subtilis] [DB:pir2]
 >gp:[GI:e1182272:g2632606] [LN:BSUB0002] [AC:Z99105:AL009126] [GN:ycgM]
 [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
 complete genome (section 2 of 21): from 194651 to415810.] [NT:similar to
 proline oxidase] [LE:149473] [RE:150384] [DI:direct]
 >gp:[GI:d1009589:g1805392] [LN:D50453] [AC:D50453] [GN:ycgM] [OR:Bacillus
 subtilis] [SR:Bacillus subtilis (strain:168 trpC2) DNA] [DB:genpept-bct1]
 [DE:Bacillus subtilis DNA for 25-36 degree region containing theamyE-srfa
 region, complete cds.] [LE:23774] [RE:24685] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000993_867187_c3_851	2342	6114	126	41		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000993_954768_c3_892	2343	6115	1053	350	611	1.3e-59

Description

sp:[LN:RIBG_BACSU] [AC:P17618] [GN:RIBG] [OR:BACILLUS SUBTILIS] [EC:3.5.4.-]
[DE:RIBOFLAVIN-SPECIFIC DEAMINASE,] [SP:P17618] [DB:swissprot]
>pir:[LN:PN0100] [AC:S45543:PN0100:E69692] [PN:riboflavin-specific
deaminase ribG] [GN:ribG] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:g410125]
[LN:BACDIA] [AC:L09228] [GN:ribG] [OR:Bacillus subtilis] [SR:Bacillus
subtilis (strain 168, sub_species Marburg) DNA] [DB:genpept-bct1]
[DE:Bacillus subtilis spoVA to serA region.] [LE:8266] [RE:9351] [DI:direct]
>gp:[GI:g40085] [LN:BSRIB] [AC:X51510] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:B.subtilis riboflavin biosynthesis operon ribG, ribB,
ribA, ribH,and ribT genes.] [NT:ribG protein product (AA 1-361)] [SP:P17618]
[LE:1212] [RE:2297] [DI:direct] >gp:[GI:e1185597:g2634763] [LN:BSUB0013]
[AC:Z99116:AL009126] [PN:riboflavin-specific deaminase] [GN:ribG]
[FN:riboflavin biosynthesis] [OR:Bacillus subtilis] [DB:genpept-bct1]
[DE:Bacillus subtilis complete genome (section 13 of 21): from 2395261to
2613730.] [SP:P17618] [LE:34232] [RE:35317] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000993_960012_c1_663	2344	6116	450	149	123	6.9e-08

Description

gp:[GI:g3283053] [LN:AF054173] [AC:AF054173] [PN:staphylococcal accessory
regulator A homolog] [GN:sarA] [OR:Staphylococcus epidermidis]
[DB:genpept-bct2] [DE:Staphylococcus epidermidis staphylococcal accessory
regulator Ahomolog (sarA) gene, complete cds.] [LE:887] [RE:1261]
[DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000993_961562_f3_433	2345	6117	126	41		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000993_9785187_c3_867	2346	6118	171	56		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000993_9845327_c1_648	2347	6119	192	63		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000993_9884378_c3_916	2348	6120	156	51		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000994_10240925_c2_505	2349	6121	252	83	65	0.024

Description

gp:[GI:d1037669:g4126667] [LN:AB016427] [AC:AB016427] [PN:transmembrane protein] [GN:bacM] [OR:Bacillus licheniformis] [SR:Bacillus licheniformis (strain:ATCC 10716) DNA] [DB:genpept-bct1] [DE:Bacillus licheniformis genes for transmembrane protein,thioesterase II-like protein and bacitracin synthetase 1 (BA1),complete and partial cds.] [NT:putative] [LE:694] [RE:>1956] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000994_10553827_c3_663	2350	6122	216	71	132	7.6e-09

Description

pir:[LN:F69808] [AC:F69808] [PN:hypothetical protein yfkK] [GN:yfkK] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1182777:g2633111] [LN:BSUB0005] [AC:Z99108:AL009126] [GN:yfkK] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.] [LE:58273] [RE:58488] [DI:complement] >gp:[GI:d1024280:g2626823] [LN:D83967] [AC:D83967] [PN:YfkK] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:AC327) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis genomic DNA, 74 degree region.] [LE:9433] [RE:9648] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000994_11125052_c1_439	2351	6123	1497	498	1715	1.4e-176

Description

pir:[LN:D70008] [AC:D70008] [PN:nicotinate phosphoribosyltransferase homolog yueK] [GN:yueK] [OR:Bacillus subtilis] [DB:pir2]
>gp:[GI:e1184252:g2635670] [LN:BSUB0017] [AC:Z99120:AL009126] [GN:yueK] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.] [NT:similar to nicotinate phosphoribosyltransferase] [LE:61479] [RE:62951] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000994_11755317_c3_655	2352	6124	759	252	135	4.4e-07

Description

pir:[LN:G70045] [AC:G70045] [PN:hypothetical protein yvqF] [GN:yvqF] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1249815:g2832819] [LN:BS43KBDNA] [AC:AJ223978] [PN:YvqF protein] [GN:yvqF] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis 42.7kB DNA fragment from yvsa to yvqA.] [LE:31389] [RE:32114] [DI:direct] >gp:[GI:e1184389:g2635807] [LN:BSUB0017] [AC:Z99120:AL009126] [GN:yvqF] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.] [LE:198173] [RE:198898] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000994_117687_c1_441	2353	6125	1377	458	1704	2.0e-175

Description

sp:[LN:PUR8_BACSU] [AC:P12047] [GN:PURB:PURE] [OR:BACILLUS SUBTILIS] [EC:4.3.2.2] [DE:ADENYLOSUCCINATE LYASE, (ADENYLOSUCCINASE) (ASL)] [SP:P12047] [DB:swissprot] >pir:[LN:WZBSDS] [AC:C29326:A69684] [PN:adenylosuccinate lyase,] [GN:purB] [CL:fumarate hydratase] [OR:Bacillus subtilis] [EC:4.3.2.2] [DB:pir1] [MP:18 min] >gp:[GI:g143366] [LN:BACPURF] [AC:J02732:K00047] [OR:Bacillus subtilis] [SR:B.subtilis (strain DE1 (prototroph DER. or W168)) DNA, clone pPZ] [DB:genpept-bct1] [DE:B.subtilis pur operon encoding purine biosynthesis enzymes, 12genes.] [NT:adenylosuccinate lyase (PUR-B)] [LE:2056] [RE:3351] [DI:direct] >gp:[GI:e1182624:g2632958] [LN:BSUB0004] [AC:Z99107:AL009126] [PN:adenylosuccinate lyase] [GN:purB] [FN:purine biosynthesis] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:4.3.2.2] [DE:Bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.] [SP:P12047] [LE:99038] [RE:100333] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000994_11959438_c2_534	2354	6126	135	44		
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Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000994_1214075_f3_332	2355	6127	507	168	328	1.3e-29
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Description

gp:[GI:g4981674] [LN:AE001770] [AC:AE001770:AE000512] [PN:ferritin]
[GN:TM1128] [OR:Thermotoga maritima] [DB:genpept-bct2] [DE:Thermotoga
maritima section 82 of 136 of the complete genome.] [NT:similar to
GB:AE000782 percent identity: 71.95;] [LE:15936] [RE:16430] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000994_12142768_f1_9	2356	6128	300	99	110	4.2e-06
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Description

pir:[LN:D71245] [AC:D71245] [PN:hypothetical protein PH0221] [GN:PH0221]
[OR:Pyrococcus horikoshii] [DB:pir2] >gp:[GI:d1030234:g3256608]
[LN:AP000001]
[AC:AP000001:AB009465:AB009464:AB009466:AB009467:AB009468:AB009469]
[PN:235aa long hypothetical protein] [GN:PH0221] [OR:Pyrococcus horikoshii]
[SR:Pyrococcus horikoshii (strain:OT3) DNA] [DB:genpept-bct1] [DE:Pyrococcus
horikoshii OT3 genomic DNA, 1-287000 nt. position (1/7).] [LE:194212]
[RE:194919] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000994_12270011_f2_269	2357	6129	180	59	239	3.5e-20
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Description

gp:[GI:e1311097:g3320009] [LN:SEHLDGN] [AC:Z49220] [GN:agrD]
[OR:Staphylococcus epidermidis] [DB:genpept-bct1] [DE:Staphylococcus
epidermidis hld and agr[A,B,C,D] genes.] [LE:1327] [RE:1467] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000994_12531558_f3_283	2358	6130	351	116		
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Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000994_12603166_f3_301	2359	6131	303	100	100	1.9e-05

Description

pir:[LN:G71244] [AC:G71244] [PN:hypothetical protein PH0217] [GN:PH0217]
[OR:Pyrococcus horikoshii] [DB:pir2] >gp:[GI:d1030229:g3256603]
[LN:AP000001]
[AC:AP000001:AB009465:AB009464:AB009466:AB009467:AB009468:AB009469]
[PN:106aa long hypothetical protein] [GN:PH0217] [OR:Pyrococcus horikoshii]
[SR:Pyrococcus horikoshii (strain:OT3) DNA] [DB:genpept-bct1] [DE:Pyrococcus
horikoshii OT3 genomic DNA, 1-287000 nt. position (1/7).] [LE:191072]
[RE:191392] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000994_1287557_f1_56	2360	6132	213	70		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000994_13678131_f3_393	2361	6133	840	279	299	1.5e-26

Description

pir:[LN:E69787] [AC:E69787] [PN:hypothetical protein ydiL] [GN:ydiL]
[OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1182580:g2632914] [LN:BSUB0004]
[AC:Z99107:AL009126] [GN:ydiL] [FN:unknown] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 4 of 21):
from 600701 to813890.] [LE:47946] [RE:48680] [DI:complement]
>gp:[GI:d1020504:g1945117] [LN:D88802] [AC:D88802] [GN:ydiL] [OR:Bacillus
subtilis] [SR:Bacillus subtilis (sub_species:Marburg, strain:168,
isolate:JH642] [DB:genpept-bct1] [DE:Bacillus subtilis DNA for
phoB-rrnE-groESL region, complete cds.] [NT:transmembrane] [LE:34948]
[RE:35682] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000994_1377337_c3_668	2362	6134	840	279	602	1.2e-58

Description

gp:[GI:g310603] [LN:STAORFPHI] [AC:L19300] [OR:Staphylococcus aureus]
[SR:Staphylococcus aureus (library: NCTC 8325) DNA] [DB:genpept-bct1]
[DE:Staphylococcus aureus DNA sequence encoding three ORFs, completecds;
prophage phi-11 sequence homology, 5' flank.] [LE:2651] [RE:3100]
[DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000994_13837927_c2_518	2363	6135	1155	384	621	1.2e-60

Description

sp:[LN:TNPA_STAAU] [AC:P06696] [GN:TNPA] [OR:STAPHYLOCOCCUS AUREUS]
 [DE:TRANSPOSASE A (TRANSPOSON TN554)] [SP:P06696] [DB:swissprot]
 >pir:[LN:A24584] [AC:A24584] [PN:transposition regulatory protein tnpA]
 [GN:tnpA] [OR:Staphylococcus aureus] [DB:pir2] >gp:[GI:g581277]
 [LN:ISTN554] [AC:X03216:K02987] [PN:tnpA protein] [GN:tnpA]
 [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:Staphylococcus aureus
 transposon Tn554.] [NT:(aa 1-361)] [SP:P06696] [LE:134] [RE:1219]
 [DI:direct] >gp:[GI:d1046007:g5360831] [LN:D86934] [AC:D86934]
 [PN:transposaseA] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus
 (strain:N315) DNA, clone_lib:library of N31] [DB:genpept] [DE:Staphylococcus
 aureus genes, mec region, partial and complete cds.] [NT:ORF N045; tnpA]
 [LE:29383] [RE:30468] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000994_13851088_c3_609	2364	6136	1089	362	185	6.2e-14

Description

gp:[GI:g1947171] [LN:CELE03H12] [AC:AF000299] [GN:E03H12.5]
 [OR:Caenorhabditis elegans] [SR:Caenorhabditis elegans strain=Bristol N2]
 [DB:genpept-inv2] [DE:Caenorhabditis elegans cosmid E03H12.] [NT:coded for
 by C. elegans cDNA yk170g3.5] [LE:1043:1176:1733] [RE:1131:1689:1762]
 [DI:directJoin]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000994_1385927_c1_442	2365	6137	711	236	851	4.9e-85

Description

sp:[LN:PCRB_STAAU] [AC:Q53726] [OR:STAPHYLOCOCCUS AUREUS] [DE:PCRB PROTEIN]
 [SP:Q53726] [DB:swissprot] >pir:[LN:S39922] [AC:S39922:S27666] [PN:pcrB
 protein] [CL:pcrB protein] [OR:Staphylococcus aureus] [DB:pir2]
 >gp:[GI:g153061] [LN:STAPCRA] [AC:M63176] [GN:pcrA] [OR:Staphylococcus
 aureus] [SR:Staphylococcus aureus (strain SA20) DNA] [DB:genpept-bct1]
 [DE:Staphylococcus aureus helicase required for T181 replication (pcrA)gene,
 complete cds.] [LE:256] [RE:939] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000994_1410277_f1_15	2366	6138	153	50		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000994_1414005_c1_477	2367	6139	579	192	324	3.4e-29

Description

pir:[LN:F69815] [AC:F69815] [PN:hypothetical protein ygaC] [GN:ygaC]
[OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1182857:g2633191] [LN:BSUB0005]
[AC:Z99108:AL009126] [GN:ygaC] [FN:unknown] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 5 of 21):
from 802821 to1011250.] [LE:135417] [RE:135734] [DI:direct]
>gp:[GI:e281578:g1673391] [LN:BSZ82044] [AC:Z82044] [PN:hypothetical 12.2 kd
protein] [GN:ygaC] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis
25 kb genomic DNA segment (from sspE to katA).] [LE:2267] [RE:2584]
[DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000994_14460882_c3_694	2368	6140	240	79	365	1.6e-33

Description

gp:[GI:g1022726] [LN:SHU35635] [AC:U35635] [PN:unknown] [OR:Staphylococcus
haemolyticus] [SR:Staphylococcus haemolyticus strain=Y176] [DB:genpept-bct1]
[DE:Staphylococcus haemolyticus IS1272 ORF1 and ORF2 genes, completedcds.]
[NT:ORF1] [LE:1101] [RE:1922] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000994_14460882_f2_232	2369	6141	126	41	99	9.9e-05

Description

gp:[GI:g1022726] [LN:SHU35635] [AC:U35635] [PN:unknown] [OR:Staphylococcus
haemolyticus] [SR:Staphylococcus haemolyticus strain=Y176] [DB:genpept-bct1]
[DE:Staphylococcus haemolyticus IS1272 ORF1 and ORF2 genes, completedcds.]
[NT:ORF1] [LE:1101] [RE:1922] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000994_14581306_f3_377	2370	6142	303	100	160	8.2e-12

Description

gp:[GI:g3676415] [LN:AF051917] [AC:AF051917:L19570] [PN:unknown]
[OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus
plasmid pSK41, complete sequence.] [NT:Orf149] [LE:2068] [RE:2484]
[DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000994_14642137_f3_381	2371	6143	168	55		
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Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000994_14714077_c1_445	2372	6144	1209	402	715	1.3e-70
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Description

pir:[LN:G69794] [AC:G69794] [PN:hypothetical protein yerH] [GN:yerH]
 [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1182643:g2632977] [LN:BSUB0004]
 [AC:Z99107:AL009126] [GN:yerH] [FN:unknown] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 4 of 21):
 from 600701 to813890.] [LE:122441] [RE:123631] [DI:direct]
 >gp:[GI:e1167977:g2577966] [LN:BSYERABCD] [AC:Y15254] [PN:YerH protein]
 [GN:yerH] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
 13kB DNA fragment, from yerA to sapB gene.] [LE:10086] [RE:11276]
 [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000994_14845336_f1_44	2373	6145	147	48		
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Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000994_14849093_c3_686	2374	6146	294	97	133	6.0e-09
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Description

pir:[LN:F71245] [AC:F71245] [PN:hypothetical protein PHS004] [GN:PHS004]
 [OR:Pyrococcus horikoshii] [DB:pir2] >gp:[GI:d1030236:g3256610]
 [LN:AP000001]
 [AC:AP000001:AB009465:AB009464:AB009466:AB009467:AB009468:AB009469] [PN:58aa
 long hypothetical protein] [GN:PHS004] [OR:Pyrococcus horikoshii]
 [SR:Pyrococcus horikoshii (strain:OT3) DNA] [DB:genpept-bct1] [DE:Pyrococcus
 horikoshii OT3 genomic DNA, 1-287000 nt. position (1/7).] [NT:similar to
 GENPEPT:Z47547 percent identity:50.000] [LE:195255] [RE:195431] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000994_14883592_c1_429	2375	6147	2076	691	600	2.0e-58

Description

pir:[LN:S40098] [AC:S40098] [PN:hypothetical protein] [OR:Clostridium butyricum] [DB:pir2] >gp:[GI:g436133] [LN:CBPYFOLY] [AC:Z29084] [OR:Clostridium butyricum] [DB:genpept-bct1] [DE:C.butyricum transposon containing tbcC gene.] [NT:product is similar to TnpB of transposon Tn554 from] [LE:1088] [RE:3070] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000994_14900826_c2_587	2376	6148	351	116	188	8.9e-15

Description

gp:[GI:g208931] [LN:SYNORFLAC] [AC:M15619] [OR:synthetic construct] [SR:E.coli (strain SE5000) synthetic DNA, clone pKB1] [DB:genpept-syn] [DE:Synthetic E.coli ORF16/lacZ fusion protein, partial cds.] [NT:ORF16-lacZ fusion protein] [LE:29] [RE:>232] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000994_15033167_c3_671	2377	6149	126	41		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000994_15041430_c2_563	2378	6150	249	82		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000994_15121077_c1_448	2379	6151	1476	491	1626	3.7e-167

Description

pir:[LN:B69795] [AC:B69795] [PN:amidase homolog yerM] [GN:yerM] [CL:indoleacetamide hydrolase] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1182648:g2632982] [LN:BSUB0004] [AC:Z99107:AL009126] [GN:yerM] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.] [NT:alternate gene name: yedB; similar to amidase] [LE:127844] [RE:129301] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000994_16110257_f3_287	2380	6152	126	41		
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000994_16209675_c3_674	2381	6153	159	52		
<u>Description</u>						

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000994_16219007_f3_366	2382	6154	921	306	1319	1.3e-134

Description

sp:[LN:BLAC_STAAU] [AC:P00807] [GN:BLAZ] [OR:STAPHYLOCOCCUS AUREUS]
[EC:3.5.2.6] [DE:BETA-LACTAMASE PRECURSOR, (PENICILLINASE)] [SP:P00807]
[DB:swissprot] >pir:[LN:PNSAP]
[AC:A01002:A23600:A90289:S06757:A45789:B45789:D45789::S11784:A60992]
[PN:beta-lactamase, precursor:cephalosporinase:penicillinase] [GN:blaZ]
[CL:beta-lactamase I] [OR:Staphylococcus aureus] [EC:3.5.2.6] [DB:pir1]
>gp:[GI:g551850] [LN:ENEBELAA] [AC:M60253] [PN:beta-lactamase] [GN:blaZ]
[OR:Enterococcus faecalis] [SR:Enterococcus faecalis (strain HH22) cDNA to
mRNA] [DB:genpept-bct1] [EC:3.5.2.6] [DE:E.faecalis beta-lactamase mRNA,
complete cds.] [LE:142] [RE:987] [DI:direct] >gp:[GI:g150717] [LN:PI25BLAZA]
[AC:M15526] [PN:beta-lactamase] [GN:blaZ] [OR:Plasmid pI258] [SR:Plasmid
pI258 (clone: pWN101) DNA] [DB:genpept-bct1] [EC:3.5.2.6] [DE:Plasmid pI258
(from S.aureus) beta-lactamase (blaZ), complete cds.] [LE:140] [RE:985]
[DI:direct] >gp:[GI:g581568] [LN:SAPBLAZ] [AC:X04121] [OR:Staphylococcus
aureus] [DB:genpept-bct1] [DE:S. aureus PC1 beta-lactamase gene blaZ from
plasmid pI258.] [NT:beta-lactamase (aa 1-281)] [SP:P00807] [LE:140] [RE:985]
[DI:direct] >gp:[GI:g581590] [LN:SATN552] [AC:X52734] [OR:Staphylococcus
aureus] [DB:genpept-bct1] [DE:S.aureus Tn552 transposable element.] [NT:blaZ
protein (AA 1-281)] [SP:P00807] [LE:5399] [RE:6244] [DI:direct]
>gp:[GI:g581591] [LN:SATNBLAZ] [AC:X16471] [OR:Staphylococcus aureus]
[DB:genpept-bct1] [DE:Staphylococcus aureus transposon Tn4002 blaZ gene
forbeta-lactamase.] [NT:beta-lactamase (AA 1-281)] [SP:P00807] [LE:142]
[RE:987] [DI:direct] >gp:[GI:g1575125] [LN:SAU58139] [AC:U58139]
[PN:beta-lactamase] [GN:blaZ] [OR:Staphylococcus aureus] [SR:Staphylococcus
aureus strain=a53] [DB:genpept-bct1] [DE:Staphylococcus aureus
beta-lactamase (blaZ) gene, complete cds.] [LE:142] [RE:987] [DI:direct]
>gp:[GI:g537336] [LN:STALACBAA] [AC:M25252] [PN:beta-lactamase]
[OR:Staphylococcus aureus] [SR:Staphylococcus aureus DNA] [DB:genpept-bct1]
[DE:Staphylococcus aureus (clone pPC1) beta-lactamase gene, completecds.]
[LE:123] [RE:968] [DI:direct] >gp:[GI:g537337] [LN:STALACBAB] [AC:M25253]
[PN:beta-lactamase] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus
DNA] [DB:genpept-bct1] [DE:Staphylococcus aureus (clone pS1) beta-lactamase
gene, completecds.] [LE:29] [RE:874] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000994_16677343_c1_412	2383	6155	447	148	111	1.3e-06

Description

sp:[LN:Y357_METJA] [AC:Q57803] [GN:MJ0357] [OR:METHANOCOCCUS JANNASCHII]
[DE:HYPOTHETICAL PROTEIN MJ0357] [SP:Q57803] [DB:swissprot] >pir:[LN:E64344]
[AC:E64344] [PN:hypothetical protein MJ0357] [OR:Methanococcus jannaschii]
[DB:pir2] [MP:REV326407-325940] >gp:[GI:g1591066] [LN:U67489]
[AC:U67489:L77117] [PN:M. jannaschii predicted coding region MJ0357]
[GN:MJ0357] [OR:Methanococcus jannaschii] [DB:genpept-bct2]
[DE:Methanococcus jannaschii section 31 of 150 of the complete genome.]
[NT:hypothetical protein; identified by GeneMark;] [LE:1632] [RE:2099]
[DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000994_16695300_f3_307	2384	6156	1113	370	586	5.9e-57

Description

pir:[LN:H69815] [AC:H69815] [PN:hypothetical protein ygaE] [GN:ygaE]
[OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1182859:g2633193] [LN:BSUB0005]
[AC:Z99108:AL009126] [GN:ygaE] [FN:unknown] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 5 of 21):
from 802821 to1011250.] [LE:137853] [RE:138914] [DI:complement]
>gp:[GI:e281580:g1673393] [LN:BSZ82044] [AC:Z82044] [PN:hypothetical 40.7 kd
protein] [GN:ygaE] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis
25 kb genomic DNA segment (from sspE to kata).] [LE:4703] [RE:5764]
[DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000994_19536693_c3_645	2385	6157	318	105	232	1.9e-19

Description

pir:[LN:A69795] [AC:A69795] [PN:conserved hypothetical protein yerL]
[GN:yerL] [CL:probable glu-tRNA amidotransferase C chain] [OR:Bacillus
subtilis] [DB:pir2] >gp:[GI:g2589194] [LN:AF008553] [AC:AF008553]
[PN:Glu-tRNAGln amidotransferase subunit C] [GN:gatC] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis Glu-tRNAGln amidotransferase
subunits C (gatC), A(gatA) and B (gatB) genes, complete cds.] [LE:412]
[RE:702] [DI:direct] >gp:[GI:g2114425] [LN:BSU92466] [AC:U92466]
[OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis strain JH642
amidase-like protein, partial cds,osmoregulated proline transporter (opuE)
gene, complete cds andSapB (sapB) gene, partial cds.] [NT:similar to
Synechocystis sp. hypothetical protein,] [LE:278] [RE:568] [DI:complement]
>gp:[GI:e1182647:g2632981] [LN:BSUB0004] [AC:Z99107:AL009126] [GN:yerL]
[FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
complete genome (section 4 of 21): from 600701 to813890.] [NT:alternate gene
name: yedA; similar to hypothetical] [LE:127538] [RE:127828] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000994_19570253_f2_152	2386	6158	213	70		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000994_1958183_f1_121	2387	6159	648	215	976	2.8e-98

Description

gp:[GI:e1311096:g3320008] [LN:SEHLDGN] [AC:Z49220] [GN:agrB]
[OR:Staphylococcus epidermidis] [DB:genpept-bct1] [DE:Staphylococcus
epidermidis hld and agr[A,B,C,D] genes.] [LE:759] [RE:1343] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000994_1972278_f3_306	2388	6160	300	99	316	2.4e-28

Description

sp:[LN:GSAB_BACSU] [AC:P71084] [GN:GSAB] [OR:BACILLUS SUBTILIS] [EC:5.4.3.8]
[DE:(GLUTAMATE-1-SEMIALDEHYDE AMINOTRANSFERASE) (GSA-AT)] [SP:P71084]
[DB:swissprot] >gp:[GI:e281581:g1673394] [LN:BSZ82044] [AC:Z82044]
[PN:glutamate-1-semialdehyde aminotransferase] [GN:gsaB] [OR:Bacillus
subtilis] [DB:genpept-bct1] [DE:B.subtilis 25 kb genomic DNA segment (from
sspE to ktaA).] [SP:P71084] [LE:5984] [RE:7273] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000994_1988811_c3_672	2389	6161	1083	360	779	2.1e-77

Description

pir:[LN:A69802] [AC:A69802] [PN:A/G-specific adenine glycosylase homolog
yfhQ] [GN:yfhQ] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1182852:g2633186]
[LN:BSUB0005] [AC:Z99108:AL009126] [GN:yfhQ] [FN:unknown] [OR:Bacillus
subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 5
of 21): from 802821 to1011250.] [NT:similar to A/G-specific adenine
glycosylase] [LE:132342] [RE:133451] [DI:direct] >gp:[GI:d1025399:g2804547]
[LN:D85082] [AC:D85082] [PN:YfhQ] [OR:Bacillus subtilis] [SR:Bacillus
subtilis DNA] [DB:genpept-bct1] [DE:Bacillus subtilis DNA, genome sequence,
79 to 81 degree region.] [LE:25233] [RE:26342] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000994_20100206_f2_137	2390	6162	165	54		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000994_20344411_c2_508	2391	6163	336	111	440	1.8e-41

Description

sp:[LN:CH10_STAEP] [AC:P48227] [GN:GROES:HSP10] [OR:STAPHYLOCOCCUS EPIDERMIDIS] [DE:10] [SP:P48227] [DB:swissprot] >gp:[GI:g535341] [LN:SEU13618] [AC:U13618] [PN:heat shock protein 10] [GN:hsp10] [OR:Staphylococcus epidermidis] [DB:genpept-bct1] [DE:Staphylococcus epidermidis 9759 heat shock protein 10 (hsp10) and heat shock protein 60 (hsp60) genes, complete cds.] [LE:105] [RE:389] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000994_20348427_c2_578	2392	6164	126	41		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000994_2037838_f2_223	2393	6165	249	82	122	8.8e-08

Description

pir:[LN:A71136] [AC:A71136] [PN:hypothetical protein PH0853] [GN:PH0853] [CL:isoleucine--tRNA ligase] [OR:Pyrococcus horikoshii] [DB:pir2] >gp:[GI:d1030890:g3257264] [LN:AP000003] [AC:AP000003:AB009484:AB009485:AB009486:AB009487:AB009488:AB009489] [PN:134aa long hypothetical protein] [GN:PH0853] [OR:Pyrococcus horikoshii] [SR:Pyrococcus horikoshii (strain:OT3) DNA] [DB:genpept-bct1] [DE:Pyrococcus horikoshii OT3 genomic DNA, 544001-777000 nt. position(3/7).] [LE:216446] [RE:216850] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000994_20414052_f1_49	2394	6166	129	42		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000994_20735686_f1_87	2395	6167	957	318	853	3.0e-85

Description

sp:[LN:YYBQ_BACSU] [AC:P37487] [GN:YYBQ] [OR:BACILLUS SUBTILIS]
 [DE:HYPOTHETICAL 34.0 KD PROTEIN IN COTF-TETB INTERGENIC REGION] [SP:P37487]
 [DB:swissprot] >pir:[LN:S65980] [AC:S65980:D70088] [PN:conserved
 hypothetical protein yybQ] [GN:yybQ] [CL:conserved hypothetical protein
 MJ0608] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:d1005728:g467340]
 [LN:BAC180K] [AC:D26185] [PN:unknown] [OR:Bacillus subtilis] [SR:Bacillus
 subtilis (sub_species:Marburg, strain:168) DNA] [DB:genpept-bct1] [DE:B.
 subtilis DNA, 180 kilobase region of replication origin.] [LE:16200]
 [RE:17129] [DI:direct] >gp:[GI:e1184781:g2636602] [LN:BSUB0021]
 [AC:Z99124:AL009126] [GN:yybQ] [FN:unknown] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 21 of 21):
 from 3999281to 4214814.] [NT:similar to hypothetical proteins] [SP:P37487]
 [LE:168132] [RE:169061] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000994_20881510_c2_510	2396	6168	492	163	216	9.6e-18

Description

gp:[GI:g3688823] [LN:AF084104] [AC:AF084104] [PN:hypothetical protein]
 [OR:Bacillus firmus] [DB:genpept-bct2] [DE:Bacillus firmus AcsA (acsA) gene,
 partial cds; SspA (sspA),hypothetical protein, maltose transportor
 ATP-binding protein(malK), leucine-rich protein transcriptional regulator
 (lrpR),hypothetical proteins, ABC transporter ATP-binding protein
 (natC),Nata (natA), NatB (natB), and hypothetical protein genes,
 completecds; and SpoIIIJ (spoIIIJ) gene, partial cds.] [NT:Orf15; similar to
 transcription regulator YtrA from] [LE:9870] [RE:10229] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000994_2125637_f3_294	2397	6169	150	49		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000994_21494536_c3_644	2398	6170	132	43		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000994_21516287_f1_17	2399	6171	135	44	100	1.9e-05

Description

pir:[LN:G64564] [AC:G64564] [PN:hypothetical protein HP0359]
[OR:Helicobacter pylori] [DB:pir2] >gp:[GI:g2313473] [LN:AE000553]
[AC:AE000553:AE000511] [PN:H. pylori predicted coding region HP0359]
[GN:HP0359] [OR:Helicobacter pylori 26695] [DB:genpept-bct2]
[DE:Helicobacter pylori 26695 section 31 of 134 of the complete genome.]
[NT:hypothetical protein; identified by GeneMark;] [LE:250] [RE:315]
[DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000994_21616078_c1_440	2400	6172	192	63	135	3.7e-09

Description

pir:[LN:C69792] [AC:C69792] [PN:hypothetical protein yebG] [GN:yebG]
[OR:Bacillus subtilis] [DB:pir2] >gp:[GI:g2239294] [LN:BSU51115] [AC:U51115]
[PN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
CotA (cotA), GabP (gabP), YeaB (yeaB), YeaC(yeaC), YebA (yebA), GMP
synthetase (guaA) genes, complete cds, andAIR carboxylase I (pure) gene,
partial cds.] [NT:yebG] [LE:15312] [RE:15509] [DI:direct]
>gp:[GI:e1182621:g2632955] [LN:BSUB0004] [AC:Z99107:AL009126] [GN:yebG]
[FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
complete genome (section 4 of 21): from 600701 to813890.] [LE:96901]
[RE:97098] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000994_21676433_c3_634	2401	6173	1137	378	192	3.3e-12

Description

gp:[GI:e1292355:g3127839] [LN:SC1A6] [AC:AL023496] [PN:hypothetical protein]
[GN:SC1A6.07c] [OR:Streptomyces coelicolor] [DB:genpept-bct1]
[DE:Streptomyces coelicolor cosmid 1A6.] [NT:SC1A6.07c, unknown, len: 813]
[LE:7442] [RE:9070] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000994_22289077_c2_514	2402	6174	546	181		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000994_22688428_c2_584	2403	6175	144	47		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000994_23438461_c1_413	2404	6176	687	228	103	0.029

Description

gp:[GI:g5306158] [LN:AF160864] [AC:AF160864] [PN:orf1386] [GN:orf1386]
 [OR:Mitochondrion Tetrahymena pyriformis] [SR:Tetrahymena pyriformis]
 [DB:genpept] [DE:Tetrahymena pyriformis mitochondrial DNA, complete genome.]
 [NT:Open reading frame ymf77 (CPGN); ATA initiation] [LE:22317] [RE:26477]
 [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000994_23495437_f2_262	2405	6177	1305	434	1004	3.0e-101

Description

pir:[LN:JC4864] [AC:JC4864] [PN:aspartate transaminase,] [GN:aspAT]
 [OR:Bacillus circulans] [EC:2.6.1.1] [DB:pir2] >gp:[GI:e216734:g1147557]
 [LN:BCASPAMIN] [AC:X94433] [PN:Aspartate aminotransferase] [OR:Bacillus
 circulans subsp. alkalophilus] [DB:genpept-bct1] [EC:2.6.1.1]
 [DE:B.circulans aspartate aminotransferase gene.] [LE:367] [RE:1665]
 [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000994_23572125_c2_571	2406	6178	534	177	393	1.7e-36

Description

sp:[LN:YKHA_BACSU] [AC:P49851] [GN:YKHA] [OR:BACILLUS SUBTILIS]
 [DE:HYPOTHETICAL 20.1 KD PROTEIN IN HMP 5'REGION (ORF1)] [SP:P49851]
 [DB:swissprot] >gp:[GI:d1011919:g1063246] [LN:BAC168TRP2] [AC:D78189]
 [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:168trpC2) DNA]
 [DB:genpept-bct1] [DE:Bacillus subtilis hmp DNA for 7 ORFs, complete cds.]
 [NT:low homology to P14 protein of Heamophilus] [LE:241] [RE:780]
 [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000994_23595386_c1_484	2407	6179	627	208	271	1.4e-23

Description

pir:[LN:H70032] [AC:H70032] [PN:glycerate dehydrogenase homolog yvcT]
 [GN:yvcT] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1186156:g2635981]
 [LN:BSUB0018] [AC:Z99121:AL009126] [GN:yvcT] [FN:unknown] [OR:Bacillus
 subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section
 18 of 21): from 3399551to 3609060.] [NT:similar to glycerate dehydrogenase]
 [LE:162076] [RE:163053] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000994_23600175_f2_274	2408	6180	123	40		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000994_23629202_c1_433	2409	6181	381	126	598	3.2e-58

Description

sp:[LN:BLAI_STAAU] [AC:P18415] [GN:BLAI:PENI] [OR:STAPHYLOCOCCUS AUREUS]
 [DE:REPRESSOR PROTEIN]] [SP:P18415] [DB:swissprot] >pir:[LN:S11782]
 [AC:S11782:S34446] [PN:regulatory protein blaI] [GN:blaI] [CL:regulatory
 protein blaI] [OR:Staphylococcus aureus] [DB:pir2] >gp:[GI:g46758]
 [LN:SATN552] [AC:X52734] [OR:Staphylococcus aureus] [DB:genpept-bct1]
 [DE:S.aureus Tn552 transposable element.] [NT:blaI protein (AA 1-126)]
 [SP:P18415] [LE:3165] [RE:3545] [DI:complement] >gp:[GI:g152967] [LN:STABLA]
 [AC:M62650] [GN:blaI] [FN:putative blaZ repressor] [OR:Staphylococcus
 aureus] [SR:Staphylococcus aureus DNA] [DB:genpept-bct1] [DE:Staphylococcus
 aureus blaZ gene, 5' end; blaR1 gene, complete cds;blaI gene, complete cds;
 and binR gene, 5' end.] [LE:1903] [RE:2283] [DI:direct] >gp:[GI:g152970]
 [LN:STABLAIA] [AC:M92376] [PN:beta-lactamase repressor] [GN:BlaI]
 [FN:represses the production of the blaZ product] [OR:Staphylococcus aureus]
 [SR:Staphylococcus aureus (strain RN4) DNA] [DB:genpept-bct1]
 [DE:Staphylococcus aureus beta-lactamase repressor (BlaI) gene,complete
 cds.] [NT:no obvious promoters were found in the region] [LE:16] [RE:396]
 [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000994_23672302_f3_302	2410	6182	156	51		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000994_23672562_c1_411	2411	6183	297	98	86	0.0034

Description

gp:[GI:e8900:g1335718] [LN:PFRESAR1] [AC:X05182] [PN:ring-infected erythrocyte surface antigen] [GN:RESA] [OR:Plasmodium falciparum] [SR:malaria parasite P. falciparum] [DB:genpept-inv1] [DE:P.falciparum FC27 Ag46 RESA mRNA for ring-infected erythrocytesurface antigen.] [SP:P13830] [LE:<1] [RE:>955] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000994_23727212_f2_175	2412	6184	303	100	87	0.00045

Description

pir:[LN:B69818] [AC:B69818] [PN:conserved hypothetical protein yhaH] [GN:yhaH] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1183002:g2633336] [LN:BSUB0006] [AC:Z99109:AL009126] [GN:yhaH] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.] [NT:similar to hypothetical proteins from B. subtilis] [LE:73870] [RE:74226] [DI:complement] >gp:[GI:e325179:g2226119] [LN:BSY14077] [AC:Y14077] [PN:Hypothetical protein] [GN:yhaH] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subitlis 10.6 Kb chromosomal DNA: glyB-prsA region.] [LE:6687] [RE:7043] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000994_23727250_f3_362	2413	6185	1395	464	1167	1.6e-118

Description

sp:[LN:DHA2_BACSU] [AC:P39616] [GN:YWDH:IPA-58R] [OR:BACILLUS SUBTILIS] [EC:1.2.1.3] [DE:PROBABLE ALDEHYDE DEHYDROGENASE YWDH,] [SP:P39616] [DB:swissprot] >pir:[LN:S39713] [AC:S39713:C70054] [PN:aldehyde dehydrogenase homolog ywdH:protein ipa-58r] [GN:ywdH] [CL:aldehyde dehydrogenase (NAD+):aldehyde dehydrogenase homology] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:g413982] [LN:BSGENR] [AC:X73124] [GN:ipa-58r] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis genomic region (325 to 333).] [SP:P39616] [LE:59908] [RE:61281] [DI:complement] >gp:[GI:e1186295:g2636331] [LN:BSUB0020] [AC:Z99123:AL009126] [GN:ywdH] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.] [NT:alternate gene name: ipa-58r; similar to aldehyde] [SP:P39616] [LE:96681] [RE:98054] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000994_2379658_f2_144	2414	6186	225	74		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000994_23850907_f1_109	2415	6187	201	66		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000994_24017175_f2_202	2416	6188	150	49		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000994_24218791_f1_86	2417	6189	588	195	525	1.7e-50

Description

pir:[LN:C70008] [AC:C70008] [PN:pyrazinamidase/nicotinamidase homolog yueJ]
[GN:yueJ] [CL:hypothetical protein b1011] [OR:Bacillus subtilis] [DB:pir2]
>gp:[GI:e1184253:g2635671] [LN:BSUB0017] [AC:Z99120:AL009126] [GN:yueJ]
[FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
complete genome (section 17 of 21): from 3197001to 3414420.] [NT:similar to
pyrazinamidase/nicotinamidase] [LE:62967] [RE:63518] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000994_24225632_f2_253	2418	6190	171	56		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000994_24257827_c2_511	2419	6191	387	128		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000994_24265676_f1_120	2420	6192	144	47		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000994_24350953_f2_151	2421	6193	132	43	72	0.017

Description

pir:[LN:G71244] [AC:G71244] [PN:hypothetical protein PH0217] [GN:PH0217]
 [OR:Pyrococcus horikoshii] [DB:pir2] >gp:[GI:d1030229:g3256603]
 [LN:AP000001]
 [AC:AP000001:AB009465:AB009464:AB009466:AB009467:AB009468:AB009469]
 [PN:106aa long hypothetical protein] [GN:PH0217] [OR:Pyrococcus horikoshii]
 [SR:Pyrococcus horikoshii (strain:OT3) DNA] [DB:genpept-bct1] [DE:Pyrococcus
 horikoshii OT3 genomic DNA, 1-287000 nt. position (1/7).] [LE:191072]
 [RE:191392] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000994_24353382_c3_608	2422	6194	1623	540	2592	1.6e-269

Description

gp:[GI:g535342] [LN:SEU13618] [AC:U13618] [PN:heat shock protein 60]
 [GN:hsp60] [OR:Staphylococcus epidermidis] [DB:genpept-bct1]
 [DE:Staphylococcus epidermidis 9759 heat shock protein 10 (hsp10) and heat
 shock protein 60 (hsp60) genes, complete cds.] [LE:445] [RE:2064]
 [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000994_24407787_c1_483	2423	6195	354	117	84	0.029

Description

sp:[LN:SERX_YEAST] [AC:P40054] [GN:YER081W] [OR:SACCHAROMYCES CEREVISIAE]
 [SR:,BAKER'S YEAST] [EC:1.1.1.95] [DE:(PGDH)] [SP:P40054] [DB:swissprot]
 >pir:[LN:S50584] [AC:S50584] [PN:probable phosphoglycerate dehydrogenase,
 YER081w] [OR:Saccharomyces cerevisiae] [EC:1.1.1.95] [DB:pir2] [MP:5R]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000994_24415942_c2_516	2424	6196	840	279		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
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AI7503000994_24475252_c2_533	2425	6197	162	53		
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Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
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AI7503000994_24475252_f1_2	2426	6198	159	52		
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Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
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AI7503000994_24885938_c3_639	2427	6199	642	213	302	7.4e-27
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Description

pir:[LN:B69792] [AC:B69792] [PN:hypothetical protein yebF] [GN:yebF]
 [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:g2239293] [LN:BSU51115] [AC:U51115]
 [PN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
 CotA (cotA), GabP (gabP), YeaB (yeaB), YeaC(yeaC), YebA (yebA), GMP
 synthetase (guaA) genes, complete cds, andAIR carboxylase I (purE) gene,
 partial cds.] [NT:yebF] [LE:15046] [RE:15312] [DI:direct]
 >gp:[GI:e1182620:g2632954] [LN:BSUB0004] [AC:Z99107:AL009126] [GN:yebF]
 [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
 complete genome (section 4 of 21): from 600701 to813890.] [LE:96635]
 [RE:96901] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
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AI7503000994_25428507_c1_457	2428	6200	576	191	109	0.0063
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Description

pir:[LN:G71609] [AC:G71609] [PN:hypothetical protein PFB0650w] [GN:PFB0650w
] [OR:Plasmodium falciparum] [DB:pir2] >gp:[GI:g3845240] [LN:AE001408]
 [AC:AE001408:AE001362] [PN:hypothetical protein] [GN:PFB0650w]
 [OR:Plasmodium falciparum] [SR:malaria parasite P. falciparum]
 [DB:genpept-inv2] [DE:Plasmodium falciparum chromosome 2, section 45 of 73
 of thecomplete sequence.] [NT:predicted by GlimmerM] [LE:4458] [RE:11960]
 [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000994_25595387_f1_93	2429	6201	432	143	326	2.1e-29

Description

gp:[GI:g3676415] [LN:AF051917] [AC:AF051917:L19570] [PN:unknown]
 [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus
 plasmid pSK41, complete sequence.] [NT:Orf149] [LE:2068] [RE:2484]
 [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000994_25603388_f1_122	2430	6202	1293	430	2112	1.2e-218

Description

gp:[GI:g2981295] [LN:AF012132] [AC:AF012132] [PN:histidine kinase] [GN:agrC]
 [OR:Staphylococcus epidermidis] [DB:genpept-bct2] [DE:Staphylococcus
 epidermidis agr system including response regulator(agrA), histidine kinase
 (agrC), AgrD (agrD), AgrB (agrB) and deltatoxin (hld) genes, complete cds.]
 [NT:AgrC; similar to S. aureus and S. lugdunensis AgrC] [LE:975] [RE:2264]
 [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000994_256265_c2_564	2431	6203	1092	363	538	7.3e-52

Description

pir:[LN:F70045] [AC:F70045] [PN:two-component sensor histidine kinase
 homolog yvqE] [GN:yvqE] [OR:Bacillus subtilis] [DB:pir2]
 >gp:[GI:e1249816:g2832820] [LN:BS43KBDNA] [AC:AJ223978] [PN:YvqE protein]
 [GN:yvqE] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
 42.7kB DNA fragment from yvsa to yvqA.] [LE:32111] [RE:33193] [DI:direct]
 >gp:[GI:e1184388:g2635806] [LN:BSUB0017] [AC:Z99120:AL009126] [GN:yvqE]
 [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
 complete genome (section 17 of 21): from 3197001to 3414420.] [NT:similar to
 two-component sensor histidine kinase] [LE:197094] [RE:198176]
 [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000994_25678438_c2_583	2432	6204	474	157	334	3.0e-30

Description

pir:[LN:E70344] [AC:E70344] [PN:conserved hypothetical protein aq_495]
 [GN:aq_495] [CL:bacterioferritin comigratory protein:alkyl hydroperoxidase
 c22 protein homology] [OR:Aquifex aeolicus] [DB:pir2] >gp:[GI:g2983147]
 [LN:AE000692] [AC:AE000692:AE000657] [PN:hypothetical protein] [GN:aq_495]
 [OR:Aquifex aeolicus] [DB:genpept-bct2] [DE:Aquifex aeolicus section 24 of
 109 of the complete genome.] [LE:11182] [RE:11667] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000994_25781392_f1_54	2433	6205	1029	342	225	5.7e-17

Description

pir:[LN:H69815] [AC:H69815] [PN:hypothetical protein ygaE] [GN:ygaE]
[OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1182859:g2633193] [LN:BSUB0005]
[AC:Z99108:AL009126] [GN:ygaE] [FN:unknown] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 5 of 21):
from 802821 to1011250.] [LE:137853] [RE:138914] [DI:complement]
>gp:[GI:e281580:g1673393] [LN:BSZ82044] [AC:Z82044] [PN:hypothetical 40.7 kd
protein] [GN:ygaE] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis
25 kb genomic DNA segment (from sspE to kata).] [LE:4703] [RE:5764]
[DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000994_25790718_c2_541	2434	6206	315	104	349	7.7e-32

Description

pir:[LN:B69794] [AC:B69794] [PN:hypothetical protein yecC] [GN:yecC]
[OR:Bacillus subtilis] [DB:pir2] >gp:[GI:g2465565] [LN:AF011544]
[AC:AF011544] [PN:YecD] [GN:yecD] [FN:unknown] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis
phosphoribosylaminoimidazole-carboxamideformyltransferase (purH-J) gene,
partial cds,phosphoribosylglycinamide synthetase (purD), YecA (yecA),
putativeadenine deaminase (yecB), YecC (yecC), and YecD (yecD)
genes,complete cds, and putative glutamate synthase (yecE) gene,
partialcds.] [NT:no apparent homology has been identified] [LE:6547]
[RE:6861] [DI:direct] >gp:[GI:e1182638:g2632972] [LN:BSUB0004]
[AC:Z99107:AL009126] [GN:yecC] [FN:unknown] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 4 of 21):
from 600701 to813890.] [LE:115237] [RE:115551] [DI:direct]
>gp:[GI:e1167973:g2577962] [LN:BSYERABCD] [AC:Y15254] [PN:YecC protein]
[GN:yecC] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
13kB DNA fragment, from yecA to sapB gene.] [LE:2882] [RE:3196] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000994_26177163_c1_466	2435	6207	1272	423	971	9.5e-98

Description

sp:[LN:AMPS_BACSU] [AC:P39762] [GN:AMPS] [OR:BACILLUS SUBTILIS]
[EC:3.4.11.-] [DE:AMINOPEPTIDASE AMPS,] [SP:P39762] [DB:swissprot]
>pir:[LN:C69585] [AC:C69585] [PN:aminopeptidase ampS] [GN:ampS]
[CL:Bacillus aminopeptidase] [OR:Bacillus subtilis] [DB:pir2]
>gp:[GI:e1185035:g2633816] [LN:BSUB0008] [AC:Z99111:AL009126]
[PN:aminopeptidase] [GN:ampS] [OR:Bacillus subtilis] [DB:genpept-bct1]
[EC:3.4.11.-] [DE:Bacillus subtilis complete genome (section 8 of 21): from
1394791to 1603020.] [SP:P39762] [LE:119612] [RE:120844] [DI:complement]
>gp:[GI:g3282130] [LN:AF012285] [AC:AF012285:AF012284:U51911]
[PN:aminopeptidase] [GN:ampS] [OR:Bacillus subtilis] [DB:genpept-bct2]
[DE:Bacillus subtilis mobA-nprE gene region.] [NT:similar to ampS gene with
GenBan Accession Number] [LE:20100] [RE:21332] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000994_26205151_f2_147	2436	6208	156	51	117	3.0e-07

Description

pir:[LN:B71245] [AC:B71245] [PN:hypothetical protein PH0220] [GN:PH0220]
[OR:Pyrococcus horikoshii] [DB:pir2] >gp:[GI:d1030232:g3256606]
[LN:AP0000001]
[AC:AP0000001:AB009465:AB009464:AB009466:AB009467:AB009468:AB009469]
[PN:171aa long hypothetical protein] [GN:PH0220] [OR:Pyrococcus horikoshii]
[SR:Pyrococcus horikoshii (strain:OT3) DNA] [DB:genpept-bct1] [DE:Pyrococcus
horikoshii OT3 genomic DNA, 1-287000 nt. position (1/7).] [LE:192864]
[RE:193379] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000994_26209510_c1_478	2437	6209	165	54		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000994_26209577_f3_358	2438	6210	1068	355	892	2.2e-89

Description

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pir:[LN:C69811] [AC:C69811 ] [PN:nitric-oxide synthase homolog yflM]
[GN:yflM ] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1182753:g2633087]
[LN:BSUB0005] [AC:Z99108:AL009126] [GN:yflM] [FN:unknown] [OR:Bacillus
subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 5
of 21): from 802821 to1011250.] [NT:similar to nitric-oxide synthase]
[LE:33422] [RE:34432] [DI:direct] >gp:[GI:d1023169:g2443235] [LN:D86417]
[AC:D86417] [PN:YflM] [OR:Bacillus subtilis] [SR:Bacillus subtilis
(strain:AC327) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis 35.7 kb genomic
DNA, 70-73 degree region,complete cds.] [LE:14090] [RE:15100]
[DI:complement]

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000994_26212875_c3_616	2439	6211	318	105		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000994_26354787_c2_499	2440	6212	744	247	121	0.00043

Description

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gp:[GI:g3549261] [LN:AF057019] [AC:AF057019] [PN:interaptin] [GN:abpD]
[OR:Dictyostelium discoideum] [DB:genpept-inv2] [DE:Dictyostelium discoideum
interaptin (abpD) gene, complete cds.] [LE:1861:2796:7392]
[RE:2378:7315:7570] [DI:directJoin]
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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000994_26369052_f1_91	2441	6213	141	46	101	1.5e-05

Description

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gp:[GI:g3676415] [LN:AF051917] [AC:AF051917:L19570] [PN:unknown]
[OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus
plasmid pSK41, complete sequence.] [NT:Orf149] [LE:2068] [RE:2484]
[DI:complement]
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ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000994_26593808_f2_159	2442	6214	981	326	753	1.2e-74

Description

pir:[LN:H69801] [AC:H69801] [PN:hypothetical protein yfhP] [GN:yfhP]
[OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1182851:g2633185] [LN:BSUB0005]
[AC:Z99108:AL009126] [GN:yfhP] [FN:unknown] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 5 of 21):
from 802821 to1011250.] [LE:131143] [RE:132126] [DI:complement]
>gp:[GI:d1025398:g2804546] [LN:D85082] [AC:D85082] [PN:YfhP] [OR:Bacillus
subtilis] [SR:Bacillus subtilis DNA] [DB:genpept-bct1] [DE:Bacillus subtilis
DNA, genome sequence, 79 to 81 degree region.] [LE:24034] [RE:25017]
[DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000994_26689703_c3_679	2443	6215	453	150	562	2.1e-54

Description

sp:[LN:FUR3_BACSU] [AC:P71086] [GN:YGAG] [OR:BACILLUS SUBTILIS] [DE:FERRIC
UPTAKE REGULATION PROTEIN HOMOLOG 3] [SP:P71086] [DB:swissprot]
>pir:[LN:B69816] [AC:B69816] [PN:transcription regulator Fur family homolog
ygaG] [GN:ygaG] [CL:ferric uptake regulator] [OR:Bacillus subtilis]
[DB:pir2] >gp:[GI:e1182862:g2633196] [LN:BSUB0005] [AC:Z99108:AL009126]
[GN:ygaG] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus
subtilis complete genome (section 5 of 21): from 802821 to1011250.]
[NT:similar to transcriptional regulator (Fur family)] [SP:P71086]
[LE:141173] [RE:141610] [DI:direct] >gp:[GI:e281583:g1673396] [LN:BSZ82044]
[AC:Z82044] [PN:hypothetical 16.4 kd protein] [GN:ygaG] [OR:Bacillus
subtilis] [DB:genpept-bct1] [DE:B.subtilis 25 kb genomic DNA segment (from
sspE to kata).] [NT:homology to ferric uptake regulation protein]
[SP:P71086] [LE:8023] [RE:8460] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000994_26756500_c3_654	2444	6216	777	258	721	2.9e-71

Description

pir:[LN:E69810] [AC:E69810] [PN:methionine aminopeptidase homolog yflG]
[GN:yflG] [CL:Escherichia coli methionyl aminopeptidase] [OR:Bacillus
subtilis] [DB:pir2] >gp:[GI:e1182759:g2633093] [LN:BSUB0005]
[AC:Z99108:AL009126] [GN:yflG] [FN:unknown] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 5 of 21):
from 802821 to1011250.] [NT:similar to methionine aminopeptidase] [LE:36423]
[RE:37172] [DI:complement] >gp:[GI:d1023163:g2443229] [LN:D86417]
[AC:D86417] [PN:YflG] [OR:Bacillus subtilis] [SR:Bacillus subtilis
(strain:AC327) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis 35.7 kb genomic
DNA, 70-73 degree region,complete cds.] [LE:11350] [RE:12099] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000994_26757312_f3_321	2445	6217	1197	398	577	5.3e-56

Description

gp:[GI:e1423916:g4584097] [LN:BAJ10131] [AC:AJ010131] [GN:yfkh] [OR:Bacillus cereus] [DB:genpept-bct1] [DE:Bacillus cereus yfkh gene and partial ykvW, bc333c genes.] [LE:863] [RE:1732] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000994_285808_f2_146	2446	6218	225	74		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000994_29307187_c3_687	2447	6219	165	54		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000994_29500277_f3_392	2448	6220	171	56	169	9.2e-13

Description

gp:[GI:g1196510] [LN:MSGTCWPA] [AC:M15467] [PN:unknown protein] [OR:Mycobacterium tuberculosis] [SR:Mycobacterium tuberculosis (strain Erdman) DNA] [DB:genpept-bct1] [DE:M.tuberculosis 65 kDa antigen (cell wall protein a) gene.] [NT:ORF F175; putative] [LE:242] [RE:769] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000994_2992943_c1_425	2449	6221	624	207	382	2.5e-35

Description

gp:[GI:g4981569] [LN:AE001764] [AC:AE001764:AE000512] [PN:ABC transporter, ATP-binding protein] [GN:TM1028] [OR:Thermotoga maritima] [DB:genpept-bct2] [DE:Thermotoga maritima section 76 of 136 of the complete genome.] [NT:similar to GB:AE000782 percent identity: 60.48;] [LE:5922] [RE:6803] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000994_30265640_c3_693	2450	6222	1080	359	684	2.4e-67

Description

pir:[LN:E71373] [AC:E71373] [PN:probable regulatory protein (pfoS/R)]
 [GN:TP0038] [OR:Treponema pallidum subsp. pallidum] [SR:, syphilis
 spirochete] [DB:pir2] >gp:[GI:g3322295] [LN:AE001189] [AC:AE001189:AE000520]
 [PN:regulatory protein (pfoS/R)] [GN:TP0038] [OR:Treponema pallidum]
 [DB:genpept-bct2] [DE:Treponema pallidum section 5 of 87 of the complete
 genome.] [NT:similar to GP:1354775 percent identity: 100.00;] [LE:1177]
 [RE:2229] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000994_30506437_c2_517	2451	6223	177	58		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000994_30677268_c1_419	2452	6224	171	56		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000994_31273377_f1_113	2453	6225	171	56		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000994_3128452_c1_438	2454	6226	132	43		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000994_31289637_c2_545	2455	6227	123	40		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000994_31534456_c3_689	2456	6228	156	51		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000994_32037826_c1_451	2457	6229	1476	491	1119	2.0e-113

Description

pir:[LN:E69793] [AC:E69793] [PN:RNA methyltransferase homolog yefA]
 [GN:yefA] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1182653:g2632987]
 [LN:BSUB0004] [AC:Z99107:AL009126] [GN:yefA] [FN:unknown] [OR:Bacillus
 subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 4
 of 21): from 600701 to813890.] [NT:alternate gene name: yerS; similar to
 RNA] [LE:136409] [RE:137788] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000994_3251577_c3_642	2458	6230	2190	729	3095	0.0

Description

sp:[LN:PCRA_STAAU] [AC:Q53727] [GN:PCRA] [OR:STAPHYLOCOCCUS AUREUS]
 [EC:3.6.1.-] [DE:ATP-DEPENDENT HELICASE PCRA,] [SP:Q53727] [DB:swissprot]
 >pir:[LN:S39923] [AC:S39923:S27667] [PN:DNA helicase pcrA] [GN:pcrA]
 [CL:helicase II] [OR:Staphylococcus aureus] [DB:pir2] >gp:[GI:g153062]
 [LN:STAPCRA] [AC:M63176] [PN:helicase] [GN:pcrA] [OR:Staphylococcus aureus]
 [SR:Staphylococcus aureus (strain SA20) DNA] [DB:genpept-bct1]
 [DE:Staphylococcus aureus helicase required for T181 replication (pcrA)gene,
 complete cds.] [LE:943] [RE:2970] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000994_32634387_f2_133	2459	6231	198	65		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000994_32680_c3_692	2460	6232	936	311	776	4.4e-77

Description

sp:[LN:STSP_STAAU] [AC:P04188] [OR:STAPHYLOCOCCUS AUREUS] [EC:3.4.21.19]
[DE:PROTEINASE) (V8 PROTEINASE) (ENDOPROTEINASE GLU-C)] [SP:P04188]
[DB:swissprot] >pir:[LN:PRSASK] [AC:A26812:A00966] [PN:glutamyl
endopeptidase, precursor:staphylococcal serine proteinase]
[CL:staphylococcal serine proteinase] [OR:Staphylococcus aureus]
[EC:3.4.21.19] [DB:pir1] >gp:[GI:g46687] [LN:SASP] [AC:Y00356]
[OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:Staphylococcus aureus V8
serine protease gene.] [NT:preproenzyme (AA -68 to 268)] [SP:P04188]
[LE:354] [RE:1364] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000994_32689162_f3_397	2461	6233	807	268	1384	1.6e-141

Description

gp:[GI:g2981299] [LN:AF012132] [AC:AF012132] [PN:unknown] [GN:orf5]
[OR:Staphylococcus epidermidis] [DB:genpept-bct2] [DE:Staphylococcus
epidermidis agr system including response regulator(agrA), histidine kinase
(agrC), AgrD (agrD), AgrB (agrB) and deltatoxin (hld) genes, complete cds.]
[NT:similar to S. aureus and S. lugdunensis orf5] [LE:3778] [RE:4572]
[DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000994_32696088_c2_580	2462	6234	1749	582	1899	4.3e-196

Description

pir:[LN:G69815] [AC:G69815] [PN:ABC transporter (ATP-binding protein)
homolog ygaD] [GN:ygaD] [CL:ATP-binding cassette homology] [OR:Bacillus
subtilis] [DB:pir2] >gp:[GI:e1182858:g2633192] [LN:BSUB0005]
[AC:Z99108:AL009126] [GN:ygaD] [FN:unknown] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 5 of 21):
from 802821 to1011250.] [NT:similar to ABC transporter (ATP-binding
protein)] [LE:136007] [RE:137776] [DI:direct] >gp:[GI:e281579:g1673392]
[LN:BSZ82044] [AC:Z82044] [PN:unidentified transporter-ATP binding]
[GN:ygaD] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis 25 kb
genomic DNA segment (from sspE to kata).] [LE:2857] [RE:4626] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000994_33237786_f3_316	2463	6235	132	43		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000994_3330167_f3_398	2464	6236	132	43		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000994_33456965_c2_592	2465	6237	138	45		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000994_33463542_c1_487	2466	6238	180	59		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000994_3361326_c2_588	2467	6239	207	68		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000994_33631292_c1_461	2468	6240	414	137	84	0.048

Description

gp:[GI:g2182758] [LN:BBU42599] [AC:U42599] [OR:Borrelia burgdorferi]
[SR:Lyme disease spirochete] [DB:genpept-bct1] [DE:Borrelia burgdorferi
plasmid cp18, OspE (ospE) gene, partial cds.] [NT:OrfE] [LE:1395] [RE:1967]
[DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000994_33631626_c1_489	2469	6241	132	43		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000994_3392952_c1_410	2470	6242	591	196	195	1.6e-15

Description

gp:[GI:e247149:g1926347] [LN:LBPHIG1E] [AC:X98106] [GN:Rorf172]
[OR:Bacteriophage phigle] [DB:genpept-phg] [DE:Lactobacillus bacteriophage
phigle complete genomic DNA.] [LE:29618] [RE:30136] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000994_34023427_c3_651	2471	6243	123	40		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000994_34164192_c3_640	2472	6244	138	45		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000994_34275325_c2_576	2473	6245	1521	506	238	5.0e-17

Description

sp:[LN:TAGH_BACSU] [AC:P42954] [GN:TAGH] [OR:BACILLUS SUBTILIS] [DE:TEICHOIC
ACID TRANSLOCATION ATP-BINDING PROTEIN TAGH] [SP:P42954] [DB:swissprot]
>pir:[LN:S69203] [AC:S69203:A69721] [PN:teichoic acid translocation
ATP-binding protein tagH] [GN:tagH] [CL:ATP-binding cassette homology]
[OR:Bacillus subtilis] [DB:pir2] >gp:[GI:g755153] [LN:BSU13832] [AC:U13832]
[PN:ATP-binding protein] [GN:tagH] [FN:teichoic acid translocation]
[OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis 168 highly
hydrophobic integral membrane protein(tagG) gene and ATP-binding protein
(tagH) gene, complete cds.] [LE:1134] [RE:2717] [DI:direct]
>gp:[GI:e1184476:g2636096] [LN:BSUB0019] [AC:Z99122:AL009126]
[PN:ATP-binding protein] [GN:tagH] [FN:teichoic acid translocation]
[OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete
genome (section 19 of 21): from 3597091to 3809700.] [SP:P42954] [LE:75534]
[RE:77117] [DI:complement] >gp:[GI:e1184476:g2636096] [LN:BSUB0019]
[AC:Z99122:AL009126] [PN:ATP-binding protein] [GN:tagH] [FN:teichoic acid
translocation] [OR:Bacillus subtilis] [DB:genpept] [DE:Bacillus subtilis
complete genome (section 19 of 21): from 3597091to 3809700.] [SP:P42954]
[LE:75534] [RE:77117] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000994_34383400_c3_618	2474	6246	582	193	78	0.010

Description

gp:[GI:g4726117] [LN:ATAC006436] [AC:AC006436] [GN:F13J11.13]
[OR:Arabidopsis thaliana] [SR:thale cress] [DB:genpept-pln2] [DE:Arabidopsis
thaliana chromosome II BAC F13J11 genomic sequence,complete sequence.]
[NT:unknown protein] [LE:50474] [RE:50725] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000994_34557262_c2_585	2475	6247	135	44		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000994_34572177_c2_513	2476	6248	735	244	147	1.5e-08

Description

pir:[LN:S42928] [AC:S42928] [PN:probable membrane-spanning protein]
[OR:Staphylococcus epidermidis] [DB:pir2] >gp:[GI:g459263] [LN:SESTPSMP]
[AC:Z30586] [PN:membrane spanning protein (putative)] [OR:Staphylococcus
epidermidis] [DB:genpept-bct1] [DE:S.epidermidis (968) genes for potential
ABC transporter andpotential membrane spanning protein.] [LE:896] [RE:1666]
[DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000994_34652177_c3_656	2477	6249	648	215	546	1.0e-52

Description

pir:[LN:E70045] [AC:E70045] [PN:two-component response regulator [YvqE]
homolog yvqC] [GN:yvqC] [CL:regulatory protein comA:response regulator
homology] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1249817:g2832821]
[LN:BS43KBDNA] [AC:AJ223978] [PN:YvqC protein] [GN:yvqC] [OR:Bacillus
subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis' 42.7kB DNA fragment from
yvsa to yvqa.] [LE:33171] [RE:33806] [DI:direct] >gp:[GI:e1184387:g2635805]
[LN:BSUB0017] [AC:Z99120:AL009126] [GN:yvqC] [FN:unknown] [OR:Bacillus
subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section
17 of 21): from 3197001to 3414420.] [NT:similar to two-component response
regulator [YvqE]] [LE:196481] [RE:197116] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000994_35428128_c3_635	2478	6250	141	46		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000994_35443785_c2_562	2479	6251	207	68		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000994_35885_f3_383	2480	6252	504	167		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000994_36119093_c3_643	2481	6253	2001	666	2102	1.3e-217

Description

pir:[LN:F69794] [AC:F69794] [PN:DNA ligase (NAD+),] [GN:yerG]
[CL:polydeoxyribonucleotide synthase (NAD+)] [OR:Bacillus subtilis]
[EC:6.5.1.2] [DB:pir1] >gp:[GI:e1182642:g2632976] [LN:BSUB0004]
[AC:Z99107:AL009126] [GN:yerG] [FN:unknown] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 4 of 21):
from 600701 to813890.] [NT:similar to DNA ligase] [LE:120419] [RE:122425]
[DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000994_36195250_f3_359	2482	6254	822	273	375	1.4e-34

Description

sp:[LN:PHEA_METJA] [AC:Q58054] [GN:PHEA:MJ0637] [OR:METHANOCOCCUS
JANNASCHII] [EC:4.2.1.51] [DE:PROBABLE PREPHENATE DEHYDRATASE, (PDT)]
[SP:Q58054] [DB:swissprot] >pir:[LN:E64379] [AC:E64379] [PN:prephenate
dehydratase,] [CL:prephenate dehydratase:prephenate dehydratase homology]
[OR:Methanococcus jannaschii] [EC:4.2.1.51] [DB:pir2] [MP:REV567914-567096]
>gp:[GI:g1591349] [LN:U67511] [AC:U67511:L77117] [PN:chorismate
mutase/prephenate dehydratase (pheA)] [GN:MJ0637] [OR:Methanococcus
jannaschii] [DB:genpept-bct2] [DE:Methanococcus jannaschii section 53 of 150
of the complete genome.] [NT:similar to SP:P43909 PID:683585 percent
identity:] [LE:7667] [RE:8485] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000994_36219692_c3_648	2483	6255	561	186	133	2.0e-08

Description

pir:[LN:A36886] [AC:A36886] [PN:surface protein PAg negative regulator par]
[GN:par] [OR:Streptococcus sobrinus] [DB:pir2] >gp:[GI:d1003084:g425488]
[LN:STRREPRES] [AC:D13323] [PN:repressor protein] [GN:par]
[OR:Streptococcus sobrinus] [SR:Streptococcus sobrinus (strain MT3791) DNA,
clone pPG11] [DB:genpept-bct1] [DE:Streptococcus sobrinus gene for repressor
protein of surfaceprotein antigen gene (pag), complete cds.] [NT:This ORF2
starts at the GTG codon (position 1162)] [LE:1162] [RE:1773] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000994_36220000_c2_525	2484	6256	1047	348	557	7.0e-54

Description

pir:[LN:D69856] [AC:D69856] [PN:conserved hypothetical protein ykgB]
[GN:ykgB] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1181502:g2632022]
[LN:BSAJ2571] [AC:AJ002571] [PN:YkgB] [GN:ykgB] [FN:unknown] [OR:Bacillus
subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis 168 56 kb DNA fragment
between xlyA and ykoR.] [LE:22000] [RE:23049] [DI:complement]
>gp:[GI:e1183321:g2633655] [LN:BSUB0007] [AC:Z99110:AL009126] [GN:ykgB]
[FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
complete genome (section 7 of 21): from 1194391to 1411140.] [NT:similar to
hypothetical proteins] [LE:174949] [RE:175998] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000994_36221013_f2_135	2485	6257	171	56		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000994_36336012_c3_664	2486	6258	165	54		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000994_36367302_c3_600	2487	6259	564	187	122	2.7e-06

Description

sp:[LN:Y359_METJA] [AC:Q57805] [GN:MJ0359] [OR:METHANOCOCCUS JANNASCHII]
[DE:HYPOTHETICAL PROTEIN MJ0359] [SP:Q57805] [DB:swissprot] >pir:[LN:G64344]
[AC:G64344] [PN:hypothetical protein MJ0359] [OR:Methanococcus jannaschii]
[DB:pir2] [MP:REV327449-326805] >gp:[GI:g1591068] [LN:U67489]
[AC:U67489:L77117] [PN:M. jannaschii predicted coding region MJ0359]
[GN:MJ0359] [OR:Methanococcus jannaschii] [DB:genpept-bct2]
[DE:Methanococcus jannaschii section 31 of 150 of the complete genome.]
[NT:hypothetical protein; identified by GeneMark;] [LE:2497] [RE:3141]
[DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000994_36457341_c2_593	2488	6260	135	44	81	0.019

Description

pir:[LN:S75730] [AC:S75730:S50064] [PN:8-amino-7-oxononanoate
synthase, :7-keto-8-aminopelargonic acid synthetase:protein
slr0917:7-keto-8-aminopelargonic acid synthetase:protein slr0917] [GN:bioF]
[CL:5-aminolevulinate synthase] [OR:Synechocystis sp.] [SR:PCC 6803, , PCC
6803] [SR:PCC 6803,] [EC:2.3.1.47] [DB:pir2] >gp:[GI:d1011116:g1673311]
[LN:SYCSLLE] [AC:D64003:AB001339] [PN:7-keto-8-aminopelargonic acid
synthetase] [GN:bioF] [OR:Synechocystis sp.] [SR:Synechocystis sp.
(strain:PCC6803) DNA] [DB:genpept-bct1] [DE:Synechocystis sp. PCC6803
complete genome, 22/27, 2755703-2868766.] [NT:ORF_ID:slr0917] [LE:35986]
[RE:37299] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000994_36522175_f1_69	2489	6261	1557	518	2240	3.2e-232

Description

gp:[GI:g2565311] [LN:AF024571] [AC:AF024571] [PN:high affinity proline
permease] [GN:putP] [OR:Staphylococcus aureus] [DB:genpept-bct2]
[DE:Staphylococcus aureus high affinity proline permease (putP)
gene,complete cds.] [LE:339] [RE:1832] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000994_39077_f2_270	2490	6262	717	238	1223	1.9e-124

Description

gp:[GI:g2981294] [LN:AF012132] [AC:AF012132] [PN:response regulator]
[GN:agrA] [OR:Staphylococcus epidermidis] [DB:genpept-bct2]
[DE:Staphylococcus epidermidis agr system including response
regulator(agrA), histidine kinase (agrC), AgrD (agrD), AgrB (agrB) and
deltatoxin (hld) genes, complete cds.] [NT:AgrA; similar to S. aureus and S.
lugdunensis AgrA] [LE:242] [RE:958] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000994_3939013_c2_573	2491	6263	210	69	109	2.1e-06

Description

pir:[LN:C69807] [AC:C69807] [PN:hypothetical protein yfjT] [GN:yfjT]
[OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1182787:g2633121] [LN:BSUB0005]
[AC:Z99108:AL009126] [GN:yfjT] [FN:unknown] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 5 of 21):
from 802821 to1011250.] [LE:65959] [RE:66144] [DI:direct]
>gp:[GI:d1024269:g2626812] [LN:D83967] [AC:D83967] [PN:YfjT] [OR:Bacillus
subtilis] [SR:Bacillus subtilis (strain:AC327) DNA] [DB:genpept-bct1]
[DE:Bacillus subtilis genomic DNA, 74 degree region.] [LE:1777] [RE:1962]
[DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000994_3942015_c1_471	2492	6264	528	175	790	1.4e-78

Description

sp:[LN:YLY1_STAAU] [AC:Q53719] [OR:STAPHYLOCOCCUS AUREUS] [DE:HYPOTHETICAL
18.6 KD PROTEIN IN LYTA 3'REGION (ORF1)] [SP:Q53719] [DB:swissprot]
>gp:[GI:g310602] [LN:STAORFPHI] [AC:L19300] [OR:Staphylococcus aureus]
[SR:Staphylococcus aureus (library: NCTC 8325) DNA] [DB:genpept-bct1]
[DE:Staphylococcus aureus DNA sequence encoding three ORFs, completecds;
prophage phi-11 sequence homology, 5' flank.] [LE:1798] [RE:2313]
[DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000994_4021888_c3_615	2493	6265	669	222	83	0.0039

Description

pir:[LN:D71114] [AC:D71114] [PN:hypothetical protein PH0683] [GN:PH0683]
 [OR:Pyrococcus horikoshii] [DB:pir2] >gp:[GI:d1030717:g3257091]
 [LN:AP000003]
 [AC:AP000003:AB009484:AB009485:AB009486:AB009487:AB009488:AB009489]
 [PN:107aa long hypothetical protein] [GN:PH0683] [OR:Pyrococcus horikoshii]
 [SR:Pyrococcus horikoshii (strain:OT3) DNA] [DB:genpept-bct1] [DE:Pyrococcus
 horikoshii OT3 genomic DNA, 544001-777000 nt. position(3/7).] [LE:63024]
 [RE:63347] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000994_4062500_c2_507	2494	6266	1401	466	502	3.3e-47

Description

gp:[GI:e1314011:g3393011] [LN:SAA224764] [AC:AJ224764] [PN:Clumping factor
 B] [GN:clfB] [FN:binds fibrinogen] [OR:Staphylococcus aureus]
 [DB:genpept-bct1] [DE:Staphylococcus aureus strain Newman clumping factor B
 (clfB) gene.] [LE:28] [RE:2769] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000994_4072936_c1_453	2495	6267	153	50		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000994_4093753_f3_387	2496	6268	126	41		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000994_4095277_c3_627	2497	6269	1827	608	2760	2.5e-287

Description

pir:[LN:S11783] [AC:S11783:S27371:S34445] [PN:bla regulator protein blaR1:probable beta-lactam receptor signal transducer protein] [GN:blaR1] [CL:mecR1 protein:beta-lactamase OXA2 homology] [OR:Staphylococcus aureus] [DB:pir2] >gp:[GI:g152966] [LN:STABLA] [AC:M62650] [GN:blaR1] [FN:putative beta-lactam receptor-signal] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus DNA] [DB:genpept-bct1] [DE:Staphylococcus aureus blaZ gene, 5' end; blaR1 gene, complete cds;blaI gene, complete cds; and binR gene, 5' end.] [LE:156] [RE:1913] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000994_409556_f1_10	2498	6270	135	44	112	2.5e-06

Description

pir:[LN:D71245] [AC:D71245] [PN:hypothetical protein PH0221] [GN:PH0221] [OR:Pyrococcus horikoshii] [DB:pir2] >gp:[GI:d1030234:g3256608] [LN:AP0000001] [AC:AP0000001:AB009465:AB009464:AB009466:AB009467:AB009468:AB009469] [PN:235aa long hypothetical protein] [GN:PH0221] [OR:Pyrococcus horikoshii] [SR:Pyrococcus horikoshii (strain:OT3) DNA] [DB:genpept-bct1] [DE:Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt. position (1/7).] [LE:194212] [RE:194919] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000994_4101517_f1_100	2499	6271	1068	355		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000994_4179637_c3_622	2500	6272	387	128	207	8.6e-17

Description

sp:[LN:TRAC_STAAU] [AC:P06698] [GN:TNPC] [OR:STAPHYLOCOCCUS AUREUS]
[DE:TRANSPOSASE FOR TRANSPOSON TN554] [SP:P06698] [DB:swissprot]
>pir:[LN:C24584] [AC:C24584] [PN:transposition regulatory protein tnpC]
[GN:tnpC] [CL:transposition regulatory protein tnpC] [OR:Staphylococcus
aureus] [DB:pir2] >gp:[GI:g43729] [LN:ISTN554] [AC:X03216:K02987] [PN:pot.
tnpC protein] [OR:Staphylococcus aureus] [DB:genpept-bct1]
[DE:Staphylococcus aureus transposon Tn554.] [NT:(aa 1-125)] [SP:P06698]
[LE:3115] [RE:3492] [DI:direct] >gp:[GI:d1046009:g5360833] [LN:D86934]
[AC:D86934] [PN:transposaseC] [GN:tnpC] [OR:Staphylococcus aureus]
[SR:Staphylococcus aureus (strain:N315) DNA, clone_lib:library of N31]
[DB:genpept] [DE:Staphylococcus aureus genes, mec region, partial and
complete cds.] [NT:ORF N047] [LE:32364] [RE:32741] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000994_430325_ci_456	2501	6273	1383	460	649	1.3e-63

Description

gp:[GI:g3820539] [LN:AF080002] [AC:AF080002] [PN:UDP-N-acetylmuramyl
tripeptide synthetase MurC] [GN:murC] [OR:Heliobacillus mobilis]
[DB:genpept-bct2] [DE:Heliobacillus mobilis exopolyphosphatase Ppx (ppx)
gene, partialcds; cobyric acid synthase CobQ (cobQ),
UDP-N-acetylmuramyltripeptide synthetase MurC (murC), glutamyl tRNA
reductase HemA(hemA), photosynthesis gene cluster, complete sequence, stage
II sporulation protein E Sp2E (sp2E), cell cycle protein MesJ (mesJ), and
ATP-dependent zinc metalloproteinase FtsH (ftsH) genes, completecds; and
nucleoside diphosphate kinase B NdkB (ndkB) gene, partialcds.] [LE:2000]
[RE:3367] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000994_4329635_f2_164	2502	6274	126	41		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000994_4689130_f2_272	2503	6275	306	101	81	0.029

Description

pir:[LN:A58932] [AC:A58932] [PN:cytochrome C-type biogenesis protein CCMF] [GN:yejR:ccmF] [OR:mitochondrion Cyanidioschyzon merolae] [DB:pir2]
>gp:[GI:d1037513:g4115789] [LN:D89861] [AC:D89861] [PN:cytochrome C-type biogenesis protein CCMF] [GN:yejR or ccmF] [OR:Mitochondrion Cyanidioschyzon merolae] [SR:Cyanidioschyzon merolae (strain:10D) mitochondrion DNA] [DB:genpept-pln1] [DE:Cyanidioschyzon merolae mitochondrial DNA, complete sequence.] [LE:16296] [RE:18158] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000994_4722265_c1_472	2504	6276	858	285	416	6.1e-39

Description

pir:[LN:H69800] [AC:H69800] [PN:hypothetical protein yfhG] [GN:yfhG] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1182842:g2633176] [LN:BSUB0005] [AC:Z99108:AL009126] [GN:yfhG] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.] [LE:122320] [RE:123114] [DI:direct]
>gp:[GI:d1025389:g2804537] [LN:D85082] [AC:D85082] [PN:YfhG] [OR:Bacillus subtilis] [SR:Bacillus subtilis DNA] [DB:genpept-bct1] [DE:Bacillus subtilis DNA, genome sequence, 79 to 81 degree region.] [LE:15211] [RE:16005] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000994_4726566_f2_189	2505	6277	582	193	187	3.8e-13

Description

gp:[GI:g4981093] [LN:AE001732] [AC:AE001732:AE000512] [PN:DNA polymerase III, alpha subunit] [GN:TM0576] [OR:Thermotoga maritima] [DB:genpept-bct2] [DE:Thermotoga maritima section 44 of 136 of the complete genome.] [NT:similar to GB:M22996 SP:P13267 GB:M33543 GB:S55653] [LE:5720] [RE:9823] [DI:direct] >gp:[GI:g3930535] [LN:AF065313] [AC:AF065313] [PN:DNA polymerase III] [GN:polC] [OR:Thermotoga maritima] [DB:genpept-bct2] [DE:Thermotoga maritima DNA polymerase III (polC) gene, complete cds.] [NT:family C DNA polymerase] [LE:235] [RE:4338] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000994_4728377_f2_171	2506	6278	1146	381	544	1.7e-52

Description

pir:[LN:F69807] [AC:F69807] [PN:hypothetical protein yfkB] [GN:yfkB]
 [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1182785:g2633119] [LN:BSUB0005]
 [AC:Z99108:AL009126] [GN:yfkB] [FN:unknown] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 5 of 21):
 from 802821 to1011250.] [LE:64694] [RE:65155] [DI:complement]
 >gp:[GI:d1024271:g2626814] [LN:D83967] [AC:D83967] [PN:YfkB] [OR:Bacillus
 subtilis] [SR:Bacillus subtilis (strain:AC327) DNA] [DB:genpept-bct1]
 [DE:Bacillus subtilis genomic DNA, 74 degree region.] [LE:2766] [RE:3227]
 [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000994_4876387_f3_376	2507	6279	180	59		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000994_4881313_c1_475	2508	6280	159	52		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000994_4900443_c1_449	2509	6281	1440	479	2460	1.5e-255

Description

sp:[LN:YZDD_BACSU] [AC:Q45486] [GN:YZDD] [OR:BACILLUS SUBTILIS]
 [DE:PET112-LIKE PROTEIN] [SP:Q45486] [DB:swissprot] >gp:[GI:g1354211]
 [LN:BSU49790] [AC:U49790] [PN:PET112-like protein] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:Bacillus subtilis PET112-like protein gene, complete
 cds.] [LE:433] [RE:1860] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000994_5133500_f1_48	2510	6282	480	159	358	8.6e-33

Description

pir:[LN:E69808] [AC:E69808] [PN:protein-tyrosine phosphatase homolog yfkJ] [GN:yfkJ] [CL:protein-tyrosine-phosphatase, low molecular weight] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1182778:g2633112] [LN:BSUB0005] [AC:Z99108:AL009126] [GN:yfkJ] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.] [NT:similar to protein-tyrosine phosphatase] [LE:58691] [RE:59161] [DI:direct] >gp:[GI:d1024279:g2626822] [LN:D83967] [AC:D83967] [PN:YfkJ] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:AC327) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis genomic DNA, 74 degree region.] [LE:8760] [RE:9230] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000994_5167268_c3_649	2511	6283	1080	359	613	8.2e-60

Description

sp:[LN:DINP_ECOLI] [AC:Q47155:Q47683] [GN:DINP] [OR:ESCHERICHIA COLI] [DE:DNA-DAMAGE-INDUCIBLE PROTEIN P] [SP:Q47155:Q47683] [DB:swissprot] >pir:[LN:H64747] [AC:H64747] [PN:DNA-damage-inducible protein dinP] [GN:dinP] [CL:umuC protein] [OR:Escherichia coli] [DB:pir2] >gp:[GI:d1008174:g984587] [LN:ECODINJ] [AC:D38582] [PN:DinP] [OR:Escherichia coli] [SR:Escherichia coli (sub_strain W3110, strain K-12) (library: Kohara')] [DB:genpept-bct1] [DE:Escherichia coli genes for 'YafH, YafI, YafJ, YafK, YafQ, DinJ, YafL, YafM, FhiA, MbhA, DinP, YafN, YafO and YafP.] [NT:hypothetical; similarity to YLW6_CAEEL (P34409),] [LE:8540] [RE:9595] [DI:direct] >gp:[GI:d1041669:g4902967] [LN:ECOTSF] [AC:D83536] [PN:DNA-damage-inducible protein p.] [GN:dinP] [OR:Escherichia coli] [SR:Escherichia coli (strain:K12) DNA] [DB:genpept-bct1] [DE:Escherichia coli genomic DNA. (4.1 - 6.1 min).] [NT:ORF_ID:o127#9; similar to PIR Accession Number] [LE:60446] [RE:61501] [DI:direct] >gp:[GI:g1552799] [LN:ECU70214] [AC:U70214] [PN:DinP] [GN:dinP] [OR:Escherichia coli] [DB:genpept-bct1] [DE:Escherichia coli chromosome minutes 4-6.] [LE:81973] [RE:83028] [DI:direct] >gp:[GI:g1786425] [LN:AE000131] [AC:AE000131:U00096] [PN:damage-inducible protein P; putative tRNA] [GN:dinP] [FN:putative enzyme; Not classified] [OR:Escherichia coli] [DB:genpept-bct2] [DE:Escherichia coli K-12 MG1655 section 21 of 400 of the completegenome.] [NT:o351; 100 pct identical to GB: ECODINJ_11] [LE:7487] [RE:8542] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000994_5269400_f3_291	2512	6284	138	45		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000994_570327_c1_424	2513	6285	171	56	52	0.026

Description

pir:[LN:S68156] [AC:S68156] [PN:NADH dehydrogenase (ubiquinone), chain 3] [GN:ND3] [CL:NADH dehydrogenase (ubiquinone) chain 3] [OR:mitochondrion Dictyostelium discoideum] [EC:1.6.5.3] [DB:pir2] >gp:[GI:d1041830:g4958885] [LN:AB000109] [AC:AB000109] [PN:NADH dehydrogenase subunit 3] [GN:nad3] [OR:Mitochondrion Dictyostelium discoideum] [SR:Dictyostelium discoideum (strain:AX3, partially X22 (48172-5151] [DB:genpept-inv1] [EC:1.6.5.3] [DE:Dictyostelium discoideum mitochondrial DNA, complete sequence.] [LE:24783] [RE:25145] [DI:direct] >gp:[GI:d1004450:g699592] [LN:DDID16466] [AC:D16466] [PN:NADH dehydrogenase subunit 3] [GN:nad3] [OR:Mitochondrion Dictyostelium discoideum] [SR:Dictyostelium discoideum (strain:AX3) mitochondrion DNA] [DB:genpept-inv1] [EC:1.6.5.3] [DE:Dictyostelium discoideum mitochondrial DNA.] [LE:7866] [RE:8228] [DI:direct] >gp:[GI:d1004450:g699592] [LN:DDID16466] [AC:D16466] [PN:NADH dehydrogenase subunit 3] [GN:nad3] [OR:Mitochondrion Dictyostelium discoideum] [SR:Dictyostelium discoideum (strain:AX3) mitochondrion DNA] [DB:genpept] [EC:1.6.5.3] [DE:Dictyostelium discoideum mitochondrial DNA.] [LE:7866] [RE:8228] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000994_5860052_f3_388	2514	6286	435	144	107	3.4e-06

Description

pir:[LN:H71190] [AC:H71190] [PN:hypothetical protein PH1800] [GN:PH1800] [OR:Pyrococcus horikoshii] [DB:pir2] >gp:[GI:d1031862:g3258236] [LN:AP000007] [AC:AP000007:AB009464:AB009465:AB009521:AB009522:AB009523:AB009524] [PN:133aa long hypothetical protein] [GN:PH1800] [OR:Pyrococcus horikoshii] [SR:Pyrococcus horikoshii (strain:OT3) DNA] [DB:genpept-bct1] [DE:Pyrococcus horikoshii OT3 genomic DNA, 1485001-1738505 nt. position(7/7).] [LE:80658] [RE:81059] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000994_5913882_f2_167	2515	6287	123	40		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000994_6053308_c2_538	2516	6288	903	300	815	3.2e-81

Description

sp:[LN:NADE_ECOLI] [AC:P18843:P78235] [GN:NADE:EFG:NTRL] [OR:ESCHERICHIA COLI] [EC:6.3.5.1] [DE:PROTEIN] [SP:P18843:P78235] [DB:swissprot]
 >pir:[LN:D64933] [AC:D64933:A26928] [PN:NAD+ synthase
 (glutamine-hydrolyzing), :nitrogen-regulatory protein] [GN:nadE] [CL:spore
 outgrowth factor B] [OR:Escherichia coli] [EC:6.3.5.1] [DB:pir2] [MP:34-39
 min] >gp:[GI:d1016252:g1742846] [LN:D90817] [AC:D90817:AB001340]
 [PN:NH(3)-dependent NAD(+) synthetase (EC 6.3.5.1)] [GN:nadE, efg, ntrL_
 [OR:Escherichia coli] [SR:Escherichia coli (strain:K12) DNA,
 clone_lib:Kohara lambda minise] [DB:genpept-bct1] [DE:E.coli genomic DNA,
 Kohara clone #326(39.1-39.4 min.)] [NT:ORF_ID:o326#9; similar to [SwissProt
 Accession] [LE:7818] [RE:8645] [DI:direct] >gp:[GI:d1016258:g1742853]
 [LN:D90818] [AC:D90818:AB001340] [PN:NH(3)-dependent NAD(+) synthetase (EC
 6.3.5.1)] [GN:nadE, efg, ntrL_
 [OR:Escherichia coli] [SR:Escherichia coli
 (strain:K12) DNA, clone_lib:Kohara lambda minise] [DB:genpept-bct1]
 [DE:E.coli genomic DNA, Kohara clone #327(39.2-39.5 min.)]
 [NT:ORF_ID:o326#9; similar to [SwissProt Accession] [LE:2186] [RE:3013]
 [DI:direct] >gp:[GI:g1788036] [LN:AE000269] [AC:AE000269:U00096] [PN:NAD
 synthetase, prefers NH3 over glutamine] [GN:nadE] [FN:enzyme; Biosynthesis
 of cofactors, carriers:] [OR:Escherichia coli] [DB:genpept-bct2]
 [EC:6.3.5.1] [DE:Escherichia coli K-12 MG1655 section 159 of 400 of the
 completegenome.] [NT:o275; residues 32-274 are 100 pct identical to]
 [LE:1232] [RE:2059] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000994_6147252_c1_473	2517	6289	846	281	150	1.6e-08

Description

sp:[LN:TAGG_BACSU] [AC:P42953] [GN:TAGG] [OR:BACILLUS SUBTILIS] [DE:TEICHOIC
 ACID TRANSLOCATION PERMEASE PROTEIN TAGG] [SP:P42953] [DB:swissprot]
 >pir:[LN:S69202] [AC:S69202:H69720] [PN:teichoic acid permease
 tagG:integral membrane protein tagG] [GN:tagG] [OR:Bacillus subtilis]
 [DB:pir2] >gp:[GI:g755152] [LN:BSU13832] [AC:U13832] [PN:highly hydrophobic
 integral membrane protein] [GN:tagG] [FN:teichoic acid translocation]
 [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis 168 highly
 hydrophobic integral membrane protein(tagG) gene and ATP-binding protein
 (tagH) gene, complete cds.] [LE:287] [RE:1114] [DI:direct]
 >gp:[GI:e1184477:g2636097] [LN:BSUB0019] [AC:Z99122:AL009126] [PN:permease]
 [GN:tagG] [FN:teichoic acid translocation] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 19 of 21):
 from 3597091to 3809700.] [SP:P42953] [LE:77137] [RE:77964] [DI:complement]
 >gp:[GI:e1184477:g2636097] [LN:BSUB0019] [AC:Z99122:AL009126] [PN:permease]
 [GN:tagG] [FN:teichoic acid translocation] [OR:Bacillus subtilis]
 [DB:genpept] [DE:Bacillus subtilis complete genome (section 19 of 21): from
 3597091to 3809700.] [SP:P42953] [LE:77137] [RE:77964] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000994_632661_c2_560	2518	6290	777	258	490	8.8e-47

Description

gp:[GI:g3820538] [LN:AF080002] [AC:AF080002] [PN:cobyric acid synthase CobQ] [GN:cobQ] [OR:Heliobacillus mobilis] [DB:genpept-bct2] [DE:Heliobacillus mobilis exopolyphosphatase Ppx (ppx) gene, partialcds; cobyric acid synthase CobQ (cobQ), UDP-N-acetylmuramyltripeptide synthetase MurC (murC), glutamyl tRNA reductase Hema(hemA), photosynthesis gene cluster, complete sequence, stage II sporulation protein E Sp2E (sp2E), cell cycle protein MesJ (mesJ), and ATP-dependent zinc metalloproteinase FtsH (ftsH) genes, completecds; and nucleoside diphosphate kinase B NdkB (ndkB) gene, partialcds.] [LE:1238] [RE:1996] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000994_6682627_c3_604	2519	6291	357	118	123	6.9e-08

Description

gp:[GI:g624123] [LN:PBU42580] [AC:U42580:U17055:U32570] [GN:a58L] [OR:Paramecium bursaria Chlorella virus 1] [DB:genpept-vrl] [DE:Paramecium bursaria Chlorella virus 1, complete genome.] [NT:contains Glu-, Gln-rich regions: QVQVV (11X), KEVWE] [LE:31140] [RE:31628] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000994_6829687_c2_512	2520	6292	618	205	355	1.8e-32

Description

pir:[LN:S42925] [AC:S42925] [PN:probable transport protein] [CL:ATP-binding cassette homology] [OR:Staphylococcus aureus] [DB:pir2] >gp:[GI:g459256] [LN:SASTPSMP] [AC:Z30588] [PN:Potential ABC transporter] [GN:stpC] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:S.aureus (RN4220) genes for potential ABC transporter and potentialmembrane spanning protein.] [LE:199] [RE:894] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000994_6931261_c1_409	2521	6293	537	178	128	2.0e-08

Description

gp:[GI:g2689551] [LN:U93688] [AC:U93688] [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus toxic shock syndrome toxin-1 (tst), enterotoxin (ent), and integrase (int) genes, complete cds.] [NT:orf4] [LE:3868] [RE:4395] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000994_7164087_c2_575	2522	6294	333	110	217	7.5e-18

Description

pir:[LN:A69801] [AC:A69801] [PN:hypothetical protein yfhH] [GN:yfhH]
 [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1182843:g2633177] [LN:BSUB0005]
 [AC:Z99108:AL009126] [GN:yfhH] [FN:unknown] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 5 of 21):
 from 802821 to1011250.] [LE:123116] [RE:123430] [DI:direct]
 >gp:[GI:d1025390:g2804538] [LN:D85082] [AC:D85082] [PN:YfhH] [OR:Bacillus
 subtilis] [SR:Bacillus subtilis DNA] [DB:genpept-bct1] [DE:Bacillus subtilis
 DNA, genome sequence, 79 to 81 degree region.] [LE:16007] [RE:16321]
 [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000994_7207518_f2_267	2523	6295	375	124	151	7.4e-11

Description

pir:[LN:B27059] [AC:B27059] [PN:hypothetical protein 2] [OR:Glycine max]
 [SR:, soybean] [DB:pir2]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000994_789010_c3_620	2524	6296	132	43		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000994_799188_f1_118	2525	6297	468	155	252	9.8e-20

Description

gp:[GI:g3929312] [LN:AF100426] [AC:AF100426] [PN:fimbriae-associated protein
 Fap1] [GN:fap1] [OR:Streptococcus parasanguinis] [DB:genpept-bct2]
 [DE:Streptococcus parasanguis fimbriae-associated protein Fap1 (fap1)gene,
 complete cds.] [NT:invovled in fimbriae assembly and fimbriae-mediated]
 [LE:284] [RE:7996] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000994_815903_c1_423	2526	6298	141	46		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000994_820325_f2_156	2527	6299	948	315	1131	1.1e-114

Description

sp:[LN:GSAB_BACSU] [AC:P71084] [GN:GSAB] [OR:BACILLUS SUBTILIS] [EC:5.4.3.8]
 [DE:(GLUTAMATE-1-SEMIALDEHYDE AMINOTRANSFERASE) (GSA-AT)] [SP:P71084]
 [DB:swissprot] >gp:[GI:e281581:g1673394] [LN:BSZ82044] [AC:Z82044]
 [PN:glutamate-1-semialdehyde aminotransferase] [GN:gsaB] [OR:Bacillus
 subtilis] [DB:genpept-bct1] [DE:B.subtilis 25 kb genomic DNA segment (from
 sspE to katA).] [SP:P71084] [LE:5984] [RE:7273] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000994_860677_f1_3	2528	6300	177	58	72	0.017

Description

gp:[GI:g3845668] [LN:AF021254] [AC:AF021254] [PN:unknown] [GN:RTL5]
 [OR:avian adenovirus type 8] [DB:genpept-vrl] [DE:Avian adenovirus type 8
 strain ATCC A-2A 100 K protein homologgene, partial cds; RTL10, RTR1, late
 33 K protein homolog, pVIIIfhomolog, RTL9, RTR2, fibre homolog, RTL8, RTL7,
 RTL6, RTL5, andRTR3 genes, complete cds; and RTL4 gene, partial cds.]
 [LE:8905] [RE:9216] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000994_885756_c3_662	2529	6301	180	59		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000994_979712_c1_430	2530	6302	1422	473	111	0.023

Description

pir:[LN:C71610] [AC:C71610] [PN:probable membrane associated protein
 PFB0615c] [GN:PFB0615c] [OR:Plasmodium falciparum] [DB:pir2]
 >gp:[GI:g3845231] [LN:AE001406] [AC:AE001406:AE001362] [PN:predicted
 membrane associated protein] [GN:PFB0615c] [OR:Plasmodium falciparum]
 [SR:malaria parasite P. falciparum] [DB:genpept-inv2] [DE:Plasmodium
 falciparum chromosome 2, section 43 of 73 of thecomplete sequence.]
 [NT:predicted by GlimmerM] [LE:1921:2496:6961] [RE:2310:6749:8358]
 [DI:complementJoin]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000994_985678_c3_646	2531	6303	975	324	889	4.6e-89

Description

pir:[LN:F69795] [AC:F69795] [PN:conserved hypothetical protein yerQ]
 [GN:yerQ] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1182652:g2632986]
 [LN:BSUB0004] [AC:Z99107:AL009126] [GN:yerQ] [FN:unknown] [OR:Bacillus
 subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 4
 of 21): from 600701 to813890.] [NT:similar to hypothetical proteins]
 [LE:135242] [RE:136153] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000994_9859433_c2_561	2532	6304	126	41		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000995_10580443_c1_140	2533	6305	237	78	246	6.4e-21

Description

sp:[LN:YEED_ECOLI] [AC:P33014] [GN:YEED] [OR:ESCHERICHIA COLI]
 [DE:HYPOTHETICAL 8.1 KD PROTEIN IN SBCB-HISL INTERGENIC REGION] [SP:P33014]
 [DB:swissprot] >pir:[LN:C64966] [AC:C64966] [PN:yeeD protein] [GN:yeeD]
 [CL:conserved hypothetical protein HI0721] [OR:Escherichia coli] [DB:pir2]
 >gp:[GI:d1016564:g1736686] [LN:D90839] [AC:D90839:AB001340] [GN:yeeD]
 [OR:Escherichia coli] [SR:Escherichia coli (strain:K12) DNA,
 clone_lib:Kohara lambda minise] [DB:genpept-bct1] [DE:E.coli genomic DNA,
 Kohara clone #349(44.6-45.0 min.)] [NT:ORF_ID:o349#3; similar to [SwissProt
 Accession] [LE:12878] [RE:13105] [DI:complement] >gp:[GI:d1016569:g1736692]
 [LN:D90840] [AC:D90840:AB001340] [GN:yeeD] [OR:Escherichia coli]
 [SR:Escherichia coli (strain:K12) DNA, clone_lib:Kohara lambda minise]
 [DB:genpept-bct1] [DE:E.coli genomic DNA, Kohara clone #350(44.9-45.2
 min.)] [NT:ORF_ID:o349#3; similar to [SwissProt Accession] [LE:1569]
 [RE:1796] [DI:complement] >gp:[GI:g405955] [LN:ECOHU43] [AC:U00009]
 [PN:yeeD] [OR:Escherichia coli] [SR:Escherichia coli K12 BHB2600]
 [DB:genpept-bct1] [DE:sbcB region of E.coli K12 BHB2600.] [NT:similar to ORF
 in fliE-amyA intergenic region] [LE:4083] [RE:4310] [DI:complement]
 >gp:[GI:g1788322] [LN:AE000292] [AC:AE000292:U00096] [PN:orf, hypothetical
 protein] [GN:yeeD] [FN:orf; Unknown] [OR:Escherichia coli] [DB:genpept-bct2]
 [DE:Escherichia coli K-12 MG1655 section 182 of 400 of the completegenome.]
 [NT:f75; 100 pct identical to YEED_ECOLI SW: P33014] [LE:9541] [RE:9768]
 [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000995_12142768_f1_32	2534	6306	300	99	110	4.2e-06

Description

pir:[LN:D71245] [AC:D71245] [PN:hypothetical protein PH0221] [GN:PH0221]
 [OR:Pyrococcus horikoshii] [DB:pir2] >gp:[GI:d1030234:g3256608]
 [LN:AP000001]
 [AC:AP000001:AB009465:AB009464:AB009466:AB009467:AB009468:AB009469]
 [PN:235aa long hypothetical protein] [GN:PH0221] [OR:Pyrococcus horikoshii]
 [SR:Pyrococcus horikoshii (strain:OT3) DNA] [DB:genpept-bct1] [DE:Pyrococcus
 horikoshii OT3 genomic DNA, 1-287000 nt. position (1/7).] [LE:194212]
 [RE:194919] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000995_13907566_c1_148	2535	6307	144	47		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000995_14493812_c1_131	2536	6308	465	154	289	1.8e-25

Description

pir:[LN:C69786] [AC:C69786] [PN:conserved hypothetical protein ydiB]
 [GN:ydiB] [CL:hypothetical protein HI0065] [OR:Bacillus subtilis] [DB:pir2]
 >gp:[GI:e1182570:g2632904] [LN:BSUB0004] [AC:Z99107:AL009126] [GN:ydiB]
 [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
 complete genome (section 4 of 21): from 600701 to813890.] [NT:similar to
 hypothetical proteins] [LE:40670] [RE:41146] [DI:direct]
 >gp:[GI:d1020494:g1945107] [LN:D88802] [AC:D88802] [GN:ydiB] [OR:Bacillus
 subtilis] [SR:Bacillus subtilis (sub_species:Marburg, strain:168,
 isolate:JH642] [DB:genpept-bct1] [DE:Bacillus subtilis DNA for
 phoB-rrnE-groESL region, complete cds.] [NT:E. coli hypothetical protein;
 P31805 (267)] [LE:27672] [RE:28148] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000995_1461637_f2_60	2537	6309	249	82	123	6.9e-08

Description

sp:[LN:ILVN_BACSU] [AC:P37252] [GN:ILVN] [OR:BACILLUS SUBTILIS]
 [EC:4.1.3.18] [DE:(ACETOHYDROXY-ACID SYNTHASE SMALL SUBUNIT) (ALS)]
 [SP:P37252] [DB:swissprot] >pir:[LN:E69644] [AC:E69644] [PN:acetolactate
 synthase (small subunit) ilvN] [GN:ilvN] [CL:acetolactate synthase small
 chain] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:g143092] [LN:BACILNB]
 [AC:L03181] [PN:acetolactate synthase small subunit] [GN:ilvN] [OR:Bacillus
 subtilis] [SR:Bacillus subtilis DNA] [DB:genpept-bct1] [DE:Bacillus subtilis
 ilvB, ilvN and ilvC genes, complete ilv-leuoperon.] [LE:2438] [RE:2962]
 [DI:direct] >gp:[GI:e1184079:g2635295] [LN:BSUB0015] [AC:Z99118:AL009126]
 [PN:acetolactate synthase (acetohydroxy-acid) [GN:ilvN]
 [FN:valine/isoleucine biosynthesis] [OR:Bacillus subtilis] [DB:genpept-bct1]
 [EC:4.1.3.18] [DE:Bacillus subtilis complete genome (section 15 of 21): from
 2795131to 3013540.] [SP:P37252] [LE:98696] [RE:99220] [DI:complement]
 >gp:[GI:e1165365:g1770067] [LN:BSZ75208] [AC:Z75208] [PN:acetolactate
 synthase small subunit] [GN:ilvN] [OR:Bacillus subtilis] [DB:genpept-bct1]
 [EC:4.1.3.18] [DE:B.subtilis genomic sequence 89009bp.] [NT:acetolactate
 synthase (acetohydroxy-acid synthase)] [SP:P37252] [LE:70687] [RE:71211]
 [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000995_14849093_c3_180	2538	6310	294	97	133	6.0e-09

Description

pir:[LN:F71245] [AC:F71245] [PN:hypothetical protein PHS004] [GN:PHS004]
 [OR:Pyrococcus horikoshii] [DB:pir2] >gp:[GI:d1030236:g3256610]
 [LN:AP000001]
 [AC:AP000001:AB009465:AB009464:AB009466:AB009467:AB009468:AB009469] [PN:58aa
 long hypothetical protein] [GN:PHS004] [OR:Pyrococcus horikoshii]
 [SR:Pyrococcus horikoshii (strain:OT3) DNA] [DB:genpept-bct1] [DE:Pyrococcus
 horikoshii OT3 genomic DNA, 1-287000 nt. position (1/7).] [NT:similar to
 GENPEPT:Z47547 percent identity:50.000] [LE:195255] [RE:195431] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000995_14897837_f1_29	2539	6311	1275	424	1161	4.3e-128

Description

sp:[LN:THD1_LACLA] [AC:Q02145] [GN:ILVA] [OR:LACTOCOCCUS LACTIS]
 [SR:,SUBSPLACTIS:STREPTOCOCCUS LACTIS] [EC:4.2.1.16] [DE:DEAMINASE)]
 [SP:Q02145] [DB:swissprot] >pir:[LN:S35141] [AC:S35141] [PN:probable
 threonine dehydratase,] [GN:ilvA] [CL:threonine dehydratase]
 [OR:Lactococcus lactis subsp. lactis] [EC:4.2.1.16] [DB:pir2]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
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AI7503000995_157802_c1_135	2540	6312	141	46		
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Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
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AI7503000995_1702_f2_36	2541	6313	522	173	88	0.0089
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Description

pir:[LN:T00168] [AC:T00168] [PN:hypothetical protein 33] [OR:Staphylococcus aureus phage phi PVL] [DB:pir3] >gp:[GI:d1032869:g3341942] [LN:AB009866] [AC:AB009866] [OR:bacteriophage phi PVL] [SR:bacteriophage phi PVL (specific_host:Staphylococcus aureus ATC] [DB:genpept-phg] [DE:Bacteriophage phi PVL proviral DNA, complete sequence.] [NT:orf 33] [LE:28172] [RE:28582] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
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AI7503000995_19564128_c2_172	2542	6314	315	104		
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Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
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AI7503000995_20422318_f3_73	2543	6315	417	138	105	2.2e-05
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Description

pir:[LN:D69633] [AC:D69633] [PN:glutamine ABC transporter (glutamine-binding protein) glnH] [GN:glnH] [CL:lysine-arginine-ornithine-binding protein] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1183973:g2635189] [LN:BSUB0014] [AC:Z99117:AL009126] [PN:glutamine ABC transporter (glutamine-binding) [GN:glnH] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.] [LE:202928] [RE:203749] [DI:direct] >gp:[GI:e1183991:g2635207] [LN:BSUB0015] [AC:Z99118:AL009126] [PN:glutamine ABC transporter (glutamine-binding) [GN:glnH] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.] [LE:7248] [RE:8069] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000995_2114077_c2_166	2544	6316	156	51	115	1.1e-06

Description

pir:[LN:D69786] [AC:D69786] [PN:glycoprotein endopeptidase homolog ydiC]
 [GN:ydiC] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1182571:g2632905]
 [LN:BSUB0004] [AC:Z99107:AL009126] [GN:ydiC] [FN:unknown] [OR:Bacillus
 subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 4
 of 21): from 600701 to813890.] [NT:similar to glycoprotein endopeptidase]
 [LE:41127] [RE:41816] [DI:direct] >gp:[GI:d1020495:g1945108] [LN:D88802]
 [AC:D88802] [GN:ydiC] [OR:Bacillus subtilis] [SR:Bacillus subtilis
 (sub_species:Marburg, strain:168, isolate:JH642] [DB:genpept-bct1]
 [DE:Bacillus subtilis DNA for phoB-rrnE-groESL region, complete cds.] [NT:H.
 influenzae hypothetical protein; P43990 (182)] [LE:28129] [RE:28818]
 [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000995_2125637_f3_111	2545	6317	150	49		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000995_22441907_f2_58	2546	6318	1869	622	1924	9.7e-199

Description

sp:[LN:ILVD_BACSU] [AC:P51785] [GN:ILVD] [OR:BACILLUS SUBTILIS] [EC:4.2.1.9]
 [DE:110) (VEG110)] [SP:P51785] [DB:swissprot]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000995_22766502_f1_18	2547	6319	135	44		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000995_23478463_f3_99	2548	6320	1755	584	1667	1.7e-171

Description

pir:[LN:B69644] [AC:B69644:I39865] [PN:acetolactate synthase, large chain] [GN:ilvB] [CL:acetolactate synthase large chain:thiamine pyrophosphate-binding domain homology] [OR:Bacillus subtilis] [EC:4.1.3.18] [DB:pir2] >gp:[GI:e1184080:g2635296] [LN:BSUB0015] [AC:Z99118:AL009126] [PN:acetolactate synthase (acetohydroxy-acid) [GN:ilvB] [FN:valine/isoleucine biosynthesis] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:4.1.3.18] [DE:Bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.] [LE:99217] [RE:100941] [DI:complement] >gp:[GI:e1165364:g1770066] [LN:BSZ75208] [AC:Z75208] [PN:acetolactate synthase large subunit] [GN:ilvB] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:4.1.3.18] [DE:B.subtilis genomic sequence 89009bp.] [NT:acetolactate synthase (acetohydroxy-acid synthase)] [LE:68966] [RE:70690] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000995_23867325_f2_64	2549	6321	570	189	561	2.6e-54

Description

sp:[LN:LEUD_LACLA] [AC:Q02144] [GN:LEUD] [OR:LACTOCOCCUS LACTIS] [SR:,SUBSP LACTIS:STREPTOCOCCUS LACTIS] [EC:4.2.1.33] [DE:(ISOPROPYLMALATE ISOMERASE) (ALPHA-IPM ISOMERASE)] [SP:Q02144] [DB:swissprot] >pir:[LN:E36889] [AC:E36889:S35135] [PN:probable 3-isopropylmalate dehydratase, chain leuD] [GN:leuD] [CL:3-isopropylmalate dehydratase small chain] [OR:Lactococcus lactis subsp. lactis] [EC:4.2.1.33] [DB:pir2] >gp:[GI:g2565154] [LN:LLU92974] [AC:U92974:M90760:M90761] [PN:LeuD] [GN:leuD] [OR:Lactococcus lactis] [DB:genpept-bct1] [DE:Lactococcus lactis unknown gene, partial cds, and HisC (hisC), unknown, HisG (hisG), unknown, HisB (hisB), unknown, HisH (hish), HisA (hisA), HisF (hisF), HisIE (hisIE), unknown, unknown, LeuA(leuA), LeuB (leuB), LeuC (leuC), LeuD (leuD), unknown, IlvD(ilvD), IlvB (ilvB), IlvN, IlvC (ilvC), IlvA (ilvA), AldB (aldB) and aldR (aldR) genes, complete cds.] [NT:isopropylmalate dehydratase subunit] [LE:16590] [RE:17165] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000995_24343813_c1_139	2550	6322	1119	372	1075	9.0e-109

Description

sp:[LN:YEEE_ECOLI] [AC:P33015] [GN:YEEE] [OR:ESCHERICHIA COLI]
 [DE:HYPOTHETICAL 38.1 KD PROTEIN IN SBCB-HISL INTERGENIC REGION] [SP:P33015]
 [DB:swissprot] >pir:[LN:D64966] [AC:D64966] [PN:membrane protein yeeE]
 [GN:yeeE] [OR:Escherichia coli] [DB:pir2] >gp:[GI:d1016565:g1736687]
 [LN:D90839] [AC:D90839:AB001340] [GN:yeeE] [OR:Escherichia coli]
 [SR:Escherichia coli (strain:K12) DNA, clone_lib:Kohara lambda minise]
 [DB:genpept-bct1] [DE:E.coli genomic DNA, Kohara clone #349(44.6-45.0
 min.)] [NT:ORF_ID:o349#4; similar to [SwissProt Accession] [LE:13119]
 [RE:14177] [DI:complement] >gp:[GI:d1016570:g1736693] [LN:D90840]
 [AC:D90840:AB001340] [GN:yeeE] [OR:Escherichia coli] [SR:Escherichia coli
 (strain:K12) DNA, clone_lib:Kohara lambda minise] [DB:genpept-bct1]
 [DE:E.coli genomic DNA, Kohara clone #350(44.9-45.2 min.)]
 [NT:ORF_ID:o349#4; similar to [SwissProt Accession] [LE:1810] [RE:2868]
 [DI:complement] >gp:[GI:g405956] [LN:ECOHU43] [AC:U00009] [PN:yeeE]
 [OR:Escherichia coli] [SR:Escherichia coli K12 BHB2600] [DB:genpept-bct1]
 [DE:sbcB region of E.coli K12 BHB2600.] [NT:similar to ORF in fliE-amyA
 intergenic region] [LE:4324] [RE:5382] [DI:complement] >gp:[GI:g1788323]
 [LN:AE000292] [AC:AE000292:U00096] [PN:putative transport system permease
 protein] [GN:yeeE] [FN:putative transport; Not classified] [OR:Escherichia
 coli] [DB:genpept-bct2] [DE:Escherichia coli K-12 MG1655 section 182 of 400
 of the completegenome.] [NT:f352; 100 pct identical to YEEE_ECOLI SW:
 P33015] [LE:9782] [RE:10840] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000995_24640625_c2_175	2551	6323	960	319	954	6.0e-96

Description

sp:[LN:SCRR_STAXY] [AC:P74892] [GN:SCRR] [OR:STAPHYLOCOCCUS XYLOSUS]
 [DE:SUCROSE OPERON REPRESSOR (SCR OPERON REGULATORY PROTEIN)] [SP:P74892]
 [DB:swissprot] >gp:[GI:e264641:g949974] [LN:SXSCRBA] [AC:X67744] [PN:sucrose
 repressor] [GN:scrR] [OR:Staphylococcus xylosus] [DB:genpept-bct1]
 [DE:S.xylosus scrB and scrR genes.] [SP:P74892] [LE:495] [RE:1457]
 [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000995_24646962_c1_150	2552	6324	210	69	79	0.0032

Description

gp:[GI:g2564351] [LN:VCU83795] [AC:U83795] [PN:RstR] [GN:rstR] [FN:repressor of rstA transcription] [OR:Vibrio cholerae] [DB:genpept-bct1] [DE:Vibrio cholerae RstR (rstR), RstA1 (rstA1), RstB1 (rstB1) and RstC(rstC) genes, complete cds.] [LE:496] [RE:834] [DI:complement] >gp:[GI:g2564356] [LN:VCU83796] [AC:U83796] [PN:RstR] [GN:rstR] [FN:repressor of rstA transcription] [OR:Vibrio cholerae] [DB:genpept-bct1] [DE:Vibrio cholerae RstR (rstR), RstA2 (rstA2), and RstB2 (rstB2)genes, complete cds.] [LE:496] [RE:834] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000995_24814812_f3_90	2553	6325	1950	649	1516	1.7e-155

Description

sp:[LN:YDIF_BACSU] [AC:O05519] [GN:YDIF] [OR:BACILLUS SUBTILIS] [DE:HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YDIF] [SP:O05519] [DB:swissprot] >pir:[LN:G69786] [AC:G69786] [PN:ABC transporter (ATP-binding protein) homolog ydiF] [GN:ydiF] [CL:ATP-binding cassette homology] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1182574:g2632908] [LN:BSUB0004] [AC:Z99107:AL009126] [GN:ydiF] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.] [NT:similar to ABC transporter (ATP-binding protein)] [SP:O05519] [LE:43544] [RE:45472] [DI:complement] >gp:[GI:d1020498:g1945111] [LN:D88802] [AC:D88802] [GN:ydiF] [OR:Bacillus subtilis] [SR:Bacillus subtilis (sub_species:Marburg, strain:168, isolate:JH642] [DB:genpept-bct1] [DE:Bacillus subtilis DNA for phoB-rrnE-groESL region, complete cds.] [NT:H. influenzae hypothetical ABC transporter; P44808] [LE:30546] [RE:32474] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000995_24823588_f2_63	2554	6326	1386	461	1633	6.7e-168

Description

sp:[LN:LEU2_LACLA] [AC:Q02142] [GN:LEUC] [OR:LACTOCOCCUS LACTIS]
[SR:,SUBSPLACTIS:STREPTOCOCCUS LACTIS] [EC:4.2.1.33] [DE:(ISOPROPYLMALATE
ISOMERASE) (ALPHA-IPM ISOMERASE) (IPMI)] [SP:Q02142] [DB:swissprot]
>pir:[LN:S35134] [AC:S35134] [PN:probable 3-isopropylmalate dehydratase,
chain leuC] [GN:leuC] [OR:Lactococcus lactis subsp. lactis] [SR:strain
NCDO2118, , strain NCDO2118] [SR:strain NCDO2118,] [EC:4.2.1.33] [DB:pir2]
>gp:[GI:g2565153] [LN:LLU92974] [AC:U92974:M90760:M90761] [PN:LeuC]
[GN:leuC] [OR:Lactococcus lactis] [DB:genpept-bct1] [DE:Lactococcus lactis
unknown gene, partial cds, and HisC (hisC), unknown, HisG (hisG), unknown,
HisB (hisB), unknown, HisH (hish), HisA (hisA), HisF (hisF), HisIE (hisIE),
unknown, unknown, LeuA(leuA), LeuB (leuB), LeuC (leuC), LeuD (leuD),
unknown, IlvD(ilvD), IlvB (ilvB), IlvN, IlvC (ilvC), IlvA (ilvA), AldB
(aldB) and aldR (aldR) genes, complete cds.] [NT:isopropylmalate dehydratase
subunit] [LE:15188] [RE:16570] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000995_25900300_c3_212	2555	6327	330	110	297	2.5e-26

Description

gp:[GI:g2689561] [LN:U93688] [AC:U93688] [OR:Staphylococcus aureus]
[DB:genpept-bct2] [DE:Staphylococcus aureus toxic shock syndrome toxin-1
(tst), enterotoxin (ent), and integrase (int) genes, complete cds.]
[NT:orf14] [LE:10769] [RE:11029] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000995_26615912_c3_206	2556	6328	1479	492	1943	9.5e-201

Description

sp:[LN:SCRB_STAXY] [AC:Q05936] [GN:SCRB] [OR:STAPHYLOCOCCUS XYLOSUS]
[EC:3.2.1.26] [DE:SUCROSE-6-PHOSPHATE HYDROLASE, (SUCRASE) (INVERTASE)]
[SP:Q05936] [DB:swissprot] >pir:[LN:A47059] [AC:A47059] [PN:sucrase ScrB]
[OR:Staphylococcus xylosus] [DB:pir2] >gp:[GI:e264653:g288269] [LN:SXSCRBA]
[AC:X67744] [PN:beta-fructofuranosidase] [GN:scrB] [OR:Staphylococcus
xylosus] [DB:genpept-bct1] [EC:3.2.1.26] [DE:S.xylosus scrB and scrR genes.]
[SP:Q05936] [LE:1541] [RE:3025] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000995_2866090_f2_35	2557	6329	1254	417	1250	2.6e-127

Description

gp:[GI:g2689564] [LN:U93688] [AC:U93688] [PN:integrase] [GN:int]
 [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus toxic
 shock syndrome toxin-1 (tst), enterotoxin (ent), and integrase (int) genes,
 complete cds.] [NT:similar to staphylococcal phage integrase] [LE:13871]
 [RE:15091] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000995_29307312_c3_181	2558	6330	165	54		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000995_31436_f1_15	2559	6331	177	58		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000995_31680342_f3_74	2560	6332	546	181	176	4.6e-12

Description

gp:[GI:g1633572] [LN:KSU52064] [AC:U52064] [OR:Kaposi's sarcoma-associated
 herpesvirus] [SR:Kaposi's sarcoma-associated herpesvirus - Human herpesvirus
 8] [DB:genpept-vr1] [DE:Kaposi's sarcoma-associated herpes-like virus ORF73
 homolog gene, complete cds.] [NT:Herpesvirus saimiri ORF73 homolog] [LE:1]
 [RE:3489] [DI:direct] >gp:[GI:g1718329] [LN:KSU75698] [AC:U75698]
 [OR:Kaposi's sarcoma-associated herpesvirus] [SR:Kaposi's sarcoma-associated
 herpesvirus - Human herpesvirus 8] [DB:genpept-vr1] [DE:Kaposi's
 sarcoma-associated herpesvirus long unique region, 80putative ORF's and
 kaposin gene, complete cds.] [NT:ORF 73; extensive acidic domains, potential
 leucine] [LE:123809] [RE:127297] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000995_33203138_c1_133	2561	6333	159	52		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000995_3361326_c2_151	2562	6334	207	68		
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Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000995_34257878_f2_62	2563	6335	1065	354	894	1.4e-89
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Description

sp:[LN:LEU3_LACLA] [AC:Q02143] [GN:LEUB] [OR:LACTOCOCCUS LACTIS]
 [SR:,SUBSPLACTIS:STREPTOCOCCUS LACTIS] [EC:1.1.1.85] [DE:(IMDH) (3-IPM-DH)]
 [SP:Q02143] [DB:swissprot] >pir:[LN:S35133] [AC:S35133:C36889]
 [PN:3-isopropylmalate dehydrogenase,] [GN:leuB] [CL:3-isopropylmalate
 dehydrogenase] [OR:Lactococcus lactis subsp. lactis] [SR:strain NCDO2118, ,
 strain NCDO2118] [SR:strain NCDO2118,] [EC:1.1.1.85] [DB:pir2]
 >gp:[GI:g2565152] [LN:LLU92974] [AC:U92974:M90760:M90761] [PN:LeuB]
 [GN:leuB] [OR:Lactococcus lactis] [DB:genpept-bct1] [DE:Lactococcus lactis
 unknown gene, partial cds, and HisC (hisC), unknown, HisG (hisG), unknown,
 HisB (hisB), unknown, HisH (hish), HisA (hisA), HisF (hisF), HisIE (hisIE),
 unknown, unknown, LeuA (leuA), LeuB (leuB), LeuC (leuC), LeuD (leuD),
 unknown, IlvD (ilvD), IlvB (ilvB), IlvN, IlvC (ilvC), IlvA (ilvA), AldB
 (aldB) and aldR (aldR) genes, complete cds.] [NT:isopropylmalate
 dehydrogenase] [LE:13788] [RE:14825] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000995_34412750_c3_207	2564	6336	966	321	1031	4.2e-104
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Description

pir:[LN:S20799] [AC:S58482:S20799] [PN:hypothetical protein 7]
 [CL:ribokinase] [OR:Staphylococcus aureus] [DB:pir2] >gp:[GI:g46512]
 [LN:SAAGRAB] [AC:X52543:M32737] [OR:Staphylococcus aureus] [DB:genpept-bct1]
 [DE:S.aureus agrA, agrB and hld genes.] [NT:orf 7] [LE:4896] [RE:5855]
 [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000995_35598750_f3_72	2565	6337	849	282	112	3.9e-06

Description

gp:[GI:g2897106] [LN:AF020798] [AC:AF020798] [PN:repressor]
[OR:Streptococcus thermophilus bacteriophage TP-J34] [DB:genpept-phg]
[DE:Streptococcus thermophilus bacteriophage lysogeny module,
integrasehomolog (int), putative host cell surface-exposed
lipoprotein,putative metallo-proteinase, repressor, Cro-like
regulatoryprotein, and P1-antirepressor homolog genes, complete cds.]
[NT:CI-like regulatory protein; orf121] [LE:4825] [RE:5190] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000995_36132937_f2_53	2566	6338	1641	546	273	9.6e-20

Description

sp:[LN:HEXA_STRPN] [AC:P10564] [GN:HEXA] [OR:STREPTOCOCCUS PNEUMONIAE]
[DE:DNA MISMATCH REPAIR PROTEIN HEXA] [SP:P10564] [DB:swissprot]
>pir:[LN:C28667] [AC:C28667] [PN:DNA mismatch repair protein hexA] [GN:hexA]
] [CL:DNA mismatch repair protein mutS] [OR:Streptococcus pneumoniae]
[DB:pir2] >gp:[GI:g153655] [LN:STRHEXA] [AC:M18729] [PN:mismatch repair
protein] [GN:hexA] [OR:Streptococcus pneumoniae] [SR:Streptococcus
pneumoniae (strain 175) (clone: pLS141.) DNA] [DB:genpept-bct1]
[DE:S.pneumoniae mismatch repair protein (hexA) gene, complete cds.]
[LE:971] [RE:3505] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000995_36206502_c3_197	2567	6339	483	160	340	7.0e-31

Description

pir:[LN:E69786] [AC:E69786] [PN:ribosomal-protein-alanine N-acetyltransfer
homolog ydiD] [GN:ydiD] [CL:Escherichia coli peptide N-acetyltransferase
rimI] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1182572:g2632906]
[LN:BSUB0004] [AC:Z99107:AL009126] [GN:ydiD] [FN:unknown] [OR:Bacillus
subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 4
of 21): from 600701 to813890.] [NT:similar to ribosomal-protein-alanine]
[LE:41826] [RE:42281] [DI:direct] >gp:[GI:d1020496:g1945109] [LN:D88802]
[AC:D88802] [GN:ydiD] [OR:Bacillus subtilis] [SR:Bacillus subtilis
(sub_species:Marburg, strain:168, isolate:JH642] [DB:genpept-bct1]
[DE:Bacillus subtilis DNA for phoB-rrnE-groESL region, complete cds.] [NT:H.
influenzae, ribosomal protein alanine] [LE:28828] [RE:29283] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000995_409556_f1_33	2568	6340	135	44	112	2.5e-06

Description

pir:[LN:D71245] [AC:D71245] [PN:hypothetical protein PH0221] [GN:PH0221]
[OR:Pyrococcus horikoshii] [DB:pir2] >gp:[GI:d1030234:g3256608]
[LN:AP000001]
[AC:AP000001:AB009465:AB009464:AB009466:AB009467:AB009468:AB009469]
[PN:235aa long hypothetical protein] [GN:PH0221] [OR:Pyrococcus horikoshii]
[SR:Pyrococcus horikoshii (strain:OT3) DNA] [DB:genpept-bct1] [DE:Pyrococcus
horikoshii OT3 genomic DNA, 1-287000 nt. position (1/7).] [LE:194212]
[RE:194919] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000995_4707506_c2_174	2569	6341	1314	437	1156	2.4e-117

Description

sp:[LN:NRGA_BACSU] [AC:Q07429] [GN:NRGA] [OR:BACILLUS SUBTILIS] [DE:PROBABLE
AMMONIUM TRANSPORTER (MEMBRANE PROTEIN NRGA)] [SP:Q07429] [DB:swissprot]
>pir:[LN:A36865] [AC:A36865:D69667] [PN:ammonium transporter nrgA] [GN:nrgA
] [CL:ammonium transporter nrgA] [OR:Bacillus subtilis] [DB:pir2]
>gp:[GI:g143264] [LN:BACNRGABO] [AC:L03216] [PN:membrane-associated protein]
[GN:nrgA] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain 168) DNA]
[DB:genpept-bct1] [DE:Bacillus subtilis operon membrane-associated protein
(nrgA), andPII-like protein (nrgB) genes, complete cds.] [NT:putative]
[LE:126] [RE:1340] [DI:direct] >gp:[GI:e1184557:g2636176] [LN:BSUB0019]
[AC:Z99122:AL009126] [PN:ammonium transporter] [GN:nrgA] [OR:Bacillus
subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section
19 of 21): from 3597091to 3809700.] [SP:Q07429] [LE:158754] [RE:159968]
[DI:direct] >gp:[GI:e283112:g1684645] [LN:BSZ82987] [AC:Z82987] [PN:unknown]
[GN:nrgA] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B. subtilis
ywo[A,B,C,D,E,F,G,H], nrg[A,B], spoIIID and mbl genes.] [SP:Q07429]
[LE:1335] [RE:2549] [DI:complement] >gp:[GI:e1184557:g2636176] [LN:BSUB0019]
[AC:Z99122:AL009126] [PN:ammonium transporter] [GN:nrgA] [OR:Bacillus
subtilis] [DB:genpept] [DE:Bacillus subtilis complete genome (section 19 of
21): from 3597091to 3809700.] [SP:Q07429] [LE:158754] [RE:159968]
[DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000995_4958387_c1_132	2570	6342	537	178	305	3.6e-27

Description

pir:[LN:D69786] [AC:D69786] [PN:glycoprotein endopeptidase homolog ydiC] [GN:ydiC] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1182571:g2632905] [LN:BSUB0004] [AC:Z99107:AL009126] [GN:ydiC] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.] [NT:similar to glycoprotein endopeptidase] [LE:41127] [RE:41816] [DI:direct] >gp:[GI:d1020495:g1945108] [LN:D88802] [AC:D88802] [GN:ydiC] [OR:Bacillus subtilis] [SR:Bacillus subtilis (sub_species:Marburg, strain:168, isolate:JH642) [DB:genpept-bct1] [DE:Bacillus subtilis DNA for phoB-rrnE-groESL region, complete cds.] [NT:H. influenzae hypothetical protein; P43990 (182)] [LE:28129] [RE:28818] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000995_5359438_c2_167	2571	6343	1107	368	1096	5.4e-111

Description

sp:[LN:YDIE_BACSU] [AC:O05518] [GN:YDIE] [OR:BACILLUS SUBTILIS] [DE:HYPOTHETICAL 36.8 KD PROTEIN IN PHOB-GROES INTERGENIC REGION] [SP:O05518] [DB:swissprot] >pir:[LN:F69786] [AC:F69786] [PN:glycoprotein endopeptidase homolog ydiE] [GN:ydiE] [CL:O-sialoglycoprotein endopeptidase] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1182573:g2632907] [LN:BSUB0004] [AC:Z99107:AL009126] [GN:ydiE] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.] [NT:similar to glycoprotein endopeptidase] [SP:O05518] [LE:42274] [RE:43314] [DI:direct] >gp:[GI:d1020497:g1945110] [LN:D88802] [AC:D88802] [GN:ydiE] [OR:Bacillus subtilis] [SR:Bacillus subtilis (sub_species:Marburg, strain:168, isolate:JH642) [DB:genpept-bct1] [DE:Bacillus subtilis DNA for phoB-rrnE-groESL region, complete cds.] [NT:P. haemolytica o-sialoglycoprotein endopeptidase;] [LE:29276] [RE:30316] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000995_5909428_c3_203	2572	6344	750	249	582	1.6e-56

Description

gp:[GI:d1039124:g4514349] [LN:AB013375] [AC:AB013375] [PN:YdiH] [GN:ydiH] [OR:Bacillus halodurans] [SR:Bacillus halodurans (strain:C-125) DNA] [DB:genpept-bct1] [DE:Bacillus halodurans C-125 ydiH, ydiI, ydiJ, yhcA and yxaA genes, complete and partial cds.] [LE:235] [RE:870] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
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AI7503000995_6836010_c2_153	2573	6345	171	56		
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Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
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AI7503000995_860790_f3_101	2574	6346	1593	530	1391	3.0e-142
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Description

sp:[LN:LEU1_LACLA] [AC:Q02141] [GN:LEUA] [OR:LACTOCOCCUS LACTIS]
 [SR:,SUBSPLACTIS:STREPTOCOCCUS LACTIS] [EC:4.1.3.12] [DE:SYNTHASE)
 (ALPHA-IPM SYNTHETASE)] [SP:Q02141] [DB:swissprot] >pir:[LN:S35132]
 [AC:S35132:B36889] [PN:2-isopropylmalate synthase,:alpha-isopropylmalate
 synthase] [GN:leuA] [CL:2-isopropylmalate synthase leuA] [OR:Lactococcus
 lactis subsp. lactis] [EC:4.1.3.12] [DB:pir2]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
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AI7503000995_9843800_f1_8	2575	6347	192	63	47	0.020
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Description

gp:[GI:e236301:g1263146] [LN:MTMCECYTB] [AC:Z70776] [PN:cytochrome b]
 [OR:Mitochondrion Mugil cephalus] [SR:Mugil cephalus] [DB:genpept-vrt]
 [DE:M.cephalus mitochondrial cytochrome b gene.] [LE:<1] [RE:>292]
 [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000995_995451_f2_61	2576	6348	1020	339	1139	1.5e-115

Description

sp:[LN:ILVC_BACSU] [AC:P37253] [GN:ILVC] [OR:BACILLUS SUBTILIS]
[EC:1.1.1.86] [DE:ISOMEROREDUCTASE) (ALPHA-KETO-BETA-HYDROXYLACIL
REDUCTOISOMERASE)] [SP:P37253] [DB:swissprot] >pir:[LN:C69644] [AC:C69644]
[PN:ketol-acid reductoisomerase ilvC] [GN:ilvC] [CL:Methanococcus
ketol-acid reductoisomerase: ketol-acid reductoisomerase homology]
[OR:Bacillus subtilis] [DB:pir2] >gp:[GI:g143093] [LN:BACILNB] [AC:L03181]
[PN:ketol-acid reductoisomerase] [GN:ilvC] [OR:Bacillus subtilis]
[SR:Bacillus subtilis DNA] [DB:genpept-bct1] [DE:Bacillus subtilis ilvB,
ilvN and ilvC genes, complete ilv-leuoperon.] [LE:2979] [RE:4007]
[DI:direct] >gp:[GI:e1184078:g2635294] [LN:BSUB0015] [AC:Z99118:AL009126]
[PN:ketol-acid reductoisomerase (acetohydroxy-acid) [GN:ilvC]
[FN:valine/isoleucine biosynthesis] [OR:Bacillus subtilis] [DB:genpept-bct1]
[EC:1.1.1.86] [DE:Bacillus subtilis complete genome (section 15 of 21): from
2795131to 3013540.] [SP:P37253] [LE:97651] [RE:98679] [DI:complement]
>gp:[GI:e1165366:g1770068] [LN:BSZ75208] [AC:Z75208] [PN:ketol-acid
reductoisomerase] [GN:ilvC] [OR:Bacillus subtilis] [DB:genpept-bct1]
[EC:1.1.1.86] [DE:B.subtilis genomic sequence 89009bp.] [NT:ketol-acid
reductoisomerase (acetohydroxy-acid) [SP:P37253] [LE:71228] [RE:72256]
[DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000996_10719452_c3_376	2577	6349	684	227	371	3.6e-34

Description

sp:[LN:HLY3_BACSU] [AC:P54175] [GN:YPLQ] [OR:BACILLUS SUBTILIS]
[DE:HEMOLYSIN III HOMOLOG] [SP:P54175] [DB:swissprot] >pir:[LN:D69938]
[AC:D69938] [PN:hemolysin III homolog homolog yplQ] [GN:yplQ]
[CL:hemolysin III yplQ] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:g1256643]
[LN:BACYACA] [AC:L77246] [GN:yplQ] [OR:Bacillus subtilis] [DB:genpept-bct1]
[DE:Bacillus subtilis (YAC10-9 clone) DNA region between the serA andkdg
loci.] [NT:20.2% identity with NADH dehydrogenase of the] [LE:25508]
[RE:26149] [DI:complement] >gp:[GI:e1183626:g2634599] [LN:BSUB0012]
[AC:Z99115:AL009126] [GN:yplQ] [FN:unknown] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 12 of 21):
from 2195541to 2409220.] [NT:similar to hemolysin III homolog] [SP:P54175]
[LE:99003] [RE:99644] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000996_10734567_f3_197	2578	6350	249	82		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000996_10752342_c2_327	2579	6351	981	326	773	9.1e-77

Description

pir:[LN:D69812] [AC:D69812] [PN:ferrichrome ABC transporter (permease) homolog yfmE] [GN:yfmE] [CL:vitamin B12 transport protein btuC] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1182740:g2633074] [LN:BSUB0005] [AC:Z99108:AL009126] [GN:yfmE] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.] [NT:similar to ferrichrome ABC transporter (permease)] [LE:20404] [RE:21405] [DI:complement] >gp:[GI:d1023182:g2443248] [LN:D86417] [AC:D86417] [PN:YfmE] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:AC327) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis 35.7 kb genomic DNA, 70-73 degree region,complete cds.] [LE:27116] [RE:28117] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000996_10759818_c1_271	2580	6352	1008	335	669	9.5e-66

Description

pir:[LN:B69812] [AC:B69812] [PN:ferrichrome ABC transporter (binding prote) homolog yfmC] [GN:yfmC] [CL:iron(III) dicitrate transport protein] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1182742:g2633076] [LN:BSUB0005] [AC:Z99108:AL009126] [GN:yfmC] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.] [NT:similar to ferrichrome ABC transporter (binding)] [LE:22475] [RE:23422] [DI:complement] >gp:[GI:d1023180:g2443246] [LN:D86417] [AC:D86417] [PN:YfmC] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:AC327) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis 35.7 kb genomic DNA, 70-73 degree region,complete cds.] [LE:25099] [RE:26046] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000996_11913877_f1_49	2581	6353	123	40		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000996_11961568_c2_311	2582	6354	945	314	1007	1.5e-101

Description

sp:[LN:LACC_STAAU] [AC:P11099] [GN:LACC] [OR:STAPHYLOCOCCUS AUREUS]
[EC:2.7.1.144] [DE:TAGATOSE-6-PHOSPHATE KINASE, (PHOSPHOTAGATOKINASE)]
[SP:P11099] [DB:swissprot] >pir:[LN:S04358] [AC:S04358] [PN:lacC protein]
[GN:lacC] [CL:6-phosphofructokinase 2] [OR:Staphylococcus aureus] [DB:pir2]
>gp:[GI:g46605] [LN:SALACCD] [AC:X14827] [OR:Staphylococcus aureus]
[DB:genpept-bct1] [DE:Staphylococcus aureus lacC and lacD genes.] [NT:lacC
polypeptide (AA 1-310)] [SP:P11099] [LE:55] [RE:987] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000996_12578885_f2_109	2583	6355	366	121		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000996_12603166_f2_89	2584	6356	303	100	110	1.6e-06

Description

pir:[LN:G71244] [AC:G71244] [PN:hypothetical protein PH0217] [GN:PH0217]
[OR:Pyrococcus horikoshii] [DB:pir2] >gp:[GI:d1030229:g3256603]
[LN:AP000001]
[AC:AP000001:AB009465:AB009464:AB009466:AB009467:AB009468:AB009469]
[PN:106aa long hypothetical protein] [GN:PH0217] [OR:Pyrococcus horikoshii]
[SR:Pyrococcus horikoshii (strain:OT3) DNA] [DB:genpept-bct1] [DE:Pyrococcus
horikoshii OT3 genomic DNA, 1-287000 nt. position (1/7).] [LE:191072]
[RE:191392] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000996_1287875_f3_173	2585	6357	123	40		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000996_13680468_c2_336	2586	6358	1080	359	1133	6.4e-115

Description

sp:[LN:YBAL_BACSU] [AC:P50863] [GN:YBAL:REC233] [OR:BACILLUS SUBTILIS]
[DE:HYPOTHETICAL 38.6 KD PROTEIN IN CWLD-GERD INTERGENIC REGION] [SP:P50863]
[DB:swissprot] >pir:[LN:A69743] [AC:A69743] [PN:ATP-binding Mrp-like
protein homolog ybaL] [GN:ybaL] [CL:conserved probable membrane protein
YIL003w] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e95614:g1177249]
[LN:BSCWLD] [AC:X74737] [GN:rec233] [OR:Bacillus subtilis] [DB:genpept-bct1]
[DE:B.subtilis cwld, rec223 and gerD genes.] [SP:P50863] [LE:1376] [RE:2434]
[DI:direct] >gp:[GI:e1182087:g2632421] [LN:BSUB0001] [AC:Z99104:AL009126]
[GN:ybaL] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus
subtilis complete genome (section 1 of 21): from 1 to213080.] [NT:alternate
gene name: ybxI; similar to ATP-binding] [LE:157420] [RE:158478] [DI:direct]
>gp:[GI:d1011652:g1644213] [LN:D64126] [AC:D64126] [PN:unknown] [GN:orf14]
[OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:168) DNA]
[DB:genpept-bct1] [DE:Bacillus subtilis genes for ribosomal proteins L13 and
S9, putativecell wall hydrolase Cwld, gerD protein, 16S ribosomal RNA and
23Sribosomal RNA.] [LE:6981] [RE:8039] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000996_13871068_c1_247	2587	6359	666	221	893	1.7e-89

Description

gp:[GI:d1039013:g4512410] [LN:AB017508] [AC:AB017508] [GN:rpsC] [OR:Bacillus
halodurans] [SR:Bacillus halodurans (strain:C-125) DNA] [DB:genpept-bct1]
[DE:Bacillus halodurans C-125 genomic DNA, 32 kb fragment, completecds.]
[NT:rpsC homologue (identity of 87% to B. subtilis)] [LE:16781] [RE:17440]
[DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000996_13886593_c2_318	2588	6360	252	83	96	5.0e-05

Description

gp:[GI:g727435] [LN:LLU23376] [AC:U23376] [OR:Lactococcus lactis]
[DB:genpept-bct1] [DE:Lactococcus lactis N5-(1-carboxyethyl)-L-ornithine
synthase (ceo)gene, complete cds.] [NT:putative 6-kDa protein] [LE:165]
[RE:353] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000996_1408450_f2_158	2589	6361	564	187	104	9.8e-06

Description

pir:[LN:E71186] [AC:E71186] [PN:hypothetical protein PH1769] [GN:PH1769]
 [OR:Pyrococcus horikoshii] [DB:pir2] >gp:[GI:d1031827:g3258201]
 [LN:AP000007]
 [AC:AP000007:AB009464:AB009465:AB009521:AB009522:AB009523:AB009524]
 [PN:100aa long hypothetical protein] [GN:PH1769] [OR:Pyrococcus horikoshii]
 [SR:Pyrococcus horikoshii (strain:OT3) DNA] [DB:genpept-bct1] [DE:Pyrococcus
 horikoshii OT3 genomic DNA, 1485001-1738505 nt. position(7/7).] [LE:59186]
 [RE:59488] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000996_1410277_f1_4	2590	6362	153	50		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000996_14277217_c2_297	2591	6363	516	171	626	3.4e-61

Description

sp:[LN:RS5_BACSU] [AC:P21467] [GN:RPSE:SPCA] [OR:BACILLUS SUBTILIS] [DE:30S
 RIBOSOMAL PROTEIN S5 (BS5)] [SP:P21467] [DB:swissprot] >pir:[LN:R3BS5S]
 [AC:D69699:S12680:S11355] [PN:ribosomal protein S5] [GN:rpsE]
 [CL:Escherichia coli ribosomal protein S5] [OR:Bacillus subtilis] [DB:pir1]
 >gp:[GI:g1044981] [LN:BACRPLP] [AC:L47971] [PN:ribosomal protein S5]
 [GN:rpsE] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
 ribosomal protein (rplPNXEFROQ, rpmCDJ, rpsQNHEMK) genes, integral membrane
 protein (secY) gene, adenylatekinase (adk) gene, methionine aminopeptidase
 (map) gene, initiation factor 1 (infA) gene, RNA polymerase alpha (rpoA)
 gene.] [LE:3585] [RE:4085] [DI:direct] >gp:[GI:e1182066:g2632400]
 [LN:BSUB0001] [AC:Z99104:AL009126] [PN:ribosomal protein S5] [GN:rpsE]
 [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete
 genome (section 1 of 21): from 1 to213080.] [SP:P21467] [LE:143359]
 [RE:143859] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000996_14312750_c3_354	2592	6364	492	163	665	2.5e-65

Description

sp:[LN:RL13_STACA] [AC:Q00990] [GN:RPLM] [OR:STAPHYLOCOCCUS CARNOSUS]
 [DE:50S RIBOSOMAL PROTEIN L13] [SP:Q00990] [DB:swissprot] >pir:[LN:S23063]
 [AC:S23063] [PN:ribosomal protein L13] [GN:rplM] [CL:Escherichia coli
 ribosomal protein L13] [OR:Staphylococcus carnosus] [DB:pir2]
 >gp:[GI:g46912] [LN:SCRPLM] [AC:X63912:S79454] [PN:ribosomal protein L13]
 [GN:rplM] [OR:Staphylococcus carnosus] [DB:genpept-bct1] [DE:S.carnosus rplM
 gene for ribosomal protein L13.] [SP:Q00990] [LE:309] [RE:746] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000996_14346067_c2_316	2593	6365	1023	340	561	2.6e-54

Description

gp:[GI:g4321580] [LN:AF050114] [AC:AF050114] [PN:alginate lyase]
 [OR:Pseudomonas sp. W7] [DB:genpept-bct2] [DE:Pseudomonas sp. W7 alginate
 lyase gene, complete cds.] [LE:1] [RE:1038] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000996_14531558_f1_53	2594	6366	126	41		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000996_14900826_c3_386	2595	6367	351	116	188	8.9e-15

Description

gp:[GI:g208931] [LN:SYNORFLAC] [AC:M15619] [OR:synthetic construct]
 [SR:E.coli (strain SE5000) synthetic DNA, clone pKB1] [DB:genpept-syn]
 [DE:Synthetic E.coli ORF16/lacZ fusion protein, partial cds.] [NT:ORF16-lacZ
 fusion protein] [LE:29] [RE:>232] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000996_157750_c3_379	2596	6368	195	64		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000996_15879002_f2_96	2597	6369	123	40		
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Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000996_16829627_c2_300	2598	6370	372	123	484	3.8e-46
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Description

gp:[GI:g1044989] [LN:BACRPLP] [AC:L47971] [PN:ribosomal protein S13] [GN:rpsM] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis ribosomal protein (rplPNXEFRQ, rpmCDJ, rpsQNHEMK) genes, integral membrane protein (secY) gene, adenylatekinase (adk) gene, methionine aminopeptidase (map) gene, initiation factor 1 (infA) gene, RNA polymerase alpha (rpoA) gene.] [LE:8197] [RE:8562] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000996_16835333_c2_288	2599	6371	840	279	1198	8.3e-122
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Description

gp:[GI:g1165306] [LN:BSU43929] [AC:U43929] [PN:L2] [GN:rplB] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis ribosomal protein gene cluster, rpsJ, rplC, rplD, rplW, rplB, rpsS, rplV and rpsC genes, complete cds, and rplP gene, partial cds.] [NT:ribosomal protein] [LE:2266] [RE:3099] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000996_197127_f2_121	2600	6372	1965	654	285	9.0e-22
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Description

sp:[LN:Y4XN_RHISN] [AC:P55706] [GN:Y4XN] [OR:RHIZOBIUM SP] [SR:NGR234,] [DE:HYPOTHETICAL 71.0 KD PROTEIN Y4XN] [SP:P55706] [DB:swissprot]
>gp:[GI:g2182722] [LN:AE000106] [AC:AE000106:U00090] [PN:Y4xN] [GN:y4xN] [OR:Rhizobium sp. NGR234] [DB:genpept-bct2] [DE:Rhizobium sp. NGR234 plasmid pNGR234a, section 43 of 46 of the complete plasmid sequence.] [NT:hypothetical 71 kd protein; similar to Escherichia] [LE:6573] [RE:8459] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000996_19730052_c1_278	2601	6373	1479	492	990	9.2e-100

Description

pir:[LN:F69763] [AC:F69763] [PN:multidrug resistance protein homolog ycnB] [GN:ycnB] [CL:lincomycin-resistance protein lmrB] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1182351:g2632685] [LN:BSUB0003] [AC:Z99106:AL009126] [GN:ycnB] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.] [NT:similar to multidrug resistance protein] [LE:32866] [RE:34284] [DI:complement] >gp:[GI:d1009651:g1805454] [LN:D50453] [AC:D50453] [PN:homologue of multidrug resistance protein B,] [GN:ycnB] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:168 trpC2) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis DNA for 25-36 degree region containing theamyE-srfa region, complete cds.] [LE:115269] [RE:116687] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000996_19822151_c2_302	2602	6374	372	123	433	9.7e-41

Description

pir:[LN:F32307] [AC:F32307:C69696] [PN:ribosomal protein L17:ribosomal protein BL15 (rplQ)] [GN:rplQ] [CL:Escherichia coli ribosomal protein L17] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:g142464] [LN:BACALPHA] [AC:M26414] [PN:ribosomal protein L17] [GN:rplQ] [OR:Bacillus subtilis] [SR:Bacillus subtilis DNA] [DB:genpept-bct1] [DE:B.subtilis initiation factor 1, ribosomal proteins B, S13, S11, L17and RNA polymerase alpha core protein genes, complete cds.] [LE:2603] [RE:2965] [DI:direct] >gp:[GI:g1044992] [LN:BACRPLP] [AC:L47971] [PN:ribosomal protein L17] [GN:rplQ] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis ribosomal protein (rplPNXEFROQ, rpmCDJ,rpsQNHEMK) genes, integral membrane protein (secY) gene, adenylatekinase (adk) gene, methionine aminopeptidase (map) gene,inititation factor 1 (infA) gene, RNA polymerase alpha (rpoA) gene.] [LE:10177] [RE:10539] [DI:direct] >gp:[GI:e1182077:g2632411] [LN:BSUB0001] [AC:Z99104:AL009126] [PN:ribosomal protein L17 (BL15)] [GN:rplQ] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 1 of 21): from 1 to213080.] [SP:P20277] [LE:149951] [RE:150313] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000996_20363762_c3_375	2603	6375	1215	404	587	4.7e-57

Description

gp:[GI:g5052662] [LN:AF145686] [AC:AF145686] [PN:BcDNA.LD24639] [GN:BcDNA.LD24639] [OR:Drosophila melanogaster] [SR:fruit fly] [DB:genpept-inv2] [DE:Drosophila melanogaster clone LD24639 BcDNA.LD24639 (BcDNA.LD24639)mRNA, complete cds.] [LE:199] [RE:1761] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000996_2125637_f3_165	2604	6376	150	49		
<u>Description</u>						

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000996_21516287_f1_6	2605	6377	126	41		
<u>Description</u>						

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000996_21751063_c1_245	2606	6378	579	192	621	1.2e-60
<u>Description</u>						

sp:[LN:RL3_BACST] [AC:P28600] [GN:RPLC] [OR:BACILLUS STEAROTHERMOPHILUS] [DE:50S RIBOSOMAL PROTEIN L3] [SP:P28600] [DB:swissprot] >pir:[LN:S24363] [AC:S24363:S36085] [PN:ribosomal protein L3] [GN:rpl3] [CL:Escherichia coli ribosomal protein L3] [OR:Bacillus stearothermophilus] [DB:pir2] >gp:[GI:g40102] [LN:BSRPLCLD] [AC:X67014:S42397] [PN:ribosomal protein L3] [GN:rplC] [OR:Bacillus stearothermophilus] [DB:genpept-bct1] [DE:B.stearothermophilus genes rplC and rplD for ribosomal proteins L3and L4, respectively.] [SP:P28600] [LE:52] [RE:693] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000996_21915941_c1_250	2607	6379	372	123	571	2.3e-55
<u>Description</u>						

sp:[LN:RL14_BACSU] [AC:P12875] [GN:RPLN] [OR:BACILLUS SUBTILIS] [DE:50S RIBOSOMAL PROTEIN L14] [SP:P12875] [DB:swissprot] >pir:[LN:R5BS4B] [AC:S05992:H69695] [PN:ribosomal protein L14] [GN:rplN] [CL:Escherichia coli ribosomal protein L14] [OR:Bacillus subtilis] [DB:pir1] >gp:[GI:g1044974] [LN:BACRPLP] [AC:L47971] [PN:ribosomal protein L14] [GN:rplN] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis ribosomal protein (rplPNXEFROQ, rpmCDJ,rpsQNHEMK) genes, integral membrane protein (secY) gene, adenylatekinase (adk) gene, methionine aminopeptidase (map) gene,inititation factor 1 (infA) gene, RNA polymerase alpha (rpoA) gene.] [LE:675] [RE:1043] [DI:direct] >gp:[GI:g40150] [LN:BSSPC] [AC:X15664] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis S10/spc operon rpmC, rpsQ, rplN, rplX, rplE, rpsN genes.] [NT:L14 protein (AA 1-122)] [SP:P12875] [LE:840] [RE:1208] [DI:direct] >gp:[GI:e1182059:g2632393] [LN:BSUB0001] [AC:Z99104:AL009126] [PN:ribosomal protein L14] [GN:rplN] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 1 of 21): from 1 to213080.] [SP:P12875] [LE:140449] [RE:140817] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000996_22002318_c3_342	2608	6380	330	109	390	3.5e-36

Description

sp:[LN:RL24_BACST] [AC:P04455] [GN:RPLX] [OR:BACILLUS STEAROTHERMOPHILUS] [DE:50S RIBOSOMAL PROTEIN L24] [SP:P04455] [DB:swissprot] >pir:[LN:R5BS24] [AC:A02819] [PN:ribosomal protein L24] [CL:Escherichia coli ribosomal protein L24] [OR:Bacillus stearothermophilus] [DB:pir1]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000996_22455303_f3_190	2609	6381	165	54		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000996_22688428_c3_383	2610	6382	144	47		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000996_22900877_c1_252	2611	6383	132	43		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000996_23460931_f2_100	2612	6384	429	142		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000996_23572128_c3_346	2613	6385	183	60	282	9.7e-25

Description

sp:[LN:RL30_STAAU] [AC:O06444] [GN:RPM] [OR:STAPHYLOCOCCUS AUREUS] [DE:50S RIBOSOMAL PROTEIN L30] [SP:O06444] [DB:swissprot] >gp:[GI:g2078380] [LN:SAU96620] [AC:U96620] [PN:ribosomal protein L30] [GN:L30] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:Staphylococcus aureus NCTC 8325 ribosomal protein L30 (L30),ribosomal protein L15 (L15) and SecY (secY) genes, complete cds.] [LE:65] [RE:244] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000996_23572180_c3_349	2614	6386	222	73	326	2.1e-29

Description

pir:[LN:F69644] [AC:F69644] [PN:translation initiation factor IF-1]
 [GN:infA] [CL:translation initiation factor IF-1] [OR:Bacillus subtilis]
 [DB:pir2] >gp:[GI:g142459] [LN:BACALPHA] [AC:M26414] [PN:initiation factor
 1] [GN:infA] [OR:Bacillus subtilis] [SR:Bacillus subtilis DNA]
 [DB:genpept-bct1] [DE:B.subtilis initiation factor 1, ribosomal proteins B,
 S13, S11, L17and RNA polymerase alpha core protein genes, complete cds.]
 [LE:235] [RE:453] [DI:direct] >gp:[GI:g1044987] [LN:BACRPLP] [AC:L47971]
 [PN:initiation factor IF-1] [GN:infA] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:Bacillus subtilis ribosomal protein (rplPNXEFRQ,
 rpmCDJ,rpsQNHEMK) genes, integral membrane protein (secY) gene,
 adenylatekinase (adk) gene, methionine aminopeptidase (map) gene,inititation
 factor 1 (infA) gene, RNA polymerase alpha (rpoA) gene.] [LE:7809] [RE:8027]
 [DI:direct] >gp:[GI:e1182072:g2632406] [LN:BSUB0001] [AC:Z99104:AL009126]
 [PN:initiation factor IF-I] [GN:infA] [FN:protein synthesis] [OR:Bacillus
 subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 1
 of 21): from 1 to213080.] [SP:P20458] [LE:147583] [RE:147801] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000996_23573587_c2_294	2615	6387	201	66	287	2.9e-25

Description

gp:[GI:d1039020:g4512417] [LN:AB017508] [AC:AB017508] [GN:rpsN] [OR:Bacillus
 halodurans] [SR:Bacillus halodurans (strain:C-125) DNA] [DB:genpept-bct1]
 [DE:Bacillus halodurans C-125 genomic DNA, 32 kb fragment, completecds.]
 [NT:rpsN homologue (identity of 92% to B. subtilis)] [LE:19712] [RE:19897]
 [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000996_23603450_c2_317	2616	6388	585	194	85	0.0017

Description

pir:[LN:S77761] [AC:S77761] [PN:probable phosphotransferase system enzyme
 II,:protein MC456:protein-Npi-phosphohistidine--sugar phosphotransferase]
 [OR:Mycoplasma capricolum] [EC:2.7.1.69] [DB:pir2]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000996_23632750_c3_365	2617	6389	525	174	726	8.7e-72

Description

pir:[LN:JC2527] [AC:JC2527:PC2381] [PN:alkaline shock protein] [GN:asp23]
[OR:Staphylococcus aureus] [DB:pir2] >gp:[GI:g894289] [LN:S76213]
[AC:S76213] [PN:alkaline shock protein 23] [GN:asp23] [OR:Staphylococcus
aureus] [SR:Staphylococcus aureus 912] [DB:genpept-bct1] [DE:asp23=alkaline
shock protein 23 {methicillin resistant}[Staphylococcus aureus, 912,
Genomic, 1360 nt].] [NT:Method: conceptual translation with partial peptide]
[LE:343] [RE:852] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000996_23634813_c3_355	2618	6390	771	256	970	1.2e-97

Description

sp:[LN:LACR_STAAU] [AC:P16644] [GN:LACR] [OR:STAPHYLOCOCCUS AUREUS]
[DE:LACTOSE PHOSPHOTRANSFERASE SYSTEM REPRESSOR] [SP:P16644] [DB:swissprot]
>pir:[LN:A44506] [AC:A44506] [PN:lactose operon repressor lacR]
[OR:Staphylococcus aureus] [DB:pir2] >gp:[GI:g153035] [LN:STALACR]
[AC:M32103] [PN:lacR repressor] [OR:Staphylococcus aureus]
[SR:Staphylococcus aureus (strain 8325-4) DNA] [DB:genpept-bct1]
[DE:Staphylococcus aureus lac repressor (lacR) gene, complete cds andlacA
repressor (lacA), partial cds.] [LE:1058] [RE:1813] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000996_23642761_f1_22	2619	6391	228	75	80	0.0064

Description

gp:[GI:d1000903:g220579] [LN:MUSPRIMP] [AC:D00570:J00614] [OR:Mus musculus]
[SR:Mus musculus male cDNA to mRNA] [DB:genpept-rod] [DE:Mus musculus mRNA
for ORFs (putative primordial protein), completecds.] [NT:open reading frame
(196 AA)] [LE:584] [RE:1174] [DI:direct] >gp:[GI:d1000903:g220579]
[LN:MUSPRIMP] [AC:D00570:J00614] [OR:Mus musculus] [SR:Mus musculus male
cDNA to mRNA] [DB:genpept] [DE:Mus musculus mRNA for ORFs (putative
primordial protein), completecds.] [NT:open reading frame (196 AA)] [LE:584]
[RE:1174] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000996_23683375_c3_356	2620	6392	507	168	583	1.2e-56

Description

sp:[LN:LACA_STRMU] [AC:P26423] [GN:LACA] [OR:STREPTOCOCCUS MUTANS]
[EC:5.3.1.26] [DE:GALACTOSE-6-PHOSPHATE ISOMERASE LACA SUBUNIT,] [SP:P26423]
[DB:swissprot] >pir:[LN:C43258] [AC:C43258:S27701] [PN:galactoside
O-acetyltransferase,] [GN:lacA] [OR:Streptococcus mutans] [EC:2.3.1.18]
[DB:pir2] >gp:[GI:g153673] [LN:STRLACOP] [AC:M80797] [PN:galactosidase
acetyltransferase] [GN:lacA] [OR:Streptococcus mutans] [SR:Streptococcus
mutans (strain PS14) DNA] [DB:genpept-bct1] [EC:2.3.1.18] [DE:Streptococcus
mutans lac operon.] [LE:1534] [RE:1962] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000996_2379658_f2_82	2621	6393	225	74		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000996_23882135_c2_303	2622	6394	873	290	665	2.5e-65

Description

sp:[LN:YBXA_BACSU] [AC:P40735] [GN:YBXA] [OR:BACILLUS SUBTILIS]
[DE:HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YBXA] [SP:P40735]
[DB:swissprot] >pir:[LN:E69751] [AC:E69751:G32307] [PN:ABC transporter
(ATP-binding protein) homolog ybxA] [GN:ybxA] [CL:ATP-binding cassette
homology] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1182078:g2632412]
[LN:BSUB0001] [AC:Z99104:AL009126] [GN:ybxA] [FN:unknown] [OR:Bacillus
subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 1
of 21): from 1 to213080.] [NT:alternate gene name: ybaD; similar to ABC]
[SP:P40735] [LE:150441] [RE:151286] [DI:direct] >gp:[GI:d1011641:g1644202]
[LN:D64126] [AC:D64126] [PN:unknown] [GN:orf4] [OR:Bacillus subtilis]
[SR:Bacillus subtilis (strain:168) DNA] [DB:genpept-bct1] [DE:Bacillus
subtilis genes for ribosomal proteins L13 and S9, putativecell wall
hydrolase Cwld, gerD protein, 16S ribosomal RNA and 23Sribosomal RNA.]
[LE:1] [RE:846] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000996_23944052_f1_36	2623	6395	150	49		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000996_24223787_c1_258	2624	6396	156	51	221	2.8e-18

Description

sp:[LN:RPOA_BACSU] [AC:P20429] [GN:RPOA] [OR:BACILLUS SUBTILIS] [EC:2.7.7.6] [DE:ALPHA CHAIN) (RNA POLYMERASE ALPHA SUBUNIT)] [SP:P20429] [DB:swissprot] >pir:[LN:E32307] [AC:E32307:C24972:E69698] [PN:DNA-directed RNA polymerase, alpha chain rpoA:transcriptase alpha chain] [GN:rpoA] [CL:DNA-directed RNA polymerase alpha chain] [OR:Bacillus subtilis] [EC:2.7.7.6] [DB:pir2] >gp:[GI:g142463] [LN:BACALPHA] [AC:M26414] [PN:RNA polymerase alpha-core-subunit] [GN:rpoA] [OR:Bacillus subtilis] [SR:Bacillus subtilis DNA] [DB:genpept-bct1] [DE:B.subtilis initiation factor 1, ribosomal proteins B, S13, S11, L17and RNA polymerase alpha core protein genes, complete cds.] [LE:1581] [RE:2525] [DI:direct] >gp:[GI:g1044991] [LN:BACRPLP] [AC:L47971] [PN:RNA polymerase alpha-core-subunit] [GN:rpoA] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis ribosomal protein (rplPNXEFROQ, rpmCDJ,rpsQNHEMK) genes, integral membrane protein (secY) gene, adenylatekinase (adk) gene, methionine aminopeptidase (map) gene,inititation factor 1 (infA) gene, RNA polymerase alpha (rpoA) gene.] [LE:9155] [RE:10099] [DI:direct] >gp:[GI:e1182076:g2632410] [LN:BSUB0001] [AC:Z99104:AL009126] [PN:RNA polymerase (alpha subunit)] [GN:rpoA] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:2.7.7.6] [DE:Bacillus subtilis complete genome (section 1 of 21): from 1 to213080.] [SP:P20429] [LE:148929] [RE:149873] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000996_24244012_c3_374	2625	6397	546	181	280	1.6e-24

Description

pir:[LN:C70048] [AC:C70048] [PN:conserved hypothetical protein yvsG] [GN:yvsG] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1249789:g2832793] [LN:BS43KBDNA] [AC:AJ223978] [PN:YvsG protein] [GN:yvsG] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis 42.7kB DNA fragment from yvsA to yvqA.] [LE:5971] [RE:6453] [DI:complement] >gp:[GI:e1186023:g2635848] [LN:BSUB0018] [AC:Z99121:AL009126] [GN:yvsG] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.] [NT:similar to hypothetical proteins] [LE:21284] [RE:21766] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000996_24252318_c1_256	2626	6398	126	41	191	4.3e-15

Description

sp:[LN:RL36_BACST] [AC:P07841] [GN:RPMJ] [OR:BACILLUS STEAROTHERMOPHILUS]
[DE:(BL38)] [SP:P07841] [DB:swissprot] >pir:[LN:R5BS36] [AC:S08566:S59066]
[PN:ribosomal protein L36:ribosomal protein BL38:ribosomal protein II]
[CL:Escherichia coli ribosomal protein L36] [OR:Bacillus stearothermophilus]
[DB:pir1]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000996_24328927_f1_39	2627	6399	201	66		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000996_24337750_c2_312	2628	6400	981	326	1524	2.4e-156

Description

sp:[LN:LACD_STAAU] [AC:P11100] [GN:LACD] [OR:STAPHYLOCOCCUS AUREUS]
[EC:4.1.2.40] [DE:ALDOLASE] (D-TAGATOSE-1,6-BISPHOSPHATE ALDOLASE)]
[SP:P11100] [DB:swissprot] >pir:[LN:S04359] [AC:S04359] [PN:lacD protein]
[GN:lacD] [OR:Staphylococcus aureus] [DB:pir2] >gp:[GI:g46606] [LN:SALACCD]
[AC:X14827] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:Staphylococcus
aureus lacC and lacD genes.] [NT:lacD polypeptide (AA 1-326)] [SP:P11100]
[LE:991] [RE:1971] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000996_24339718_c2_335	2629	6401	483	160	93	0.033

Description

gp:[GI:e246715:g1617437] [LN:SGCOM7865] [AC:X98110] [PN:pheromone receptor]
[GN:comD2] [OR:Streptococcus gordonii] [DB:genpept-bct1] [DE:S.gordonii
tRNA-Arg, comC2, comD2 & comE2 genes.] [NT:histidine kinase] [LE:656]
[RE:2014] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000996_24402217_c3_350	2632	6404	405	134	560	3.4e-54

Description

sp:[LN:RS11_BACSU] [AC:P04969] [GN:RPSK] [OR:BACILLUS SUBTILIS] [DE:30S RIBOSOMAL PROTEIN S11 (BS11)] [SP:P04969] [DB:swissprot] >pir:[LN:R3BSS1] [AC:D32307:B24972:S11361:B69700] [PN:ribosomal protein S11:ribosomal protein BS11] [GN:rpsK] [CL:Escherichia coli ribosomal protein S11] [OR:Bacillus subtilis] [DB:pir1] >gp:[GI:g142462] [LN:BACALPHA] [AC:M26414] [PN:ribosomal protein S11] [GN:rpsK] [OR:Bacillus subtilis] [SR:Bacillus subtilis DNA] [DB:genpept-bct1] [DE:B.subtilis initiation factor 1, ribosomal proteins B, S13, S11, L17and RNA polymerase alpha core protein genes, complete cds.] [LE:1009] [RE:1404] [DI:direct] >gp:[GI:g1044990] [LN:BACRPLP] [AC:L47971] [PN:ribosomal protein S11] [GN:rpsK] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis ribosomal protein (rplPNXEFRQ, rpmCDJ,rpsQNHEMK) genes, integral membrane protein (secY) gene, adenylatekinase (adk) gene, methionine aminopeptidase (map) gene,inititation factor 1 (infA) gene, RNA polymerase alpha (rpoA) gene.] [LE:8583] [RE:8978] [DI:direct] >gp:[GI:g143451] [LN:BACRPOA] [AC:M13957] [OR:Bacillus subtilis] [SR:B.subtilis (strain 168 Marburg) DNA clone lambda-gt11-11-1] [DB:genpept-bct1] [DE:B.subtilis DNA sequence of the rpsM-rpoA interval.] [NT:ribosomal protein S11] [LE:133] [RE:528] [DI:direct] >gp:[GI:e1182075:g2632409] [LN:BSUB0001] [AC:Z99104:AL009126] [PN:ribosomal protein S11 (BS11)] [GN:rpsK] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 1 of 21): from 1 to213080.] [SP:P04969] [LE:148357] [RE:148752] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000996_24641927_c1_273	2633	6405	1380	459	978	1.7e-98

Description

sp:[LN:YKAA_BACFI] [AC:P30267] [OR:BACILLUS FIRMUS] [DE:HYPOTHETICAL 50.9 KD PROTEIN IN KATA 3'REGION (ORF A)] [SP:P30267] [DB:swissprot] >pir:[LN:S27491] [AC:S27491] [PN:hypothetical protein A] [OR:Bacillus firmus] [DB:pir2] >gp:[GI:g143121] [LN:BACKATA2] [AC:L02548:M74194] [OR:Bacillus firmus] [SR:Bacillus firmus DNA] [DB:genpept-bct1] [DE:B.firmus ORF A and ORF B, complete cds.] [NT:ORF A; putative] [LE:225] [RE:1616] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000996_24648312_f1_48	2634	6406	747	248	905	9.3e-91

Description

gp:[GI:g845686] [LN:STALACR] [AC:M32103] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus (strain 8325-4) DNA] [DB:genpept-bct1] [DE:Staphylococcus aureus lac repressor (lacR) gene, complete cds andlacA repressor (lacA), partial cds.] [NT:ORF-27] [LE:76] [RE:807] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000996_24744040_c1_270	2635	6407	1065	354	361	4.1e-33

Description

gp:[GI:g4982168] [LN:AE001804] [AC:AE001804:AE000512] [PN:hypothetical protein] [GN:TM1597] [OR:Thermotoga maritima] [DB:genpept-bct2] [DE:Thermotoga maritima section 116 of 136 of the complete genome.] [NT:similar to percent identity: 0.00; identified by] [LE:7299] [RE:8363] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000996_24806662_c1_248	2636	6408	237	78	252	1.5e-21

Description

sp:[LN:RL29_BACSU] [AC:P12873] [GN:RPMC] [OR:BACILLUS SUBTILIS] [DE:50S RIBOSOMAL PROTEIN L29] [SP:P12873] [DB:swissprot] >pir:[LN:R5BS2L] [AC:S05990:E69697] [PN:ribosomal protein L29] [GN:rpmC] [CL:Escherichia coli ribosomal protein L29] [OR:Bacillus subtilis] [DB:pir1] >gp:[GI:g1044972] [LN:BACRPLP] [AC:L47971] [PN:ribosomal protein L29] [GN:rpmC] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis ribosomal protein (rplPNXEFROQ, rpmCDJ, rpsQNHEMK) genes, integral membrane protein (secY) gene, adenylatekinase (adk) gene, methionine aminopeptidase (map) gene, initiation factor 1 (infA) gene, RNA polymerase alpha (rpoA) gene.] [LE:142] [RE:342] [DI:direct] >gp:[GI:g40148] [LN:BSSPC] [AC:X15664] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B. subtilis S10/spc operon rpmC, rpsQ, rplN, rplX, rplE, rpsN genes.] [NT:L29 protein (AA 1-66)] [SP:P12873] [LE:313] [RE:513] [DI:direct] >gp:[GI:e1182057:g2632391] [LN:BSUB0001] [AC:Z99104:AL009126] [PN:ribosomal protein L29] [GN:rpmC] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 1 of 21): from 1 to213080.] [SP:P12873] [LE:139922] [RE:140122] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000996_24855303_c3_368	2637	6409	1047	348	784	6.2e-78

Description

pir:[LN:C69812] [AC:C69812] [PN:ferrichrome ABC transporter (permease) homolog yfmD] [GN:yfmD] [CL:ferrichrome ABC transporter] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1182741:g2633075] [LN:BSUB0005] [AC:Z99108:AL009126] [GN:yfmD] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.] [NT:similar to ferrichrome ABC transporter (permease)] [LE:21402] [RE:22403] [DI:complement] >gp:[GI:d1023181:g2443247] [LN:D86417] [AC:D86417] [PN:YfmD] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:AC327) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis 35.7 kb genomic DNA, 70-73 degree region, complete cds.] [LE:26118] [RE:27119] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000996_25908568_c1_253	2638	6410	453	150	706	1.1e-69

Description

sp:[LN:RL15_STAAU] [AC:O06445] [GN:RPLO] [OR:STAPHYLOCOCCUS AUREUS] [DE:50S RIBOSOMAL PROTEIN L15] [SP:O06445] [DB:swissprot] >gp:[GI:g2078381] [LN:SAU96620] [AC:U96620] [PN:ribosomal protein L15] [GN:L15] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:Staphylococcus aureus NCTC 8325 ribosomal protein L30 (L30), ribosomal protein L15 (L15) and SecY (secY) genes, complete cds.] [LE:261] [RE:701] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000996_26205151_f2_85	2639	6411	156	51	123	6.9e-08

Description

pir:[LN:B71245] [AC:B71245] [PN:hypothetical protein PH0220] [GN:PH0220] [OR:Pyrococcus horikoshii] [DB:pir2] >gp:[GI:d1030232:g3256606] [LN:AP0000001] [AC:AP000001:AB009465:AB009464:AB009466:AB009467:AB009468:AB009469] [PN:171aa long hypothetical protein] [GN:PH0220] [OR:Pyrococcus horikoshii] [SR:Pyrococcus horikoshii (strain:OT3) DNA] [DB:genpept-bct1] [DE:Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt. position (1/7).] [LE:192864] [RE:193379] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000996_26360036_c3_345	2640	6412	387	128	429	2.6e-40

Description

sp:[LN:RL18_BACSU] [AC:P46899:P70969] [GN:RPLR] [OR:BACILLUS SUBTILIS] [DE:50S RIBOSOMAL PROTEIN L18] [SP:P46899:P70969] [DB:swissprot] >gp:[GI:g1044980] [LN:BACRPLP] [AC:L47971] [PN:ribosomal protein L18] [GN:rplR] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis ribosomal protein (rplPNXEFROQ, rpmCDJ, rpsQNHEMK) genes, integral membrane protein (secY) gene, adenylatekinase (adk) gene, methionine aminopeptidase (map) gene, initiation factor 1 (infA) gene, RNA polymerase alpha (rpoA) gene.] [LE:3198] [RE:3560] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000996_26773450_c1_249	2641	6413	285	94	380	4.0e-35

Description

sp:[LN:RS17_BACST] [AC:P23828] [GN:RPSQ] [OR:BACILLUS STEAROTHERMOPHILUS] [DE:30S RIBOSOMAL PROTEIN S17] [SP:P23828] [DB:swissprot] >pir:[LN:S17865] [AC:S17865:S59056] [PN:ribosomal protein S17] [GN:rps17] [CL:Escherichia coli ribosomal protein S17] [OR:Bacillus stearothermophilus] [DB:pir2]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000996_26776678_c2_290	2642	6414	372	123	431	1.6e-40

Description

sp:[LN:RL22_BACST] [AC:P23311] [GN:RPLV] [OR:BACILLUS STEAROTHERMOPHILUS]
[DE:50S RIBOSOMAL PROTEIN L22] [SP:P23311] [DB:swissprot] >pir:[LN:S10612]
[AC:S10612] [PN:ribosomal protein L22] [CL:Escherichia coli ribosomal
protein L22] [OR:Bacillus stearothermophilus] [DB:pir2] >gp:[GI:g40107]
[LN:BSRPLS] [AC:X54994] [PN:ribosomal protein L22] [OR:Bacillus
stearothermophilus] [DB:genpept-bct1] [DE:B.stearothermophilus gene for
ribosomal proteins L2, S19, L22, S3,and L16.] [SP:P23311] [LE:923] [RE:1264]
[DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000996_2735801_c1_269	2643	6415	1848	615	274	1.3e-20

Description

sp:[LN:Y4XN_RHISN] [AC:P55706] [GN:Y4XN] [OR:RHIZOBIUM SP] [SR:NGR234,]
[DE:HYPOTHETICAL 71.0 KD PROTEIN Y4XN] [SP:P55706] [DB:swissprot]
>gp:[GI:g2182722] [LN:AE000106] [AC:AE000106:U00090] [PN:Y4xN] [GN:y4xN]
[OR:Rhizobium sp. NGR234] [DB:genpept-bct2] [DE:Rhizobium sp. NGR234 plasmid
pNGR234a, section 43 of 46 of thecomplete plasmid sequence.]
[NT:hypothetical 71 kd protein; similar to Escherichia] [LE:6573] [RE:8459]
[DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000996_277312_c1_276	2644	6416	1353	450	452	9.4e-43

Description

gp:[GI:e1391039:g4467970] [LN:MXEGLBG] [AC:X76640] [PN:hypothetical protein]
[FN:transmembrane protein, putative] [OR:Myxococcus xanthus]
[DB:genpept-bct1] [DE:Myxococcus xanthus ceaA gene and ORFX.] [NT:ORFX]
[LE:669] [RE:2192] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000996_285808_f2_84	2645	6417	225	74		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000996_29314381_f2_151	2646	6418	138	45	79	0.0032

Description

pir:[LN:QOECR3] [AC:A04439] [PN:hypothetical protein E-116] [OR:Escherichia coli] [DB:pir1] [MP:72 min]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000996_29328312_c2_289	2647	6419	339	112	431	1.6e-40

Description

gp:[GI:g4927744] [LN:AF126059] [AC:AF126059] [PN:RpS19] [GN:rpsS]
[OR:Streptococcus pneumoniae] [DB:genpept-bct2] [DE:Streptococcus pneumoniae isolate R6 ribosomal protein operon,partial sequence.] [NT:30S ribosomal protein S19] [LE:934] [RE:1215] [DI:direct] >gp:[GI:g4927753] [LN:AF126060] [AC:AF126060] [PN:RpS19] [GN:rpsS] [OR:Streptococcus pneumoniae] [DB:genpept-bct2] [DE:Streptococcus pneumoniae isolate ZR1 ribosomal protein operon,partial sequence.] [NT:30S ribosomal protein S19] [LE:934] [RE:1215] [DI:direct] >gp:[GI:g4927762] [LN:AF126061] [AC:AF126061] [PN:RpS19] [GN:rpsS] [OR:Streptococcus pneumoniae] [DB:genpept-bct2] [DE:Streptococcus pneumoniae isolate SP#5 ribosomal protein operon,partial sequence.] [NT:30S ribosomal protein S19] [LE:934] [RE:1215] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000996_29562550_f3_218	2648	6420	156	51		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000996_30742165_c3_347	2649	6421	1323	440	1919	3.3e-198

Description

sp:[LN:SECY_STACA] [AC:Q05217] [GN:SECY] [OR:STAPHYLOCOCCUS CARNOSUS]
[DE:PREPROTEIN TRANSLOCASE SECY SUBUNIT] [SP:Q05217] [DB:swissprot]
>pir:[LN:S30115] [AC:S30115] [PN:preprotein translocase secY] [GN:secY]
[CL:preprotein translocase secY] [OR:Staphylococcus carnosus] [DB:pir2]
>gp:[GI:g49189] [LN:SCSECY] [AC:X70086:S47913:X68981] [GN:secY]
[OR:Staphylococcus carnosus] [DB:genpept-bct1] [DE:S.carnosus secY gene.]
[SP:Q05217] [LE:223] [RE:1515] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000996_3131677_f2_99	2650	6422	123	40		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000996_31377318_c1_246	2651	6423	291	96	297	2.5e-26

Description

sp:[LN:RL23_BACSU] [AC:P42924] [GN:RPLW] [OR:BACILLUS SUBTILIS] [DE:50S RIBOSOMAL PROTEIN L23] [SP:P42924] [DB:swissprot] >pir:[LN:A69697] [AC:A69697] [PN:ribosomal protein L23] [GN:rplW] [CL:Escherichia coli ribosomal protein L23] [OR:Bacillus subtilis] [DB:pir1] >gp:[GI:d1009466:g786155] [LN:BACRPL1] [AC:D50302] [PN:Ribosomal Protein L23] [GN:rplW] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:168) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis genes for ribosomal proteins L13, L4, L23, L2, S19, L22, S3 and L16, partial and complete cds.] [LE:1140] [RE:1427] [DI:direct] >gp:[GI:e1182051:g2632385] [LN:BSUB0001] [AC:Z99104:AL009126] [PN:ribosomal protein L23] [GN:rplW] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 1 of 21): from 1 to213080.] [SP:P42924] [LE:136990] [RE:137277] [DI:direct] >gp:[GI:g1165305] [LN:BSU43929] [AC:U43929] [PN:L23] [GN:rplW] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis ribosomal protein gene cluster, rpsJ, rplC, rplD, rplW, rplB, rpsS, rplV and rpsC genes, complete cds, and rplP gene, partial cds.] [NT:ribosomal protein] [LE:1947] [RE:2234] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000996_3304562_c3_359	2652	6424	366	121	411	2.1e-38

Description

sp:[LN:PTLA_STAAU] [AC:P02909] [GN:LACF] [OR:STAPHYLOCOCCUS AUREUS] [EC:2.7.1.69] [DE:(EC 2.7.1.69) (EIII-LAC)] [SP:P02909] [DB:swissprot] >gp:[GI:g153037] [LN:STALACS] [AC:J03479:M17729] [OR:Staphylococcus aureus] [SR:S.aureus (strain 8325-4) DNA, clone pFB34] [DB:genpept-bct1] [DE:S.aureus enzyme III-lac (lacF), enzyme II-lac (lacE), andphospho-beta-galactosidase (lacG) genes, complete cds.] [NT:enzyme III-lac (lacF)] [LE:102] [RE:413] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000996_33437802_c2_299	2653	6425	669	222	772	1.2e-76

Description

sp:[LN:KAD_BACSU] [AC:P16304] [GN:ADK] [OR:BACILLUS SUBTILIS] [EC:2.7.4.3]
 [DE:(SUPEROXIDE-INDUCIBLE PROTEIN 16) (SOI16)] [SP:P16304] [DB:swissprot]
 >pir:[LN:JS0492] [AC:JS0492:S12684:S08630:E69583] [PN:adenylate
 kinase, :ATP-AMP transphosphorylase] [GN:adk] [CL:adenylate kinase]
 [OR:Bacillus subtilis] [EC:2.7.4.3] [DB:pir2] >gp:[GI:g1044985] [LN:BACRPLP]
 [AC:L47971] [PN:adenylate kinase] [GN:adk] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:Bacillus subtilis ribosomal protein (rplPNXEFRQ,
 rpmCDJ,rpsQNHEMK) genes, integral membrane protein (secY) gene,
 adenylatekinase (adk) gene, methionine aminopeptidase (map) gene,inititation
 factor 1 (infA) gene, RNA polymerase alpha (rpoA) gene.] [LE:6101] [RE:6754]
 [DI:direct] >gp:[GI:d1000951:g216340] [LN:BACSECY] [AC:D00619] [PN:adenylate
 kinase] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:207-21) DNA]
 [DB:genpept-bct1] [DE:Bacillus subtilis genes for ribosomal proteins, SecY,
 adenylatekinase and methionine amino peptidase, complete cds.] [LE:2055]
 [RE:2708] [DI:direct] >gp:[GI:e1182070:g2632404] [LN:BSUB0001]
 [AC:Z99104:AL009126] [PN:adenylate kinase] [GN:adk] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [EC:2.7.4.3] [DE:Bacillus subtilis complete genome
 (section 1 of 21): from 1 to213080.] [SP:P16304] [LE:145875] [RE:146528]
 [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000996_33463542_c2_337	2654	6426	180	59		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000996_34017517_c2_304	2655	6427	828	275	714	1.6e-70

Description

pir:[LN:F69742] [AC:F69742] [PN:hypothetical protein ybaF] [GN:ybaF]
 [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1182080:g2632414] [LN:BSUB0001]
 [AC:Z99104:AL009126] [GN:ybaF] [FN:unknown] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 1 of 21):
 from 1 to213080.] [LE:152128] [RE:152925] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000996_34188213_c2_295	2656	6428	423	140	579	3.3e-56

Description

gp:[GI:g1044978] [LN:BACRPLP] [AC:L47971] [PN:ribosomal protein S8]
[GN:rpsH] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
ribosomal protein (rplPNXEFRQ, rpmCDJ, rpsQNHEMK) genes, integral membrane
protein (secY) gene, adenylatekinase (adk) gene, methionine aminopeptidase
(map) gene, initiation factor 1 (infa) gene, RNA polymerase alpha (rpoA)
gene.] [LE:2198] [RE:2596] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000996_34406562_c1_259	2657	6429	867	288	644	4.2e-63

Description

pir:[LN:E69742] [AC:E69742] [PN:ABC transporter (ATP-binding protein)
homolog ybaE] [GN:ybaE] [CL:ATP-binding cassette homology] [OR:Bacillus
subtilis] [DB:pir2] >gp:[GI:e1182079:g2632413] [LN:BSUB0001]
[AC:Z99104:AL009126] [GN:ybaE] [FN:unknown] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 1 of 21):
from 1 to213080.] [NT:similar to ABC transporter (ATP-binding protein)]
[LE:151301] [RE:152131] [DI:direct] >gp:[GI:d1011642:g1644203] [LN:D64126]
[AC:D64126] [PN:unknown] [GN:orf5] [OR:Bacillus subtilis] [SR:Bacillus
subtilis (strain:168) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis genes for
ribosomal proteins L13 and S9, putativecell wall hydrolase CwID, gerD
protein, 16S ribosomal RNA and 23Sribosomal RNA.] [LE:861] [RE:1691]
[DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000996_34557262_c3_384	2658	6430	135	44		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000996_34647177_c2_296	2659	6431	558	185	638	1.8e-62

Description

gp:[GI:d1039022:g4512419] [LN:AB017508] [AC:AB017508] [GN:rplF] [OR:Bacillus
halodurans] [SR:Bacillus halodurans (strain:C-125) DNA] [DB:genpept-bct1]
[DE:Bacillus halodurans C-125 genomic DNA, 32 kb fragment, completecds.]
[NT:rplF homologue (identity of 78% to B. subtilis)] [LE:20357] [RE:20893]
[DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000996_36226575_c1_251	2663	6435	558	185	766	5.0e-76

Description

sp:[LN:RL5_BACSU] [AC:P12877] [GN:RPLE] [OR:BACILLUS SUBTILIS] [DE:50S RIBOSOMAL PROTEIN L5 (BL6)] [SP:P12877] [DB:swissprot] >pir:[LN:R5BS5] [AC:S05994:A69695] [PN:ribosomal protein L5:BL6] [GN:rplE] [CL:Escherichia coli ribosomal protein L5] [OR:Bacillus subtilis] [DB:pir1]
>gp:[GI:g1044976] [LN:BACRPLP] [AC:L47971] [PN:ribosomal protein L5] [GN:rplE] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis ribosomal protein (rplPNXEFROQ, rpmCDJ,rpsQNHMK) genes, integral membrane protein (secY) gene, adenylatekinase (adk) gene, methionine aminopeptidase (map) gene,inititation factor 1 (infA) gene, RNA polymerase alpha (rpoA) gene.] [LE:1419] [RE:1958] [DI:direct] >gp:[GI:g40152] [LN:BSSPC] [AC:X15664] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis S10/spc operon rpmC, rpsQ, rplN, rplX, rplE, rpsN genes.] [NT:L5 protein (AA 1-179)] [SP:P12877] [LE:1584] [RE:2123] [DI:direct] >gp:[GI:e1182061:g2632395] [LN:BSUB0001] [AC:Z99104:AL009126] [PN:ribosomal protein L5 (BL6)] [GN:rplE] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 1 of 21): from 1 to213080.] [SP:P12877] [LE:141193] [RE:141732] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000996_4062510_f3_217	2664	6436	168	55		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000996_4100327_f3_181	2665	6437	360	119	133	6.0e-09

Description

pir:[LN:D69798] [AC:D69798] [PN:hypothetical protein yetG] [GN:yetG] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1182694:g2633028] [LN:BSUB0004] [AC:Z99107:AL009126] [GN:yetG] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.] [LE:183921] [RE:184298] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000996_4165677_c2_305	2666	6438	807	268	544	1.7e-52

Description

sp:[LN:TRUA_BACSU] [AC:P70973] [GN:TRUA] [OR:BACILLUS SUBTILIS]
[EC:4.2.1.70] [DE:I] (PSEUDOURIDINE SYNTHASE I) (URACIL HYDROLYASE)]
[SP:P70973] [DB:swissprot] >pir:[LN:F69726] [AC:F69726] [PN:pseudouridylate
synthase I truA] [GN:truA] [CL:tRNA-pseudouridine synthase I] [OR:Bacillus
subtilis] [DB:pir2] >gp:[GI:e1182081:g2632415] [LN:BSUB0001]
[AC:Z99104:AL009126] [PN:pseudouridylate synthase I] [GN:truA] [OR:Bacillus
subtilis] [DB:genpept-bct1] [EC:4.2.1.70] [DE:Bacillus subtilis complete
genome (section 1 of 21): from 1 to213080.] [NT:alternate gene name: ybaH]
[SP:P70973] [LE:152935] [RE:153678] [DI:direct] >gp:[GI:d1011645:g1644206]
[LN:D64126] [AC:D64126] [PN:unknown] [GN:orf8] [OR:Bacillus subtilis]
[SR:Bacillus subtilis (strain:168) DNA] [DB:genpept-bct1] [DE:Bacillus
subtilis genes for ribosomal proteins L13 and S9, putativecell wall
hydrolase Cwld, gerD protein, 16S ribosomal RNA and 23Sribosomal RNA.]
[LE:2496] [RE:3239] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000996_4305287_f3_211	2667	6439	123	40		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000996_4564036_c3_363	2668	6440	1044	347	898	5.2e-90

Description

pir:[LN:A69813] [AC:A69813] [PN:quinone oxidoreductase homolog yfmJ]
[GN:yfmJ] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1182735:g2633069]
[LN:BSUB0005] [AC:Z99108:AL009126] [GN:yfmJ] [FN:unknown] [OR:Bacillus
subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 5
of 21): from 802821 to1011250.] [NT:similar to quinone oxidoreductase]
[LE:14498] [RE:15517] [DI:complement] >gp:[GI:d1023187:g2443253] [LN:D86417]
[AC:D86417] [PN:YfmJ] [OR:Bacillus subtilis] [SR:Bacillus subtilis
(strain:AC327) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis 35.7 kb genomic
DNA, 70-73 degree region,complete cds.] [LE:33004] [RE:34023] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000996_4694030_c3_367	2669	6441	1236	411	362	3.2e-33

Description

gp:[GI:g5354197] [LN:AF157493] [AC:AF157493] [PN:putative transporter]
[GN:ditE] [OR:Zymomonas mobilis] [DB:genpept] [DE:Zymomonas mobilis ZM4
fosmid clone 42D7, complete sequence.] [LE:17549] [RE:18844] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000996_4697262_c2_310	2670	6442	540	179	806	2.9e-80

Description

pir:[LN:D43258] [AC:D43258] [PN:galactose-6-phosphate isomerase subunit
LacB] [OR:Streptococcus mutans] [DB:pir2]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000996_4714817_c2_315	2671	6443	879	292	200	1.0e-14

Description

gp:[GI:g4206189] [LN:LLU60828] [AC:U60828] [PN:unknown] [OR:Lactococcus
lactis] [DB:genpept-bct2] [DE:Lactococcus lactis galactose-lactose operon,
complete sequence.] [NT:orfx] [LE:12631] [RE:13554] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000996_4886592_c3_341	2672	6444	450	149	614	6.4e-60

Description

sp:[LN:RL16_BACSU] [AC:P14577] [GN:RPLP] [OR:BACILLUS SUBTILIS] [DE:50S
RIBOSOMAL PROTEIN L16] [SP:P14577] [DB:swissprot] >pir:[LN:B69696]
[AC:B69696:S05989] [PN:ribosomal protein L16 (rplP)] [GN:rplP]
[CL:Escherichia coli ribosomal protein L16] [OR:Bacillus subtilis] [DB:pir2]
>gp:[GI:e1182056:g2632390] [LN:BSUB0001] [AC:Z99104:AL009126] [PN:ribosomal
protein L16] [GN:rplP] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus
subtilis complete genome (section 1 of 21): from 1 to213080.] [LE:139498]
[RE:139932] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000996_4897202_c1_257	2673	6445	768	255	996	2.1e-100

Description

sp:[LN:RPOA_BACS5] [AC:O50634] [GN:RPOA] [OR:BACILLUS SP] [SR:C-125,]
[EC:2.7.7.6] [DE:ALPHA CHAIN) (RNA POLYMERASE ALPHA SUBUNIT)] [SP:O50634]
[DB:swissprot] >gp:[GI:d1025104:g2760185] [LN:AB010082] [AC:AB010082]
[PN:RNA polymerase alpha subunit] [GN:rpoA] [OR:Bacillus halodurans]
[SR:Bacillus halodurans (strain:C-125) DNA] [DB:genpept-bct1] [DE:Bacillus
halodurans C-125 gene for initiation factor IF-I, RNApolymerase alpha
subunit and ribosomal proteins, partial andcomplete cds.] [LE:1701]
[RE:2645] [DI:direct] >gp:[GI:d1039034:g4512431] [LN:AB017508] [AC:AB017508]
[GN:rpoA] [OR:Bacillus halodurans] [SR:Bacillus halodurans (strain:C-125)
DNA] [DB:genpept-bct1] [DE:Bacillus halodurans C-125 genomic DNA, 32 kb
fragment, completecds.] [NT:rpoA homologue (identity of 85% to B. subtilis
)] [LE:26934] [RE:27878] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000996_4897253_f3_189	2674	6446	129	42		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000996_4901712_c1_261	2675	6447	408	135	496	2.0e-47

Description

pir:[LN:H69699] [AC:H69699:S11359] [PN:ribosomal protein S9
(rpsI):ribosomal protein BS10] [GN:rpsI] [CL:Escherichia coli ribosomal
protein S9] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1182083:g2632417]
[LN:BSUB0001] [AC:Z99104:AL009126] [PN:ribosomal protein S9] [GN:rpsI]
[OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete
genome (section 1 of 21): from 1 to213080.] [SP:P21470] [LE:154299]
[RE:154691] [DI:direct] >gp:[GI:d1011647:g1644208] [LN:D64126] [AC:D64126]
[PN:ribosomal protein S9] [GN:rpsI] [OR:Bacillus subtilis] [SR:Bacillus
subtilis (strain:168) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis genes for
ribosomal proteins L13 and S9, putativecell wall hydrolase CwID, gerD
protein, 16S ribosomal RNA and 23Sribosomal RNA.] [LE:3860] [RE:4252]
[DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000996_5110637_c2_306	2676	6448	129	42		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000996_5189012_f1_55	2677	6449	168	55		
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Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000996_55437_c2_314	2678	6450	1428	475	2439	2.6e-253
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Description

sp:[LN:LACG_STAAU] [AC:P11175] [GN:LACG] [OR:STAPHYLOCOCCUS AUREUS]
[EC:3.2.1.85] [DE:GALACTOXYDROLASE) (PGALASE) (P-BETA-GAL) (PBG)]
[SP:P11175] [DB:swissprot] >pir:[LN:A27233] [AC:A27233]
[PN:beta-galactosidase,:lactase] [CL:Agrobacterium beta-glucosidase]
[OR:Staphylococcus aureus] [EC:3.2.1.23] [DB:pir2] >gp:[GI:g153039]
[LN:STALACS] [AC:J03479:M17729] [OR:Staphylococcus aureus] [SR:S.aureus
(strain 8325-4) DNA, clone pFB34] [DB:genpept-bct1] [DE:S.aureus enzyme
III-lac (lacF), enzyme II-lac (lacE), andphospho-beta-galactosidase (lacG)
genes, complete cds.] [NT:phospho-beta-galactosidase (lacG)] [LE:2149]
[RE:3561] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000996_6854675_f1_20	2679	6451	279	92	119	1.8e-07
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Description

pir:[LN:A69895] [AC:A69895] [PN:hypothetical protein ynzG] [GN:ynzG]
[CL:hypothetical protein yofF] [OR:Bacillus subtilis] [DB:pir2]
>gp:[GI:e1183408:g2634133] [LN:BSUB0010] [AC:Z99113:AL009126] [GN:ynzG]
[FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
complete genome (section 10 of 21): from 1781201to 2014980.] [LE:99142]
[RE:99393] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000996_797308_f2_112	2680	6452	189	62		
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Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000996_812840_c1_260	2681	6453	144	47		
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Description

NO-HIT

AI7503000996_9771907_c2_334	2682	6454	165	54
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NO-HIT

AI7503000997_10406642_f1_38	2683	6455	342	113	165	2.8e-12
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sp:[LN:NARQ_BACSU] [AC:P39756] [GN:NARQ:NARAA] [OR:BACILLUS SUBTILIS]
[DE:NARQ PROTEIN] [SP:P39756] [DB:swissprot] >pir:[LN:B69665] [AC:B69665 ]
[PN:required for formate dehydrogenase activity narQ] [GN:narQ ]
[OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e276834:g1648855] [LN:BSATPC]
[AC:Z81356] [PN:unknown] [GN:narQ] [OR:Bacillus subtilis] [DB:genpept-bct1]
[DE:B.subtilis atpC gene.] [SP:P39756] [LE:7048] [RE:7836] [DI:direct]
>gp:[GI:g580895] [LN:BSNARAAB] [AC:Z35277] [PN:unknown] [GN:narAA]
[OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis (168) narA gene.]
[SP:P39756] [LE:490] [RE:1278] [DI:direct] >gp:[GI:e1184577:g2636196]
[LN:BSUB0019] [AC:Z99122:AL009126] [GN:narQ] [FN:required for formate
dehydrogenase activity] [OR:Bacillus subtilis] [DB:genpept-bct1]
[DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091to
3809700.] [NT:alternate gene name: narAA] [SP:P39756] [LE:175331]
[RE:176119] [DI:complement] >gp:[GI:e1184577:g2636196] [LN:BSUB0019]
[AC:Z99122:AL009126] [GN:narQ] [FN:required for formate dehydrogenase
activity] [OR:Bacillus subtilis] [DB:genpept] [DE:Bacillus subtilis complete
genome (section 19 of 21): from 3597091to 3809700.] [NT:alternate gene name:
narAA] [SP:P39756] [LE:175331] [RE:176119] [DI:complement]
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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000997_1054640_f3_189	2684	6456	213	70	170	7.2e-13

Description

sp:[LN:NARQ_BACSU] [AC:P39756] [GN:NARQ:NARAA] [OR:BACILLUS SUBTILIS]
 [DE:NARQ PROTEIN] [SP:P39756] [DB:swissprot] >pir:[LN:B69665] [AC:B69665]
 [PN:required for formate dehydrogenase activity narQ] [GN:narQ]
 [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e276834:g1648855] [LN:BSATPC]
 [AC:Z81356] [PN:unknown] [GN:narQ] [OR:Bacillus subtilis] [DB:genpept-bct1]
 [DE:B.subtilis atpC gene.] [SP:P39756] [LE:7048] [RE:7836] [DI:direct]
 >gp:[GI:g580895] [LN:BSNARAAB] [AC:Z35277] [PN:unknown] [GN:narAA]
 [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis (168) narA gene.]
 [SP:P39756] [LE:490] [RE:1278] [DI:direct] >gp:[GI:e1184577:g2636196]
 [LN:BSUB0019] [AC:Z99122:AL009126] [GN:narQ] [FN:required for formate
 dehydrogenase activity] [OR:Bacillus subtilis] [DB:genpept-bct1]
 [DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091to
 3809700.] [NT:alternate gene name: narAA] [SP:P39756] [LE:175331]
 [RE:176119] [DI:complement] >gp:[GI:e1184577:g2636196] [LN:BSUB0019]
 [AC:Z99122:AL009126] [GN:narQ] [FN:required for formate dehydrogenase
 activity] [OR:Bacillus subtilis] [DB:genpept] [DE:Bacillus subtilis complete
 genome (section 19 of 21): from 3597091to 3809700.] [NT:alternate gene name:
 narAA] [SP:P39756] [LE:175331] [RE:176119] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000997_10580182_f1_9	2685	6457	123	40		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000997_10646887_f1_25	2686	6458	126	41		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000997_11756250_f3_197	2687	6459	144	47		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000997_11767205_f3_213	2688	6460	126	41		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000997_1209800_c2_304	2689	6461	282	93	72	0.0011

Description

sp:[LN:LACF_AGRRD] [AC:P29823] [GN:LACF] [OR:AGROBACTERIUM RADIOBACTER]
 [DE:LACTOSE TRANSPORT SYSTEM PERMEASE PROTEIN LACF] [SP:P29823]
 [DB:swissprot] >pir:[LN:MMAGCF] [AC:S25248:S22740] [PN:membrane protein
 lacF] [GN:lacF] [CL:inner membrane protein ugpA] [OR:Agrobacterium
 radiobacter] [DB:pir1] >gp:[GI:g38969] [LN:ARLACOP]
 [AC:X66596:S40378:S40757] [GN:lacF] [OR:Agrobacterium radiobacter]
 [DB:genpept-bct1] [DE:A.radiobacter lac operon.] [SP:P29823] [LE:1897]
 [RE:2793] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000997_12270176_c2_349	2690	6462	180	59		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000997_12595175_f2_140	2691	6463	498	165	261	1.6e-22

Description

sp:[LN:YKKC_BACSU] [AC:P49856] [GN:YKKC] [OR:BACILLUS SUBTILIS]
 [DE:HYPOTHETICAL 11.9 KD PROTEIN IN HMP 3'REGION] [SP:P49856] [DB:swissprot]
 >pir:[LN:A69857] [AC:A69857] [PN:chaperonin homolog ykkC] [GN:ykkC]
 [CL:sugE protein] [OR:Bacillus subtilis] [DB:pir2]
 >gp:[GI:d1011924:g1063251] [LN:BAC168TRP2] [AC:D78189] [OR:Bacillus
 subtilis] [SR:Bacillus subtilis (strain:168trpC2) DNA] [DB:genpept-bct1]
 [DE:Bacillus subtilis hmp DNA for 7 ORFs, complete cds.] [NT:unnamed protein
 product] [LE:4724] [RE:5062] [DI:direct] >gp:[GI:e1181509:g2632029]
 [LN:BSAJ2571] [AC:AJ002571] [PN:YkkC] [GN:ykkC] [FN:unknown] [OR:Bacillus
 subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis 168 56 kb DNA fragment
 between xlyA and ykoR.] [SP:P49856] [LE:28642] [RE:28980] [DI:direct]
 >gp:[GI:e1183329:g2633663] [LN:BSUB0007] [AC:Z99110:AL009126] [GN:ykkC]
 [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
 complete genome (section 7 of 21): from 1194391to 1411140.] [NT:similar to
 chaperonin] [SP:P49856] [LE:181591] [RE:181929] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000997_1375308_c2_341	2692	6464	411	136	103	9.0e-06

Description

gp:[GI:g3283053] [LN:AF054173] [AC:AF054173] [PN:staphylococcal accessory regulator A homolog] [GN:sarA] [OR:Staphylococcus epidermidis] [DB:genpept-bct2] [DE:Staphylococcus epidermidis staphylococcal accessory regulator Ahomolog (sarA) gene, complete cds.] [LE:887] [RE:1261] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000997_13849056_c1_251	2693	6465	279	92	79	0.041

Description

gp:[GI:e1313955:g3392923] [LN:LLNISG] [AC:AJ000993] [PN:hypothetical protein] [GN:orfD] [OR:Lactococcus lactis] [DB:genpept-bct1] [DE:Lactococcus lactis nisG gene, orfA, orfB, orfC, and orfD.] [LE:3153] [RE:4799] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000997_1406552_c1_252	2694	6466	123	40		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000997_14094002_c2_303	2695	6467	138	45		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000997_14097586_f3_201	2696	6468	438	145	470	1.2e-44

Description

sp:[LN:URE2_STAXY] [AC:P42874] [GN:UREB] [OR:STAPHYLOCOCCUS XYLOSUS] [EC:3.5.1.5] [DE:UREASE BETA SUBUNIT, (UREA AMIDOHYDROLASE)] [SP:P42874] [DB:swissprot] >pir:[LN:S38484] [AC:S38484] [PN:urease, beta chain] [CL:urease 12K chain:urease 12K chain homology] [OR:Staphylococcus xylosus] [EC:3.5.1.5] [DB:pir1] >gp:[GI:g410515] [LN:SXUREABC] [AC:X74600] [PN:urease beta subunit] [GN:ureB] [OR:Staphylococcus xylosus] [DB:genpept-bct1] [DE:S.xylosus gene for ureA, ureB, and ureC genes for urease gamma,beta and alpha subunits.] [SP:P42874] [LE:886] [RE:1299] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000997_14220635_c3_380	2697	6469	150	49		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000997_14454632_c2_289	2698	6470	177	58	226	8.4e-19

Description

gp:[GI:g1022726] [LN:SHU35635] [AC:U35635] [PN:unknown] [OR:Staphylococcus haemolyticus] [SR:Staphylococcus haemolyticus strain=Y176] [DB:genpept-bct1] [DE:Staphylococcus haemolyticus IS1272 ORF1 and ORF2 genes, completedcs.] [NT:ORF1] [LE:1101] [RE:1922] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000997_14460882_f1_23	2699	6471	189	62	221	2.8e-18

Description

gp:[GI:g1022726] [LN:SHU35635] [AC:U35635] [PN:unknown] [OR:Staphylococcus haemolyticus] [SR:Staphylococcus haemolyticus strain=Y176] [DB:genpept-bct1] [DE:Staphylococcus haemolyticus IS1272 ORF1 and ORF2 genes, completedcs.] [NT:ORF1] [LE:1101] [RE:1922] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000997_14501888_f2_129	2700	6472	126	41		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000997_14549010_c2_339	2701	6473	666	221	531	4.0e-51

Description

gp:[GI:e1429630:g4756162] [LN:A67171] [AC:A67171] [FN:MOBA GENE] [OR:Staphylococcus carnosus] [DB:genpept-pat] [DE:Sequence 11 from Patent EP0805205.] [NT:unnamed protein product] [LE:4821] [RE:5411] [DI:direct]
>gp:[GI:g3955208] [LN:AF022796] [AC:AF022796] [PN:MobA] [GN:mobA] [OR:Staphylococcus carnosus] [DB:genpept-bct2] [DE:Staphylococcus carnosus molybdenum cofactor biosynthetic genecluster, complete sequence.] [NT:protein similar to MobA of Escherichia coli] [LE:7042] [RE:7632] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000997_14550133_f1_14	2702	6474	543	180		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000997_15820176_f3_207	2703	6475	126	41		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000997_16129817_f1_68	2704	6476	156	51		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000997_19533567_f2_100	2705	6477	264	87	80	0.0025

Description

gp:[GI:g5306165] [LN:AF160864] [AC:AF160864] [PN:orf98] [GN:orf98]
 [OR:Mitochondrion Tetrahymena pyriformis] [SR:Tetrahymena pyriformis]
 [DB:genpept] [DE:Tetrahymena pyriformis mitochondrial DNA, complete genome.]
 [NT:Open reading frame ymf71 (CPGN); ATT initiation] [LE:37598] [RE:37894]
 [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000997_20112790_c3_399	2706	6478	126	41		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000997_20345067_c3_365	2707	6479	126	41		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000997_2126925_f3_211	2708	6480	153	50		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000997_21611592_f3_236	2709	6481	369	122	89	0.0017

Description

pir:[LN:E71805] [AC:E71805] [PN:protein-export membrane protein] [GN:secF] [CL:Escherichia coli preprotein translocase chain secF] [OR:Helicobacter pylori] [SR:strain J99, , strain J99] [SR:strain J99,] [DB:pir2]
>gp:[GI:g4156068] [LN:AE001567] [AC:AE001567:AE001439] [PN:PROTEIN-EXPORT MEMBRANE PROTEIN] [GN:secF] [OR:Helicobacter pylori J99] [DB:genpept-bct2] [DE:Helicobacter pylori, strain J99 section 128 of 132 of the completegenome.] [NT:similar to H. pylori 26695 gene HP1549] [LE:9115] [RE:10086] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000997_21646015_f2_104	2710	6482	210	69	158	1.3e-11

Description

gp:[GI:g1022725] [LN:SHU35635] [AC:U35635] [PN:unknown] [OR:Staphylococcus haemolyticus] [SR:Staphylococcus haemolyticus strain=Y176] [DB:genpept-bct1] [DE:Staphylococcus haemolyticus IS1272 ORF1 and ORF2 genes, completecds.] [NT:ORF2] [LE:394] [RE:1083] [DI:complement] >gp:[GI:g295162] [LN:STAMECRA] [AC:L14017] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus (strain COL) DNA] [DB:genpept-bct1] [DE:Staphylococcus aureus methicillin-resistance protein (mecR) geneand unknown ORF, complete cds.] [NT:unknown ORF1; putative] [LE:1492] [RE:2181] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000997_21675050_f3_230	2711	6483	360	119		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000997_21681561_f1_74	2712	6484	891	296	776	4.4e-77

Description

pir:[LN:D69744] [AC:D69744] [PN:conserved hypothetical protein ybbI]
 [GN:ybbI] [CL:conserved hypothetical protein b2428] [OR:Bacillus subtilis]
 [DB:pir2] >gp:[GI:e1182103:g2632437] [LN:BSUB0001] [AC:Z99104:AL009126]
 [GN:ybbI] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus
 subtilis complete genome (section 1 of 21): from 1 to213080.] [NT:similar to
 hypothetical proteins] [LE:192050] [RE:192964] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000997_21776942_c1_244	2713	6485	642	213	855	1.9e-85

Description

sp:[LN:YBXG_BACSU] [AC:P54425:O31438] [GN:YBXG:YBDP] [OR:BACILLUS SUBTILIS]
 [DE:HYPOTHETICAL TRANSPORT PROTEIN IN NDHF-CSGA INTERGENIC REGION (ORF1)]
 [SP:P54425:O31438] [DB:swissprot] >pir:[LN:H69751] [AC:H69751:PC6045]
 [PN:amino acid permease homolog ybxG] [GN:ybxG] [CL:arginine permease]
 [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:d1034070:g3599629] [LN:AB006424]
 [AC:AB006424] [GN:ybdP] [OR:Bacillus subtilis] [SR:Bacillus subtilis
 (strain:168) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis genomic DNA, 70 kb
 region between 17 and 23degree.] [LE:29556] [RE:30944] [DI:direct]
 >gp:[GI:e1182158:g2632492] [LN:BSUB0002] [AC:Z99105:AL009126] [GN:ybxG]
 [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
 complete genome (section 2 of 21): from 194651 to415810.] [NT:alternate gene
 name: ybdP; similar to amino acid] [SP:P54425] [LE:31905] [RE:33293]
 [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000997_2211433_f3_205	2714	6486	867	288	534	1.9e-51

Description

sp:[LN:URED_BACSB] [AC:Q07400] [GN:URED] [OR:BACILLUS SP] [SR:TB-90,]
 [DE:UREASE ACCESSORY PROTEIN URED] [SP:Q07400] [DB:swissprot]
 >pir:[LN:G36950] [AC:G36950] [PN:ureD protein] [OR:Bacillus sp.] [DB:pir2]
 >gp:[GI:d1003839:g216366] [LN:BACUREA] [AC:D14439] [PN:urease accessory
 protein] [GN:UreD] [OR:Bacillus sp.] [SR:Bacillus sp. (strain:TB-90) DNA]
 [DB:genpept-bct1] [DE:Thermophilic Bacillus genes for urease subunits and
 ureaseaccessory proteins, complete cds.] [LE:4281] [RE:5096] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000997_22290657_c3_382	2715	6487	387	128	164	3.1e-12

Description

gp:[GI:g3283053] [LN:AF054173] [AC:AF054173] [PN:staphylococcal accessory regulator A homolog] [GN:sarA] [OR:Staphylococcus epidermidis] [DB:genpept-bct2] [DE:Staphylococcus epidermidis staphylococcal accessory regulator A homolog (sarA) gene, complete cds.] [LE:887] [RE:1261] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000997_22455337_f3_217	2716	6488	168	55		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000997_22692177_c1_271	2717	6489	537	178	556	9.0e-54

Description

gp:[GI:e1429621:g4756159] [LN:A67171] [AC:A67171] [FN:MOAB GENE] [OR:Staphylococcus carnosus] [DB:genpept-pat] [DE:Sequence 11 from Patent EP0805205.] [NT:unnamed protein product] [LE:1150] [RE:1662] [DI:direct] >gp:[GI:g3955202] [LN:AF022796] [AC:AF022796] [PN:Moab] [GN:moab] [OR:Staphylococcus carnosus] [DB:genpept-bct2] [DE:Staphylococcus carnosus molybdenum cofactor biosynthetic genecluster, complete sequence.] [NT:protein similar to Moab of Escherichia coli] [LE:3371] [RE:3883] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000997_22734582_c2_293	2718	6490	141	46		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000997_23538332_f1_18	2719	6491	150	49		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000997_23609628_c2_330	2720	6492	975	324	385	1.2e-35

Description

gp:[GI:g2645495] [LN:AF017231] [AC:AF017231]
 [PN:inosine-adenosine-guanosine-nucleoside] [FN:catalyzes the hydrolysis of
 the N-ribosidic] [OR:Trypanosoma brucei brucei] [DB:genpept-inv1]
 [DE:Trypanosoma brucei brucei
 inosine-adenosine-guanosine-nucleosidehydrolase mRNA, complete cds.]
 [NT:N-ribohydrolase; IAG-nucleoside hydrolase] [LE:187] [RE:1170]
 [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000997_23620260_c2_311	2721	6493	1107	368	334	3.0e-30

Description

sp:[LN:ODH_ARTSP] [AC:Q44297] [GN:ODH] [OR:ARTHROBACTER SP] [SR:1C,]
 [EC:1.5.1.28] [DE:OPINE DEHYDROGENASE,] [SP:Q44297] [DB:swissprot]
 >pir:[LN:I39664] [AC:I39664] [PN:probable D-octopine dehydrogenase,]
 [OR:Arthrobacter sp.] [EC:1.5.1.11] [DB:pir2] >gp:[GI:d1008736:g1060848]
 [LN:ARGOD] [AC:D45211] [PN:opine dehydrogenase] [OR:Arthrobacter sp.]
 [SR:Arthrobacter sp. DNA, clone poDH1] [DB:genpept-bct1] [DE:Arthrobacter
 sp. gene for opine dehydrogenase, complete cds.] [LE:254] [RE:1333]
 [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000997_23631551_c3_395	2722	6494	792	263		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000997_23642167_f3_175	2723	6495	1218	405	611	1.3e-59

Description

pir:[LN:B70065] [AC:B70065] [PN:antibiotic resistance protein homolog ywoG] [GN:ywoG] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1184551:g2636170] [LN:BSUB0019] [AC:Z99122:AL009126] [GN:ywoG] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.] [NT:similar to antibiotic resistance protein] [LE:151451] [RE:152641] [DI:direct] >gp:[GI:e283116:g1684651] [LN:BSZ82987] [AC:Z82987] [PN:unknown similar to quinolon resistance protein] [GN:ywoG] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis ywo[A,B,C,D,E,F,G,H], nrg[A,B], spoIIID and mb1 genes.] [LE:8662] [RE:9852] [DI:complement] >gp:[GI:e1184551:g2636170] [LN:BSUB0019] [AC:Z99122:AL009126] [GN:ywoG] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept] [DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.] [NT:similar to antibiotic resistance protein] [LE:151451] [RE:152641] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000997_23678262_c3_394	2724	6496	573	190	370	4.6e-34

Description

pir:[LN:B69832] [AC:B69832] [PN:biotin biosynthesis homolog yhfU] [GN:yhfU] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1183039:g2633373] [LN:BSUB0006] [AC:Z99109:AL009126] [GN:yhfU] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.] [NT:similar to biotin biosynthesis] [LE:111897] [RE:112457] [DI:complement] >gp:[GI:e325000:g2226257] [LN:BSY14084] [AC:Y14084] [PN:hypothetical protein] [GN:yhfU] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis chromosomal DNA, region 78-80 degrees: aprE to comK.] [NT:similarity to BioY from Bacillus sphaericus (Swiss) [LE:6325] [RE:6885] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000997_24104677_c2_291	2725	6497	1656	551	1619	2.0e-166

Description

sp:[LN:PTIB_BACSU] [AC:P54715] [GN:GLVC:GLVCB:GLV-2] [OR:BACILLUS SUBTILIS] [EC:2.7.1.69] [DE:II, BC COMPONENT),] [SP:P54715] [DB:swissprot]
>pir:[LN:G69635] [AC:G69635] [PN:PTS arbutin-like enzyme IIBC component glvC] [GN:glvC] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1182810:g2633144] [LN:BSUB0005] [AC:Z99108:AL009126] [PN:phosphotransferase system (PTS) arbutin-like] [GN:glvC] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.] [NT:alternate gene name: yfiB] [SP:P54715] [LE:88901] [RE:90484] [DI:direct] >gp:[GI:d1009740:g1486243] [LN:D50543] [AC:D50543] [PN:unknown] [GN:glv-2] [FN:unknown] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:168, haplotype:haploid) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis DNA for 76-degree region, complete cds.] [LE:2577] [RE:4160] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000997_24257012_c1_268	2726	6498	735	244	927	4.4e-93

Description

gp:[GI:g3955199] [LN:AF022796] [AC:AF022796] [PN:ModB] [GN:modB] [OR:Staphylococcus carnosus] [DB:genpept-bct2] [DE:Staphylococcus carnosus molybdenum cofactor biosynthetic genecluster, complete sequence.] [NT:integral membrane-spanning protein of the] [LE:906] [RE:1577] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000997_24303812_c3_352	2727	6499	123	40		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000997_24314818_c2_340	2728	6500	1035	344	1410	2.9e-144

Description

gp:[GI:e1429633:g4756163] [LN:A67171] [AC:A67171] [PN:MOAA GENE] [OR:Staphylococcus carnosus] [DB:genpept-pat] [DE:Sequence 11 from Patent EP0805205.] [LE:5470] [RE:6492] [DI:direct] >gp:[GI:g3955209] [LN:AF022796] [AC:AF022796] [PN:MoaA] [GN:moaA] [OR:Staphylococcus carnosus] [DB:genpept-bct2] [DE:Staphylococcus carnosus molybdenum cofactor biosynthetic genecluster, complete sequence.] [NT:protein similar to MoaA of Escherichia coli] [LE:7691] [RE:8713] [DI:direct]

AI7503000997_24406502_f2_127	2729	6501	171	56
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NO-HIT

AI7503000997_24406577_c2_346	2730	6502	3156	1051	2317	2.2e-240
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pir:[LN:E69795] [AC:E69795] [PN:acriflavin resistance protein homolog yerP]
[GN:yerP] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1182651:g2632985]
[LN:BSUB0004] [AC:Z99107:AL009126] [GN:yerP] [FN:unknown] [OR:Bacillus
subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 4
of 21): from 600701 to813890.] [NT:similar to acriflavin resistance protein]
[LE:131722] [RE:134919] [DI:direct]

AY7503000997_24431532_c1_277	2731	6503	1254	417	1796	3.6e-185
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gpc:[GI:g4574235] [LN:AF106850] [AC:AF106850] [PN:FmhB] [GN:fmhB]
[OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus FmhB
(fmhB) gene, complete cds.] [NT:similar to Staphylococcus aureus FemA and
FemB] [LE:204] [RE:1469] [DI:direct]

AI7503000997_24616251_f2_148	2732	6504	696	231	139	2.6e-07
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gp:[GI:g567887] [LN:STMDNRN] [AC:L37338] [PN:putative repressor] [GN:dnrO]
[OR:Streptomyces peucetius] [SR:Streptomyces peucetius ATCC 29050 DNA]
[DB:genpept-bct2] [DE:Streptomyces peucetius TDP-D-glucose-4,6-dehydratase
(dnrM) gene,3' end, regulatory protein (dnrN) gene, complete cds, and
repressorprotein (dnrO) gene, complete cds.] [NT:putative] [LE:1085]
[RE:2107] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000997_24644008_c3_396	2733	6505	792	263	911	2.2e-91

Description

gp:[GI:g3955198] [LN:AF022796] [AC:AF022796] [PN:ModA] [GN:modA]
 [OR:Staphylococcus carnosus] [DB:genpept-bct2] [DE:Staphylococcus carnosus
 molybdenum cofactor biosynthetic genecluster, complete sequence.]
 [NT:molybdate-binding lipoprotein of the] [LE:109] [RE:894] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000997_24650452_f1_64	2734	6506	153	50		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000997_24804077_c3_358	2735	6507	153	50		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000997_25430317_c1_274	2736	6508	492	163	446	4.1e-42

Description

gp:[GI:g3955205] [LN:AF022796] [AC:AF022796] [PN:MobB] [GN:mobB]
 [OR:Staphylococcus carnosus] [DB:genpept-bct2] [DE:Staphylococcus carnosus
 molybdenum cofactor biosynthetic genecluster, complete sequence.]
 [NT:protein similar to MobB of Escherichia coli] [LE:5873] [RE:6355]
 [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000997_25443838_c2_305	2737	6509	789	262	448	2.5e-42

Description

gp:[GI:d1023468:g2506027] [LN:D42078] [AC:D42078] [GN:NAG]
 [OR:Staphylococcus aureus] [SR:Staphylococcus aureus DNA] [DB:genpept-bct1]
 [DE:Staphylococcus aureus DNA for N-acetyl-glucosaminidase, partialcds.]
 [LE:<1] [RE:1448] [DI:direct] >gp:[GI:d1023468:g2506027] [LN:D42078]
 [AC:D42078] [GN:NAG] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus
 DNA] [DB:genpept] [DE:Staphylococcus aureus DNA for
 N-acetyl-glucosaminidase, partialcds.] [LE:<1] [RE:1448] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000997_25548385_f1_7	2738	6510	144	47		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000997_25554213_f1_49	2739	6511	627	208	943	8.8e-95

Description

sp:[LN:UREG_STAXY] [AC:P42877] [GN:UREG] [OR:STAPHYLOCOCCUS XYLOSUS]
 [DE:UREASE ACCESSORY PROTEIN UREG] [SP:P42877] [DB:swissprot]
 >gp:[GI:g511070] [LN:SKUREFG] [AC:Z35136] [PN:UreG] [OR:Staphylococcus
 xylosus] [DB:genpept-bct1] [DE:S.xylosus (C2a) UreF and UreG genes.]
 [SP:P42877] [LE:781] [RE:1395] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000997_25582885_f1_22	2740	6512	453	150	153	4.6e-11

Description

pir:[LN:C70065] [AC:C70065] [PN:transcription regulator MarR family homolog
 ywoH] [GN:ywoH] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1184550:g2636169]
 [LN:BSUB0019] [AC:Z99122:AL009126] [GN:ywoH] [FN:unknown] [OR:Bacillus
 subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section
 19 of 21): from 3597091to 3809700.] [NT:similar to transcriptional regulator
 (MarR family)] [LE:151016] [RE:151429] [DI:direct] >gp:[GI:e283130:g1684652]
 [LN:BSZ82987] [AC:Z82987] [PN:unknown, similar to cytolysin SlyA from]
 [GN:ywoH] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis
 ywo[A,B,C,D,E,F,G,H], nrg[A,B], spoIIID and mb1 genes.] [LE:9874] [RE:10287]
 [DI:complement] >gp:[GI:e1184550:g2636169] [LN:BSUB0019]
 [AC:Z99122:AL009126] [GN:ywoH] [FN:unknown] [OR:Bacillus subtilis]
 [DB:genpept] [DE:Bacillus subtilis complete genome (section 19 of 21): from
 3597091to 3809700.] [NT:similar to transcriptional regulator (MarR family)]
 [LE:151016] [RE:151429] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000997_25679762_c1_248	2741	6513	831	276	374	1.7e-34

Description

sp:[LN:SUHB_BACSU] [AC:Q45499] [GN:SUHB] [OR:BACILLUS SUBTILIS]
 [DE:EXTRAGENIC SUPPRESSOR PROTEIN SUHB HOMOLOG] [SP:Q45499] [DB:swissprot]
 >pir:[LN:E69864] [AC:E69864] [PN:myo-inositol-1(or 4)-monophosphatase
 homolog yktC] [GN:yktC] [CL:suppressor protein suhB] [OR:Bacillus subtilis]
 [DB:pir2] >gp:[GI:e1185057:g2633838] [LN:BSUB0008] [AC:Z99111:AL009126]
 [GN:yktC] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus
 subtilis complete genome (section 8 of 21): from 1394791to 1603020.]
 [NT:similar to myo-inositol-1(or 4)-monophosphatase] [SP:Q45499] [LE:142056]
 [RE:142853] [DI:direct] >gp:[GI:g3282150] [LN:AF012285]
 [AC:AF012285:AF012284:U51911] [PN:unknown] [GN:yktC] [FN:unknown]
 [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis mobA-nprE
 gene region.] [NT:similar to E. coli extragenic suppressor protein]
 [LE:42544] [RE:43341] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000997_26182800_c1_276	2742	6514	813	270	90	0.045

Description

sp:[LN:YCX3_ASTLO] [AC:P34778] [OR:ASTASIA LONGA] [SR:,EUGLENOPHYCEAN ALGA]
 [DE:HYPOTHETICAL 20.1 KD PROTEIN IN TRNS-RPL20 INTERGENIC REGION (ORF170)]
 [SP:P34778] [DB:swissprot] >pir:[LN:S38600] [AC:S38600] [PN:hypothetical
 protein 170 (rpl20 5' region)] [OR:plastid Astasia longa] [DB:pir2]
 >gp:[GI:g414866] [LN:ALRIBPTR] [AC:X75653] [GN:orf170] [OR:Chloroplast
 Astasia longa] [SR:euglenophycean alga] [DB:genpept-pln1] [DE:A.longa
 plastid genes for ribosomal proteins and tRNAs.] [SP:P34778] [LE:1985]
 [RE:2497] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000997_26367127_f1_44	2743	6515	168	55		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000997_26375031_f1_8	2744	6516	195	64	86	0.015

Description

pir:[LN:A70387] [AC:A70387] [PN:conserved hypothetical protein aq_1006]
 [GN:aq_1006] [OR:Aquifex aeolicus] [DB:pir2] >gp:[GI:g2983515]
 [LN:AE000718] [AC:AE000718:AE000657] [PN:hypothetical protein] [GN:aq_1006]
 [OR:Aquifex aeolicus] [DB:genpept-bct2] [DE:Aquifex aeolicus section 50 of
 109 of the complete genome.] [LE:2797] [RE:5733] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000997_26758426_c2_316	2745	6517	750	249	121	2.8e-07

Description

gp:[GI:g3283053] [LN:AF054173] [AC:AF054173] [PN:staphylococcal accessory
 regulator A homolog] [GN:sarA] [OR:Staphylococcus epidermidis]
 [DB:genpept-bct2] [DE:Staphylococcus epidermidis staphylococcal accessory
 regulator Ahomolog (sarA) gene, complete cds.] [LE:887] [RE:1261]
 [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000997_29494067_c3_356	2746	6518	213	70	50	0.031

Description

pir:[LN:PC1133] [AC:PC1133:S18087] [PN:hypothetical protein 119 (rmpG 5'
 region)] [OR:Lactococcus lactis] [DB:pir2]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000997_29697752_c2_302	2747	6519	786	261	499	9.8e-48

Description

sp:[LN:LYTR_BACSU] [AC:Q02115] [GN:LYTR] [OR:BACILLUS SUBTILIS]
[DE:MEMBRANE-BOUND PROTEIN LYTR] [SP:Q02115] [DB:swissprot] >pir:[LN:A47679]
[AC:A47679:H69654] [PN:lyt divergon expression attenuator Lytr] [GN:lytR]
[CL:Bacillus subtilis probable transcription regulator yvhJ] [OR:Bacillus
subtilis] [DB:pir2] >gp:[GI:g143156] [LN:BACLYTABCD] [AC:M87645]
[PN:membrane bound protein] [GN:lytR] [OR:Bacillus subtilis] [SR:Bacillus
subtilis (strain W168) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis
membrane bound protein (lytA and lytR); amidaseenhancer (lytB); and amidase
(lytC) genes, complete cds's.] [LE:92] [RE:1012] [DI:complement]
>gp:[GI:e1184471:g2636091] [LN:BSUB0019] [AC:Z99122:AL009126]
[PN:membrane-bound protein] [GN:lytR] [FN:attenuator role for lytABC and
lytR expression] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus
subtilis complete genome (section 19 of 21): from 3597091to 3809700.]
[SP:Q02115] [LE:65251] [RE:66171] [DI:direct] >gp:[GI:e1184471:g2636091]
[LN:BSUB0019] [AC:Z99122:AL009126] [PN:membrane-bound protein] [GN:lytR]
[FN:attenuator role for lytABC and lytR expression] [OR:Bacillus subtilis]
[DB:genpept] [DE:Bacillus subtilis complete genome (section 19 of 21): from
3597091to 3809700.] [SP:Q02115] [LE:65251] [RE:66171] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000997_31284550_f3_237	2748	6520	174	57		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000997_3250075_f3_220	2749	6521	1008	335	705	1.5e-69

Description

pir:[LN:A71175] [AC:A71175] [PN:probable dehydrogenase] [GN:PH0597]
[OR:Pyrococcus horikoshii] [DB:pir2] >gp:[GI:d1030629:g3257003]
[LN:AP000002]
[AC:AP000002:AB009475:AB009476:AB009477:AB009478:AB009479:AB009480]
[PN:376aa long hypothetical dehydrogenase] [GN:PH0597] [OR:Pyrococcus
horikoshii] [SR:Pyrococcus horikoshii (strain:OT3) DNA] [DB:genpept-bct1]
[DE:Pyrococcus horikoshii OT3 genomic DNA, 287001-544000 nt. position(2/7).]
[NT:similar to owl:BSZ9404317 percent identity: 49.821] [LE:248539]
[RE:249669] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000997_33360910_f3_216	2750	6522	549	182	120	1.4e-07

Description

pir:[LN:S74932] [AC:S74932] [PN:hypothetical protein slr0686]
 [OR:Synechocystis sp.] [SR:PCC 6803, , PCC 6803] [SR:PCC 6803,] [DB:pir2]
 >gp:[GI:d1017705:g1652047] [LN:D90902] [AC:D90902:AB001339] [PN:hypothetical
 protein] [OR:Synechocystis sp.] [SR:Synechocystis sp. (strain:PCC6803) DNA]
 [DB:genpept-bct1] [DE:Synechocystis sp. PCC6803 complete genome, 4/27,
 402290-524345.] [NT:ORF_ID:slr0686] [LE:27521] [RE:27880] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000997_33694505_f3_198	2751	6523	162	53	47	0.0063

Description

gp:[GI:d1042768:g5103471] [LN:AP000058] [AC:AP000058] [PN:102aa long
 hypothetical protein] [GN:APE0083] [OR:Aeropyrum pernix] [SR:Aeropyrum
 pernix (strain:K1) DNA] [DB:genpept] [DE:Aeropyrum pernix genomic DNA,
 section 1/7.] [LE:56764] [RE:57072] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000997_3371062_f1_10	2752	6524	333	110	90	0.00034

Description

gp:[GI:g1040951] [LN:AOU35271] [AC:U35271] [PN:NADH dehydrogenase subunit 6]
 [OR:Mitochondrion Anopheles oswaldoi] [SR:Anopheles oswaldoi]
 [DB:genpept-inv1] [DE:Anopheles oswaldoi NADH dehydrogenase subunit 6 gene,
 mitochondrial gene encoding mitochondrial product, partial cds.] [LE:<1]
 [RE:525] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000997_34192165_f1_63	2753	6525	345	114	264	7.9e-23

Description

pir:[LN:B69857] [AC:B69857] [PN:chaperonin homolog ykkD] [GN:ykkD]
 [CL:sugE protein] [OR:Bacillus subtilis] [DB:pir2]
 >gp:[GI:e1181510:g2632030] [LN:BSAJ2571] [AC:AJ002571] [PN:YkkD] [GN:ykkD]
 [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
 168 56 kb DNA fragment between xlyA and ykoR.] [LE:28980] [RE:29297]
 [DI:direct] >gp:[GI:e1183330:g2633664] [LN:BSUB0007] [AC:Z99110:AL009126]
 [GN:ykkD] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus
 subtilis complete genome (section 7 of 21): from 1194391 to 1411140.]
 [NT:similar to chaperonin] [LE:181929] [RE:182246] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000997_34411552_f2_123	2754	6526	1722	573	2703	2.8e-281

Description

sp:[LN:URE1_STAXY] [AC:P42873] [GN:UREC] [OR:STAPHYLOCOCCUS XYLOSUS]
[EC:3.5.1.5] [DE:UREASE ALPHA SUBUNIT, (UREA AMIDOHYDROLASE)] [SP:P42873]
[DB:swissprot] >pir:[LN:S38485] [AC:S38485] [PN:urease, 62K chain:urease
alpha chain] [GN:ureC] [CL:urease 62K chain:urease 62K chain homology]
[OR:Staphylococcus xylosus] [EC:3.5.1.5] [DB:pir2] >gp:[GI:g410516]
[LN:SXUREABC] [AC:X74600] [PN:urease alpha subunit] [GN:ureC]
[OR:Staphylococcus xylosus] [DB:genpept-bct1] [DE:S.xylosus gene for ureA,
ureB, and ureC genes for urease gamma,beta and alpha subunits.] [SP:P42873]
[LE:1296] [RE:3011] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000997_34430_f2_96	2755	6527	156	51		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000997_34431300_c2_300	2756	6528	774	257	139	2.8e-09

Description

gp:[GI:d1011987:g1402529] [LN:D78257] [AC:D78257] [PN:ORF8] [GN:orf8]
[OR:Enterococcus faecalis] [SR:Enterococcus faecalis plasmid:pYI17 DNA]
[DB:genpept-bct1] [DE:Enterococcus faecalis plasmid pYI17 genes for BacA,
BacB, ORF3,ORF4, ORF5, ORF6, ORF7, ORF8, ORF9, ORF10, ORF11,partial cds.]
[LE:1899] [RE:2261] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000997_34617187_f2_156	2757	6529	207	68	74	0.00010

Description

gp:[GI:g4164553] [LN:AF081828] [AC:AF081828] [PN:NADH dehydrogenase 6]
[OR:Mitochondrion Ixodes hexagonus] [SR:Ixodes hexagonus] [DB:genpept-inv2]
[DE:Ixodes hexagonus mitochondrial DNA, complete genome.] [LE:9406]
[RE:9831] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000997_35191527_f1_19	2758	6530	156	51		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
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AI7503000997_35319025_f3_200	2759	6531	132	43		
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Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
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AI7503000997_35547892_f3_218	2760	6532	156	51	161	8.5e-12
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Description

gp: [GI:g2735506] [LN:SCU96107] [AC:U96107] [PN:SceB precursor] [GN:sceB]
 [OR:Staphylococcus carnosus] [DB:genpept-bct2] [DE:Staphylococcus carnosus
 N5,N10-methylenetetrahydromethanopterinreductase homolog, SceB precursor
 (sceB) and putative transmembraneprotein genes, complete cds, and putative
 Na+/H+ antiporter NhaC(nhaC) gene, partial cds.] [NT:major secreted protein]
 [LE:1894] [RE:2685] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
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AI7503000997_35572051_f1_72	2761	6533	129	42		
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Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
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AI7503000997_36017151_f2_110	2762	6534	141	46		
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Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000997_36113805_c1_245	2763	6535	750	249	775	5.6e-77

Description

sp:[LN:YBXG_BACSU] [AC:P54425:O31438] [GN:YBXG:YBDP] [OR:BACILLUS SUBTILIS] [DE:HYPOTHETICAL TRANSPORT PROTEIN IN NDHF-CSGA INTERGENIC REGION (ORF1)] [SP:P54425:O31438] [DB:swissprot] >pir:[LN:H69751] [AC:H69751:PC6045] [PN:amino acid permease homolog ybxG] [GN:ybxG] [CL:arginine permease] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:d1034070:g3599629] [LN:AB006424] [AC:AB006424] [GN:ybdP] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:168) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis genomic DNA, 70 kb region between 17 and 23degree.] [LE:29556] [RE:30944] [DI:direct] >gp:[GI:e1182158:g2632492] [LN:BSUB0002] [AC:Z99105:AL009126] [GN:ybxG] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.] [NT:alternate gene name: ybdP; similar to amino acid] [SP:P54425] [LE:31905] [RE:33293] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000997_36132792_c3_402	2764	6536	255	84	218	5.9e-18

Description

gp:[GI:e1429627:g4756161] [LN:A67171] [AC:A67171] [PN:MOAD GENE] [OR:Staphylococcus carnosus] [DB:genpept-pat] [DE:Sequence 11 from Patent EP0805205.] [LE:4583] [RE:4816] [DI:direct] >gp:[GI:g3955207] [LN:AF022796] [AC:AF022796] [PN:MoaD] [GN:moaD] [OR:Staphylococcus carnosus] [DB:genpept-bct2] [DE:Staphylococcus carnosus molybdenum cofactor biosynthetic genecluster, complete sequence.] [NT:protein similar to MoaD of Escherichia coli] [LE:6804] [RE:7037] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000997_36134427_c1_241	2765	6537	657	218	251	1.9e-21

Description

sp:[LN:YHCW_BACSU] [AC:P54607] [GN:YHCW] [OR:BACILLUS SUBTILIS]
 [DE:HYPOTHETICAL 24.7 KD PROTEIN IN CSPB-GLPP INTERGENIC REGION] [SP:P54607]
 [DB:swissprot] >pir:[LN:C69824] [AC:C69824] [PN:phosphoglycolate
 phosphatase homolog yhcW] [GN:yhcW] [CL:hypothetical protein b2690]
 [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e233881:g1239999] [LN:BS75DGREG]
 [AC:X96983] [PN:hypothetical protein] [GN:yhcW] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:B.subtilis chromosomal DNA (region 75 degrees: cspB
 upstream ofglpPFDK operon).] [NT:similarity to phosphoglycolate phosphatase
 from] [SP:P54607] [LE:18604] [RE:19266] [DI:direct]
 >gp:[GI:e1182913:g2633247] [LN:BSUB0005] [AC:Z99108:AL009126] [GN:yhcW]
 [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
 complete genome (section 5 of 21): from 802821 to1011250.] [NT:similar to
 phosphoglycolate phosphatase] [SP:P54607] [LE:194410] [RE:195072]
 [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000997_36209660_f2_116	2766	6538	378	125		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000997_36225625_f1_56	2767	6539	795	264	1034	2.0e-104

Description

gp:[GI:e244971:g1340128] [LN:SA1234] [AC:X97985] [OR:Staphylococcus aureus]
 [DB:genpept-bct1] [DE:S.aureus orfs 1,2,3 & 4.] [NT:ORF1] [LE:537] [RE:1304]
 [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000997_36615903_c2_329	2768	6540	1164	387	1007	1.5e-101

Description

pir:[LN:H69771] [AC:H69771] [PN:butyryl-CoA dehydrogenase homolog ydbM] [GN:ydbM] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:d1020042:g1881262] [LN:AB001488] [AC:AB001488] [GN:ydbM] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:168) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.] [NT:SIMILAR TO ACYL-COA DEHYDROGENASE.] [LE:38215] [RE:39360] [DI:direct] >gp:[GI:e1182418:g2632752] [LN:BSUB0003] [AC:Z99106:AL009126] [GN:ydbM] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.] [NT:similar to butyryl-CoA dehydrogenase] [LE:101959] [RE:103104] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000997_3943752_f2_128	2769	6541	150	49		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000997_3947153_f3_204	2770	6542	456	151	482	6.2e-46

Description

sp:[LN:UREE_BACSB] [AC:Q07401] [GN:UREE] [OR:BACILLUS SP] [SR:TB-90,] [DE:UREASE ACCESSORY PROTEIN UREE] [SP:Q07401] [DB:swissprot] >pir:[LN:D36950] [AC:D36950] [PN:ureE protein] [OR:Bacillus sp.] [DB:pir2] >gp:[GI:d1003836:g393297] [LN:BACUREA] [AC:D14439] [PN:urease accessory protein] [GN:UreE] [OR:Bacillus sp.] [SR:Bacillus sp. (strain:TB-90) DNA] [DB:genpept-bct1] [DE:Thermophilic Bacillus genes for urease subunits and ureaseaccessory proteins, complete cds.] [LE:2521] [RE:2967] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000997_3991557_f1_55	2771	6543	141	46		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000997_4042327_c3_390	2772	6544	918	305	309	1.3e-27

Description

gp:[GI:g1322222] [LN:HSU35735] [AC:U35735] [PN:RACH1] [GN:RACH1] [OR:Homo sapiens] [SR:human] [DB:genpept-pri2] [DE:Human RACH1 (RACH1) mRNA, complete cds.] [LE:169] [RE:1338] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000997_4086568_c3_381	2773	6545	1983	660	130	1.8e-07

Description

sp:[LN:SOXS_ECOLI] [AC:P22539] [GN:SOXS] [OR:ESCHERICHIA COLI] [DE:REGULATORY PROTEIN SOXS] [SP:P22539] [DB:swissprot]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000997_42500_f1_24	2774	6546	159	52		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000997_4459380_f1_84	2775	6547	207	68		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000997_4459505_c2_343	2776	6548	129	42		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000997_4486693_f2_92	2777	6549	804	267	976	2.8e-98

Description

gp:[GI:e324856:g2226002] [LN:SKY14043] [AC:Y14043] [PN:glucose-1-dehydrogenase] [GN:gdh] [OR:Staphylococcus xylosus] [DB:genpept-bct1] [DE:Staphylococcus xylosus glcU and gdh genes.] [LE:1222] [RE:2013] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000997_4491450_f2_150	2778	6550	873	290	310	1.0e-27

Description

gp:[GI:g4980827] [LN:AE001714] [AC:AE001714:AE000512] [PN:transcriptional regulator, RpiR family] [GN:TM0326] [OR:Thermotoga maritima] [DB:genpept-bct2] [DE:Thermotoga maritima section 26 of 136 of the complete genome.] [NT:similar to SP:P46118 PID:881368 GB:U00096] [LE:3706] [RE:4548] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000997_4547163_f1_48	2779	6551	699	232	741	2.2e-73

Description

sp:[LN:UREF_STAXY] [AC:P42876] [GN:UREF] [OR:STAPHYLOCOCCUS XYLOSUS] [DE:UREASE ACCESSORY PROTEIN UREF] [SP:P42876] [DB:swissprot] >gp:[GI:g511069] [LN:SKUREFG] [AC:Z35136] [PN:UreF] [OR:Staphylococcus xylosus] [DB:genpept-bct1] [DE:S.xylosus (C2a) UreF and UreG genes.] [SP:P42876] [LE:79] [RE:648] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000997_4569012_f1_79	2780	6552	588	195		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000997_4720290_f2_145	2781	6553	138	45		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000997_4720928_f1_11	2782	6554	186	61		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000997_4726550_f2_143	2783	6555	177	58		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000997_4800202_c1_269	2784	6556	621	206	694	2.1e-68

Description

gp:[GI:g3955200] [LN:AF022796] [AC:AF022796] [PN:ModC] [GN:modC]
[OR:Staphylococcus carnosus] [DB:genpept-bct2] [DE:Staphylococcus carnosus
molybdenum cofactor biosynthetic genecluster, complete sequence.]
[NT:ATP-binding protein of the molybdate-specific ABC] [LE:1578] [RE:2186]
[DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000997_4804153_f1_33	2785	6557	690	229	618	2.4e-60

Description

gp:[GI:e1429636:g4756164] [LN:A67171] [AC:A67171] [FN:MOAC GENE]
[OR:Staphylococcus carnosus] [DB:genpept-pat] [DE:Sequence 11 from Patent
EP0805205.] [NT:unnamed protein product] [LE:1846] [RE:2331] [DI:complement]
>gp:[GI:g3955203] [LN:AF022796] [AC:AF022796] [PN:Moac] [GN:moac]
[OR:Staphylococcus carnosus] [DB:genpept-bct2] [DE:Staphylococcus carnosus
molybdenum cofactor biosynthetic genecluster, complete sequence.]
[NT:protein similar to Moac of Escherichia coli] [LE:4067] [RE:4552]
[DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000997_4876675_f2_122	2786	6558	399	132	430	2.0e-40

Description

sp:[LN:URE3_STAXY] [AC:P42875] [GN:UREA] [OR:STAPHYLOCOCCUS XYLOSUS]
[EC:3.5.1.5] [DE:UREASE GAMMA SUBUNIT, (UREA AMIDOHYDROLASE)] [SP:P42875]
[DB:swissprot] >pir:[LN:S38483] [AC:S38483] [PN:urease, 11K chain:urease
gamma chain] [CL:urease 11K chain:urease 11K chain homology]
[OR:Staphylococcus xylosus] [EC:3.5.1.5] [DB:pir2] >gp:[GI:g581787]
[LN:SXUREABC] [AC:X74600] [PN:urease gamma subunit] [GN:ureA]
[OR:Staphylococcus xylosus] [DB:genpept-bct1] [DE:S.xylosus gene for ureA,
ureB, and ureC genes for urease gamma,beta and alpha subunits.] [SP:P42875]
[LE:568] [RE:870] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000997_4884662_c3_367	2787	6559	1128	375	333	1.0e-32

Description

gp:[GI:e1393931:g4490992] [LN:SCE29] [AC:AL035707] [PN:putative salicylate
hydroxylase] [GN:SCE29.14c] [OR:Streptomyces coelicolor] [DB:genpept-bct1]
[DE:Streptomyces coelicolor cosmid E29.] [NT:SCE29.14c, possible salicylate
hydroxylase, len:] [LE:19076] [RE:20338] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000997_4976687_c1_281	2788	6560	924	307	232	1.9e-19

Description

gp:[GI:g4980727] [LN:AE001707] [AC:AE001707:AE000512] [PN:conserved hypothetical protein] [GN:TM0229] [OR:Thermotoga maritima] [DB:genpept-bct2] [DE:Thermotoga maritima section 19 of 136 of the complete genome.] [NT:similar to GB:L77117 PID:1591686 percent identity:] [LE:5630] [RE:6487] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000997_5082812_c2_310	2789	6561	135	44		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000997_5087556_c2_335	2790	6562	849	282	990	9.2e-100

Description

gp:[GI:e1429618:g4756158] [LN:A67171] [AC:A67171] [FN:MOEB GENE] [OR:Staphylococcus carnosus] [DB:genpept-pat] [DE:Sequence 11 from Patent EP0805205.] [NT:unnamed protein product] [LE:117] [RE:1118] [DI:direct]
>gp:[GI:g3955201] [LN:AF022796] [AC:AF022796] [PN:MoeB] [GN:moeB] [OR:Staphylococcus carnosus] [DB:genpept-bct2] [DE:Staphylococcus carnosus molybdenum cofactor biosynthetic genecluster, complete sequence.] [NT:protein similar to the molybdopterin synthase] [LE:2338] [RE:3339] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000997_5113550_f2_149	2791	6563	1089	362	269	2.3e-23

Description

pir:[LN:C70217] [AC:C70217] [PN:outer surface protein homolog] [OR:Borrelia burgdorferi] [SR:, Lyme disease spirochete] [DB:pir2] >gp:[GI:g2689897] [LN:AE000792] [AC:AE000792] [PN:outer surface protein, putative] [GN:BBB07] [OR:Borrelia burgdorferi] [SR:Lyme disease spirochete] [DB:genpept-bct2] [DE:Borrelia burgdorferi plasmid cp26, complete plasmid sequence.] [NT:similar to GB:M88764 SP:Q09090 PID:469166] [LE:4769] [RE:5866] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000997_5266018_f2_160	2792	6564	771	256	415	7.8e-39

Description

sp:[LN:YFIA_BACSU] [AC:P54717] [GN:YFIA] [OR:BACILLUS SUBTILIS]
[DE:HYPOTHETICAL 29.3 KD PROTEIN IN GLVG-GLVBC INTERGENIC REGION]
[SP:P54717] [DB:swissprot] >pir:[LN:D69802] [AC:D69802] [PN:conserved
hypothetical protein yfiA] [GN:yfiA] [OR:Bacillus subtilis] [DB:pir2]
>gp:[GI:e1182809:g2633143] [LN:BSUB0005] [AC:Z99108:AL009126] [GN:yfiA]
[FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
complete genome (section 5 of 21): from 802821 to1011250.] [NT:similar to
hypothetical proteins] [SP:P54717] [LE:88122] [RE:88886] [DI:direct]
>gp:[GI:d1009739:g1486242] [LN:D50543] [AC:D50543] [PN:unknown] [GN:yfiA]
[FN:unknown] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:168,
haplotype:haploid) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis DNA for
76-degree region, complete cds.] [LE:1798] [RE:2562] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000997_5898328_f2_91	2793	6565	864	287	1102	1.2e-111

Description

gp:[GI:e324855:g2226001] [LN:SXY14043] [AC:Y14043] [PN:glucose uptake
protein] [GN:glcU] [OR:Staphylococcus xylosus] [DB:genpept-bct1]
[DE:Staphylococcus xylosus glcU and gdh genes.] [LE:306] [RE:1172]
[DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000997_6050010_c3_404	2794	6566	129	42		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000997_6757755_f2_121	2795	6567	171	56		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000997_6929676_c1_255	2796	6568	342	113		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000997_7031318_f2_153	2797	6569	339	112		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000997_7086677_c3_364	2798	6570	243	80	78	0.019

Description

sp:[LN:LY4F_MOUSE] [AC:Q60653] [GN:LY49F:LY-49F:LY49-F] [OR:MUS MUSCULUS] [SR:,MOUSE] [DE:T-CELL SURFACE GLYCOPROTEIN LY-49F (LY49-F ANTIGEN)] [SP:Q60653] [DB:swissprot] >pir:[LN:I49051] [AC:I49051] [PN:Ly-49F-GE antigen] [OR:Mus musculus] [SR:, house mouse] [DB:pir2] >gp:[GI:g533492] [LN:MMU10092] [AC:U10092] [PN:Ly-49F-GE antigen] [OR:Mus musculus] [SR:house mouse] [DB:genpept-rod] [DE:Mus musculus C57BL/6 Ly-49F-GE antigen mRNA, complete cds.] [LE:81] [RE:881] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000997_818812_c2_337	2799	6571	1287	428	1560	3.6e-160

Description

gp:[GI:e1429624:g4756160] [LN:A67171] [AC:A67171] [FN:MOEA GENE] [OR:Staphylococcus carnosus] [DB:genpept-pat] [DE:Sequence 11 from Patent EP0805205.] [NT:unnamed protein product] [LE:2396] [RE:3655] [DI:direct] >gp:[GI:g3955204] [LN:AF022796] [AC:AF022796] [PN:MoeA] [GN:moeA] [OR:Staphylococcus carnosus] [DB:genpept-bct2] [DE:Staphylococcus carnosus molybdenum cofactor biosynthetic genecluster, complete sequence.] [NT:protein similar to MoeA of Escherichia coli] [LE:4617] [RE:5876] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000997_829761_c1_288	2800	6572	2172	723	1751	2.1e-180

Description

pir:[LN:H69724] [AC:H69724] [PN:DNA topoisomerase III topB] [GN:topB] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:d1020016:g1881236] [LN:AB001488] [AC:AB001488] [PN:PROBABLE DNA TOPOISOMERASE III] [GN:topB] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:168) DNA] [DB:genpept-bct1] [EC:5.99.1.2] [DE:Bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.] [LE:9617] [RE:11800] [DI:direct] >gp:[GI:e1182392:g2632726] [LN:BSUB0003] [AC:Z99106:AL009126] [PN:DNA topoisomerase III] [GN:topB] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:5.99.1.2] [DE:Bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.] [LE:73361] [RE:75544] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000997_834686_c2_290	2801	6573	132	43		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000997_959427_f1_62	2802	6574	417	138	241	2.2e-20

Description

gp:[GI:g2735506] [LN:SCU96107] [AC:U96107] [PN:SceB precursor] [GN:sceB]
[OR:Staphylococcus carnosus] [DB:genpept-bct2] [DE:Staphylococcus carnosus
N5,N10-methylenetetrahydromethanopterinreductase homolog, SceB precursor
(sceB) and putative transmembraneprotein genes, complete cds, and putative
Na+/H+ antiporter NhaC(nhaC) gene, partial cds.] [NT:major secreted protein]
[LE:1894] [RE:2685] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000997_964077_c1_275	2803	6575	453	150	659	1.1e-64

Description

gp:[GI:g3955206] [LN:AF022796] [AC:AF022796] [PN:MoaE] [GN:moaE]
[OR:Staphylococcus carnosus] [DB:genpept-bct2] [DE:Staphylococcus carnosus
molybdenum cofactor biosynthetic genecluster, complete sequence.]
[NT:protein similar to MoaE of Escherichia coli] [LE:6352] [RE:6804]
[DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000997_975061_c3_377	2804	6576	1455	484	916	6.4e-92

Description

sp:[LN:YB07_HAEIN] [AC:Q57007:P96339] [GN:HI1107] [OR:HAEMOPHILUS
INFLUENZAE] [DE:HYPOTHETICAL NA+/H+ ANTIPORTER HI1107] [SP:Q57007:P96339]
[DB:swissprot] >pir:[LN:I64182] [AC:I64182] [PN:Na+/H+-exchanging protein
homolog:Na+/H+ antiporter] [CL:Na+/H+-exchanging protein] [OR:Haemophilus
influenzae] [DB:pir2] >gp:[GI:g1574661] [LN:U32790] [AC:U32790:L42023]
[PN:Na+/H+ antiporter (nhaC)] [GN:HI1107] [OR:Haemophilus influenzae Rd]
[DB:genpept-bct2] [DE:Haemophilus influenzae Rd section 105 of 163 of the
completegenome.] [NT:similar to GB:M73530 SP:P27611 PID:143245] [LE:7526]
[RE:8932] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000997_9845631_f3_222	2805	6577	156	51		
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Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000997_9928188_f1_39	2806	6578	132	43	95	0.00025
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Description

sp:[LN:NARQ_BACSU] [AC:P39756] [GN:NARQ:NARAA] [OR:BACILLUS SUBTILIS]
 [DE:NARQ PROTEIN] [SP:P39756] [DB:swissprot] >pir:[LN:B69665] [AC:B69665]
 [PN:required for formate dehydrogenase activity narQ] [GN:narQ]
 [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e276834:g1648855] [LN:BSATPC]
 [AC:Z81356] [PN:unknown] [GN:narQ] [OR:Bacillus subtilis] [DB:genpept-bct1]
 [DE:B.subtilis atpC gene.] [SP:P39756] [LE:7048] [RE:7836] [DI:direct]
 >gp:[GI:g580895] [LN:BSNARAAB] [AC:Z35277] [PN:unknown] [GN:narAA]
 [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis (168) narA gene.]
 [SP:P39756] [LE:490] [RE:1278] [DI:direct] >gp:[GI:e1184577:g2636196]
 [LN:BSUB0019] [AC:Z99122:AL009126] [GN:narQ] [FN:required for formate
 dehydrogenase activity] [OR:Bacillus subtilis] [DB:genpept-bct1]
 [DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091to
 3809700.] [NT:alternate gene name: narAA] [SP:P39756] [LE:175331]
 [RE:176119] [DI:complement] >gp:[GI:e1184577:g2636196] [LN:BSUB0019]
 [AC:Z99122:AL009126] [GN:narQ] [FN:required for formate dehydrogenase
 activity] [OR:Bacillus subtilis] [DB:genpept] [DE:Bacillus subtilis complete
 genome (section 19 of 21): from 3597091to 3809700.] [NT:alternate gene name:
 narAA] [SP:P39756] [LE:175331] [RE:176119] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000997_9928500_c1_270	2807	6579	261	86	286	3.7e-25
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Description

gp:[GI:e1429618:g4756158] [LN:A67171] [AC:A67171] [FN:MOEB GENE]
 [OR:Staphylococcus carnosus] [DB:genpept-pat] [DE:Sequence 11 from Patent
 EP0805205.] [NT:unnamed protein product] [LE:117] [RE:1118] [DI:direct]
 >gp:[GI:g3955201] [LN:AF022796] [AC:AF022796] [PN:MoeB] [GN:moeB]
 [OR:Staphylococcus carnosus] [DB:genpept-bct2] [DE:Staphylococcus carnosus
 molybdenum cofactor biosynthetic genecluster, complete sequence.]
 [NT:protein similar to the molybdopterin synthase] [LE:2338] [RE:3339]
 [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000997_9977318_f1_75	2808	6580	1437	478	700	4.9e-69

Description

pir:[LN:D65017] [AC:D65017] [PN:hypothetical protein b2429]
[CL:phosphotransferase system sucrose-specific enzyme II, factor II]
[OR:Escherichia coli] [DB:pir2] >gp:[GI:d1017042:g1799859] [LN:D90872]
[AC:D90872:AB001340] [PN:PTS SYSTEM, SUCROSE-SPECIFIC IIBC COMPONENT]
[GN:IPA-49D] [OR:Escherichia coli] [SR:Escherichia coli (strain:K12) DNA,
clone_lib:Kohara lambda minise] [DB:genpept-bct1] [DE:E.coli genomic DNA,
Kohara clone #419(54.7-55.1 min.)] [NT:similar to [SwissProt Accession
Number P05306]] [LE:9801] [RE:11225] [DI:direct] >gp:[GI:d1017045:g1799863]
[LN:D90873] [AC:D90873:AB001340] [PN:PTS SYSTEM, SUCROSE-SPECIFIC IIBC
COMPONENT] [GN:IPA-49D] [OR:Escherichia coli] [SR:Escherichia coli
(strain:K12) DNA, clone_lib:Kohara lambda minise] [DB:genpept-bct1]
[DE:E.coli genomic DNA, Kohara clone #420(54.9-55.2 min.)] [NT:similar to
[SwissProt Accession Number P05306]] [LE:611] [RE:2035] [DI:direct]
>gp:[GI:g1788769] [LN:AE000330] [AC:AE000330:U00096] [PN:putative PTS enzyme
II] [GN:b2429] [FN:putative enzyme; Not classified] [OR:Escherichia coli]
[DB:genpept-bct2] [DE:Escherichia coli K-12 MG1655 section 220 of 400 of the
completegenome.] [NT:o474; 33 pct identical (29 gaps) to 436 residues]
[LE:5237] [RE:6661] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000998_10159760_f1_50	2809	6581	156	51		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000998_10312805_f3_197	2810	6582	144	47		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000998_10646950_c1_238	2811	6583	1221	406	1151	8.0e-117

Description

pir:[LN:A69974] [AC:A69974] [PN:cystathionine gamma-synthase homolog yrhB] [GN:yrhB] [CL:O-succinylhomoserine (thiol)-lyase] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:g1934606] [LN:BSU93874] [AC:U93874] [PN:cystathionine gamma-lyase] [GN:yrhB] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis cysteine synthase (yrhA), cystathionine gamma-lyase (yrhB), YrhC (yrhC), YrhD (yrhD), formate dehydrogenase chain A (yrhE), YrhF (yrhF), formate dehydrogenase (yrhG), YrhH (yrhH), regulatory protein (yrhI), cytochrome P450 102 (yrhJ), YrhK (yrhK), hypothetical protein YrhL (yrhL), putative anti-SigV factor (yrhM), RNA polymerase sigma factor SigV (sigV) and YrhO (yrhO) genes, complete cds, and YrhP (yrhP) gene, partial cds.] [NT:similar to Rattus norvegicus cystathionine] [LE:986] [RE:2125] [DI:direct] >gp:[GI:e1183955:g2635171] [LN:BSUB0014] [AC:Z99117:AL009126] [GN:yrhB] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 14 of 21): from 2599451 to 2812870.] [NT:similar to cystathionine gamma-synthase] [LE:184821] [RE:185960] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000998_10723177_f1_59	2812	6584	255	84		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000998_11213532_c3_351	2813	6585	246	81	90	0.00022

Description

gp:[GI:g208931] [LN:SYNORFLAC] [AC:M15619] [OR:synthetic construct] [SR:E.coli (strain SE5000) synthetic DNA, clone pKB1] [DB:genpept-syn] [DE:Synthetic E.coli ORF16/lacZ fusion protein, partial cds.] [NT:ORF16-lacZ fusion protein] [LE:29] [RE:>232] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000998_1178785_c3_323	2814	6586	939	312	731	2.6e-72

Description

pir:[LN:H69973] [AC:H69973] [PN:cysteine synthase homolog yrhA] [GN:yrhA] [CL:threonine dehydratase] [OR:Bacillus subtilis] [DB:pir2]
 >gp:[GI:g1934605] [LN:BSU93874] [AC:U93874] [PN:cysteine synthase] [GN:yrhA] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis cysteine synthase (yrhA), cystathionine gamma-lyase (yrhB), YrhC (yrhC), YrhD (yrhD), formate dehydrogenase chain A (yrhE), YrhF (yrhF), formate dehydrogenase (yrhG), YrhH (yrhH), regulatory protein (yrhI), cytochrome P450 102 (yrhJ), YrhK (yrhK), hypothetical protein YrhL (yrhL), putative anti-SigV factor (yrhM), RNA polymerase sigma factor SigV (sigV) and YrhO (yrhO) genes, complete cds, and YrhP (yrhP) gene, partial cds.] [NT:similar to cysteine synthase from Spinacia] [LE:61] [RE:984] [DI:direct]
 >gp:[GI:e1183956:g2635172] [LN:BSUB0014] [AC:Z99117:AL009126] [GN:yrhA] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 14 of 21): from 2599451 to 2812870.] [NT:similar to cysteine synthase] [LE:185962] [RE:186885] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000998_11931540_f2_96	2815	6587	825	274	786	3.8e-78

Description

sp:[LN:YLAC_STAXY] [AC:O33812] [OR:STAPHYLOCOCCUS XYLOSUS] [DE:HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN LACR 5' REGION (FRAGMENT)] [SP:O33812] [DB:swissprot] >gp:[GI:e352090:g2462703] [LN:SXLACRPH] [AC:Y14599] [PN:transcriptional regulator from the LysR-type] [OR:Staphylococcus xylosus] [DB:genpept-bct1] [DE:Staphylococcus xylosus lacR, lacP, lacH genes and 2 ORF's.] [NT:ORF1] [SP:O33812] [LE:<1] [RE:814] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000998_1256387_c2_297	2816	6588	129	42		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000998_12603166_f2_86	2817	6589	303	100	100	1.9e-05

Description

pir:[LN:G71244] [AC:G71244] [PN:hypothetical protein PH0217] [GN:PH0217]
 [OR:Pyrococcus horikoshii] [DB:pir2] >gp:[GI:d1030229:g3256603]
 [LN:AP000001]
 [AC:AP000001:AB009465:AB009464:AB009466:AB009467:AB009468:AB009469]
 [PN:106aa long hypothetical protein] [GN:PH0217] [OR:Pyrococcus horikoshii]
 [SR:Pyrococcus horikoshii (strain:OT3) DNA] [DB:genpept-bct1] [DE:Pyrococcus
 horikoshii OT3 genomic DNA, 1-287000 nt. position (1/7).] [LE:191072]
 [RE:191392] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000998_126068_f1_46	2818	6590	555	184	164	3.4e-11

Description

pir:[LN:A71661] [AC:A71661] [PN:hypothetical protein RP563] [GN:RP563]
 [OR:Rickettsia prowazekii] [DB:pir2] >gp:[GI:e1342855:g3861111] [LN:RPXX03]
 [AC:AJ235272:AJ235269] [PN:unknown] [GN:RP563] [OR:Rickettsia prowazekii]
 [DB:genpept-bct1] [DE:Rickettsia prowazekii strain Madrid E, complete
 genome; segment3/4.] [LE:110476] [RE:112242] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000998_13089052_f3_214	2819	6591	123	40		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000998_13678300_c2_267	2820	6592	1233	410	1393	1.8e-142

Description

pir:[LN:B69760] [AC:B69760] [PN:conserved hypothetical protein yciC]
 [GN:yciC] [CL:conserved hypothetical protein yciC] [OR:Bacillus subtilis]
 [DB:pir2] >gp:[GI:e1182288:g2632622] [LN:BSUB0002] [AC:Z99105:AL009126]
 [GN:yciC] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus
 subtilis complete genome (section 2 of 21): from 194651 to415810.]
 [NT:similar to hypothetical proteins] [LE:170984] [RE:172177] [DI:direct]
 >gp:[GI:d1009605:g1805408] [LN:D50453] [AC:D50453] [PN:homologues to nitrile
 hydratase region] [GN:yciC] [OR:Bacillus subtilis] [SR:Bacillus subtilis
 (strain:168 trpC2) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis DNA for
 25-36 degree region containing theamyE-srfA region, complete cds.]
 [LE:45287] [RE:46480] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000998_13912712_c3_312	2821	6593	150	49	52	0.015

Description

sp:[LN:IMM1_ECOLI] [AC:P02985] [GN:IMM] [OR:ESCHERICHIA COLI] [DE:COLICIN E1 IMMUNITY PROTEIN (IMME1) (MICROCIN E1 IMMUNITY PROTEIN)] [SP:P02985]
[DB:swissprot] >gp:[GI:g455140] [LN:CE1CEA] [AC:M12543] [OR:Plasmid ColE1]
[SR:Plasmid ColE1 (a colicin-producing derivative strain from E.col)]
[DB:genpept-bct1] [DE:Plasmid ColE1 cea (3' end), imm and lys genes
(complete cds).] [NT:immunity protein] [LE:32] [RE:373] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000998_13923427_f3_196	2822	6594	135	44		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000998_14218805_c2_301	2823	6595	129	42	80	0.0095

Description

sp:[LN:TRER_BACSU] [AC:P39796] [GN:TRER] [OR:BACILLUS SUBTILIS]
[DE:TREHALOSE OPERON TRANSCRIPTIONAL REPRESSOR] [SP:P39796] [DB:swissprot]
>pir:[LN:JC5038] [AC:JC5038:S67931:D69725:I40499:S67866] [PN:transcription
repressor of trehalose operon treR] [GN:treR] [OR:Bacillus subtilis]
[DB:pir2] >gp:[GI:g1000453] [LN:BSTREAPR] [AC:Z54245] [PN:TreR] [GN:treR]
[FN:repressor of the trehalose operon] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:B.subtilis treA, treP and treR genes.] [NT:position
3684 corresponds to position 2543 of] [SP:P39796] [LE:3352] [RE:4068]
[DI:direct] >gp:[GI:e1182772:g2633106] [LN:BSUB0005] [AC:Z99108:AL009126]
[PN:transcriptional regulator (GntR family)] [GN:treR] [FN:negative
regulation of the trehalose operon] [OR:Bacillus subtilis] [DB:genpept-bct1]
[DE:Bacillus subtilis complete genome (section 5 of 21): from 802821
to1011250.] [NT:alternate gene name: yfxA] [SP:P39796] [LE:50243] [RE:50959]
[DI:direct] >gp:[GI:d1024286:g2626829] [LN:D83967] [AC:D83967] [PN:TreR]
[OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:AC327) DNA]
[DB:genpept-bct1] [DE:Bacillus subtilis genomic DNA, 74 degree region.]
[LE:16962] [RE:17678] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000998_14271068_f1_51	2824	6596	261	86	68	0.018

Description

sp:[LN:PROP_ECOLI] [AC:P30848] [GN:PROP] [OR:ESCHERICHIA COLI]
 [DE:PROLINE/BETAINE TRANSPORTER (PROLINE PORTER II) (PPII)] [SP:P30848]
 [DB:swissprot] >pir:[LN:S32331] [AC:S32331:S56339:F65220]
 [PN:proline/betaine transport protein:proline permease II:proline porter II]
 [GN:proP] [CL:citrate utilization determinant] [OR:Escherichia coli]
 [DB:pir2] [MP:93 min] >gp:[GI:g147357] [LN:ECOPROBETT] [AC:M83089] [PN:a
 proline/betaine transporter] [GN:proP] [FN:active uptake of proline or
 betaine] [OR:Escherichia coli] [DB:genpept-bct1] [DE:E. coli proline/betaine
 transporter (proP) gene, complete cds.] [NT:Evidence that this open reading
 frame encodes a] [LE:433] [RE:1935] [DI:direct] >gp:[GI:g536955]
 [LN:ECOUW93] [AC:U14003] [GN:proP] [FN:active uptake of proline or betaine]
 [OR:Escherichia coli] [DB:genpept-bct1] [DE:Escherichia coli K-12
 chromosomal region from 92.8 to 00.1 minutes.] [NT:CG Site No. 361]
 [LE:21331] [RE:22833] [DI:direct] >gp:[GI:g1790550] [LN:AE000483]
 [AC:AE000483:U00096] [PN:low-affinity transport system; proline permease]
 [GN:proP] [FN:transport; Transport of small molecules: Amino]
 [OR:Escherichia coli] [DB:genpept-bct2] [DE:Escherichia coli K-12 MG1655
 section 373 of 400 of the completegenome.] [NT:o500; 100 pct identical to
 PROP_ECOLI SW: P30848;] [LE:5301] [RE:6803] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000998_14460882_c1_217	2825	6597	1695	564	1304	4.9e-133

Description

gp:[GI:g1022726] [LN:SHU35635] [AC:U35635] [PN:unknown] [OR:Staphylococcus
 haemolyticus] [SR:Staphylococcus haemolyticus strain=Y176] [DB:genpept-bct1]
 [DE:Staphylococcus haemolyticus IS1272 ORF1 and ORF2 genes, completedcds.]
 [NT:ORF1] [LE:1101] [RE:1922] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000998_14485686_c2_287	2826	6598	153	50		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000998_15022153_f1_73	2827	6599	189	62		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000998_15900305_f3_177	2828	6600	789	262	78	0.019

Description

gp:[GI:g453517] [LN:TETRRTRNA] [AC:L28677] [OR:Mitochondrion Tetrahymena pyriformis] [SR:Mitochondrion Tetrahymena pyriformis (strain ST, organelle)] [DB:genpept-inv1] [DE:Tetrahymena pyriformis ribosomal RNA; tRNA-Trp; ORF 1-4; tRNA-Glu;cytochrome oxidase subunit 1; NADH dehydrogenase; ribosomal proteinL14.] [NT:ORF3] [LE:4384] [RE:4680] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000998_16196963_f2_133	2829	6601	192	63		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000998_16257665_f1_37	2830	6602	192	63		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000998_16281286_c3_322	2831	6603	1359	452	1059	4.5e-107

Description

pir:[LN:F69825] [AC:F69825] [PN:sodium-dependent transporter homolog yhdH] [GN:yhdH] [CL:gamma-aminobutyric acid transporter] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1182948:g2633282] [LN:BSUB0006] [AC:Z99109:AL009126] [GN:yhdH] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.] [NT:similar to sodium-dependent transporter] [LE:24845] [RE:26200] [DI:direct] >gp:[GI:e1191879:g2226203] [LN:BSY14082] [AC:Y14082] [PN:hypothetical protein] [GN:yhdH] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis chromosomal DNA, region 72 to 75 degrees: spoVRto sspB.] [NT:Similarity to sodium dependent transporters;] [LE:11493] [RE:12848] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000998_19712762_c3_347	2832	6604	600	199	813	5.2e-81

Description

sp:[LN:RECR_BACSU] [AC:P24277] [GN:RECR:RECM:RECD] [OR:BACILLUS SUBTILIS] [DE:RECOMBINATION PROTEIN RECR] [SP:P24277] [DB:swissprot] >pir:[LN:B69691] [AC:B69691:S13788:S66051] [PN:DNA repair and genetic recombination recR:recM protein] [GN:recR] [CL:recR protein] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:d1005799:g467411] [LN:BAC180K] [AC:D26185] [PN:recombination protein] [GN:recR] [OR:Bacillus subtilis] [SR:Bacillus subtilis (sub_species:Marburg, strain:168) DNA] [DB:genpept-bct1] [DE:B. subtilis DNA, 180 kilobase region of replication origin.] [LE:92467] [RE:93063] [DI:direct] >gp:[GI:g453239] [LN:BSRECM] [AC:X17014] [GN:recR] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis dnaZX and recR genes and two unidentified readingframes.] [SP:P24277] [LE:2314] [RE:2910] [DI:direct] >gp:[GI:e1181954:g2632288] [LN:BSUB0001] [AC:Z99104:AL009126] [GN:recR] [FN:DNA repair and genetic recombination] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 1 of 21): from 1 to213080.] [NT:alternate gene name: recM] [SP:P24277] [LE:28865] [RE:29461] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000998_19960162_c1_232	2833	6605	2631	876	1785	5.2e-184

Description

pir:[LN:E69745] [AC:E69745] [PN:hypothetical protein ybcd] [GN:ybcd] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1182118:g2632452] [LN:BSUB0001] [AC:Z99104:AL009126] [GN:ybcd] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 1 of 21): from 1 to213080.] [LE:207166] [RE:209430] [DI:direct] >gp:[GI:e1182136:g2632470] [LN:BSUB0002] [AC:Z99105:AL009126] [GN:ybcd] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.] [LE:12516] [RE:14780] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000998_20093_c3_311	2834	6606	306	101		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000998_20602263_c2_270	2838	6610	1512	503	1414	1.1e-144

Description

sp:[LN:NDHF_BACSU] [AC:P39755] [GN:NDHF] [OR:BACILLUS SUBTILIS] [EC:1.6.5.3] [DE:OXIDOREDUCTASE CHAIN 5)] [SP:P39755] [DB:swissprot] >pir:[LN:C69666] [AC:C69666] [PN:NADH dehydrogenase (subunit 5) ndhF] [GN:ndhF] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:d1034042:g3599601] [LN:AB006424] [AC:AB006424] [PN:NADH DEHYDROGENASE SUBUNIT 5] [GN:ndhF] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:168) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis genomic DNA, 70 kb region between 17 and 23degree.] [LE:8378] [RE:9895] [DI:direct] >gp:[GI:g903587] [LN:BSU28323] [AC:U28323] [PN:NADH dehydrogenase subunit 5] [GN:ndhF] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis NADH dehydrogenase subunit 5 (ndhF) gene,complete cds.] [LE:519] [RE:2036] [DI:direct] >gp:[GI:e1182116:g2632450] [LN:BSUB0001] [AC:Z99104:AL009126] [PN:NADH dehydrogenase (subunit 5)] [GN:ndhF] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:1.6.5.3] [DE:Bacillus subtilis complete genome (section 1 of 21): from 1 to213080.] [NT:alternate gene name: ybxE] [SP:P39755] [LE:205395] [RE:206912] [DI:direct] >gp:[GI:e1182134:g2632468] [LN:BSUB0002] [AC:Z99105:AL009126] [PN:NADH dehydrogenase (subunit 5)] [GN:ndhF] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:1.6.5.3] [DE:Bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.] [NT:alternate gene name: ybxE] [SP:P39755] [LE:10745] [RE:12262] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000998_2142316_f3_207	2839	6611	213	70	52	0.040

Description

gp:[GI:e1287275:g3063696] [LN:ATF4D11] [AC:AL022537] [PN:putative protein] [GN:F4D11.60] [OR:Arabidopsis thaliana] [SR:thale cress] [DB:genpept-pln1] [DE:Arabidopsis thaliana DNA chromosome 4, BAC clone F4D11 (ESSAIIproject).] [NT:contains EST gb:W43721] [LE:21418:21729:22060] [RE:21537:22004:22174] [DI:complementJoin]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000998_21516287_f1_2	2840	6612	126	41		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000998_2195338_c3_342	2841	6613	165	54		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000998_22305342_f3_205	2842	6614	543	180	162	8.7e-11

Description

gp:[GI:g4019275] [LN:AF083424] [AC:AF083424] [OR:Ateline herpesvirus 3]
[DB:genpept-vr1] [DE:Ateline herpesvirus 3 complete genome.] [NT:orf 48]
[LE:62159] [RE:64537] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000998_22437751_c3_307	2843	6615	489	162	160	5.5e-11

Description

pir:[LN:T03492] [AC:T03492] [PN:hypothetical protein] [OR:Rhodobacter
capsulatus] [DB:pir2] [MP:1] >gp:[GI:g3128293] [LN:AF010496] [AC:AF010496]
[PN:hypothetical protein] [OR:Rhodobacter capsulatus] [DB:genpept-bct2]
[DE:Rhodobacter capsulatus strain SB1003, partial genome.] [LE:54291]
[RE:55613] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000998_22459802_f2_135	2844	6616	156	51	117	1.0e-06

Description

gp:[GI:g1022726] [LN:SHU35635] [AC:U35635] [PN:unknown] [OR:Staphylococcus
haemolyticus] [SR:Staphylococcus haemolyticus strain=Y176] [DB:genpept-bct1]
[DE:Staphylococcus haemolyticus IS1272 ORF1 and ORF2 genes, completedcs.]
[NT:ORF1] [LE:1101] [RE:1922] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000998_22688428_c3_348	2845	6617	144	47		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000998_23484678_c2_304	2846	6618	1731	576	1263	1.1e-128

Description

pir:[LN:S13786] [AC:S13786:S00745:S66049:B69618] [PN:DNA-directed DNA polymerase, III chain dnaX:DNA polymerase III (gamma and tau subunits) dnaX] [GN:dnaX:dnaZX] [OR:Bacillus subtilis] [EC:2.7.7.7] [DB:pir2]
 >gp:[GI:d1005797:g467409] [LN:BAC180K] [AC:D26185] [PN:DNA polymerase III subunit] [GN:dnaH] [OR:Bacillus subtilis] [SR:Bacillus subtilis (sub_species:Marburg, strain:168) DNA] [DB:genpept-bct1] [DE:B. subtilis DNA, 180 kilobase region of replication origin.] [LE:90414] [RE:92105] [DI:direct] >gp:[GI:g580914] [LN:BSRECM] [AC:X17014] [GN:dnaZX] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis dnaZX and recR genes and two unidentified readingframes.] [SP:P09122] [LE:261] [RE:1952] [DI:direct] >gp:[GI:e1181952:g2632286] [LN:BSUB0001] [AC:Z99104:AL009126] [PN:DNA polymerase III (gamma and tau subunits)] [GN:dnaX] [FN:DNA synthesis] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:2.7.7.7] [DE:Bacillus subtilis complete genome (section 1 of 21): from 1 to213080.] [NT:alternate gene name: dnaH, dna-8132] [SP:P09122] [LE:26812] [RE:28503] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000998_23556500_f1_33	2847	6619	282	93		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000998_2359675_c3_329	2848	6620	141	46	68	0.047

Description

pir:[LN:S72295] [AC:S72295] [PN:ribosomal protein S8] [GN:rps8] [OR:plastid Plasmodium falciparum] [DB:pir2] >gp:[GI:e220199:g1171601] [LN:PFCOMPIRB] [AC:X95276] [GN:rps8] [OR:Plasmodium falciparum] [SR:malaria parasite P. falciparum] [DB:genpept-inv1] [DE:P.falciparum complete gene map of plastid-like DNA (IR-B).] [LE:5492] [RE:5878] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000998_23631262_f2_94	2849	6621	150	49		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000998_23994687_f1_45	2850	6622	132	43		
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Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000998_24016916_c3_341	2851	6623	1044	347	396	8.1e-37
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Description

sp:[LN:YEIH_ECOLI] [AC:P33019] [GN:YEIH] [OR:ESCHERICHIA COLI]
 [DE:HYPOTHETICAL 36.9 KD PROTEIN IN LYSP-NFO INTERGENIC REGION] [SP:P33019]
 [DB:swissprot] >pir:[LN:E64984] [AC:E64984] [PN:hypothetical 36.9 kD
 protein in lysP-nfo intergenic region] [GN:yeiH] [OR:Escherichia coli]
 [DB:pir2] >gp:[GI:g405879] [LN:ECOHU47] [AC:U00007] [PN:yeiH]
 [OR:Escherichia coli] [SR:Escherichia coli K12 BHB2600] [DB:genpept-bct1]
 [DE:47 to 48 centisome region of E.coli K12 BHB2600.] [LE:57462] [RE:58511]
 [DI:direct] >gp:[GI:g1788482] [LN:AE000305] [AC:AE000305:U00096] [PN:orf,
 hypothetical protein] [GN:yeiH] [FN:orf; Unknown] [OR:Escherichia coli]
 [DB:genpept-bct2] [DE:Escherichia coli K-12 MG1655 section 195 of 400 of the
 completegenome.] [NT:o349; 100 pct identical to YEIH_ECOLI SW: P33019]
 [LE:2831] [RE:3880] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000998_24220967_c1_228	2852	6624	138	45		
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Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000998_24227192_c3_343	2853	6625	147	48		
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Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000998_24235626_c1_257	2854	6626	159	52		
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Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000998_24272337_f3_204	2855	6627	432	143	96	0.0025

Description

pir:[LN:D69633] [AC:D69633] [PN:glutamine ABC transporter (glutamine-binding protein) glnH] [GN:glnH] [CL:lysine-arginine-ornithine-binding protein] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1183973:g2635189] [LN:BSUB0014] [AC:Z99117:AL009126] [PN:glutamine ABC transporter (glutamine-binding) [GN:glnH] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.] [LE:202928] [RE:203749] [DI:direct] >gp:[GI:e1183991:g2635207] [LN:BSUB0015] [AC:Z99118:AL009126] [PN:glutamine ABC transporter (glutamine-binding) [GN:glnH] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.] [LE:7248] [RE:8069] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000998_24350953_f1_6	2856	6628	132	43	72	0.017

Description

pir:[LN:G71244] [AC:G71244] [PN:hypothetical protein PH0217] [GN:PH0217] [OR:Pyrococcus horikoshii] [DB:pir2] >gp:[GI:d1030229:g3256603] [LN:AP000001] [AC:AP000001:AB009465:AB009464:AB009466:AB009467:AB009468:AB009469] [PN:106aa long hypothetical protein] [GN:PH0217] [OR:Pyrococcus horikoshii] [SR:Pyrococcus horikoshii (strain:OT3) DNA] [DB:genpept-bct1] [DE:Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt. position (1/7).] [LE:191072] [RE:191392] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000998_24390937_f3_198	2857	6629	156	51		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000998_24391885_f3_178	2858	6630	183	60		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000998_24475252_f3_213	2859	6631	159	52		
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Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000998_24664802_c1_234	2860	6632	747	248	380	4.0e-35
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Description

pir:[LN:H70027] [AC:H70027] [PN:carboxylesterase homolog yvaK] [GN:yvaK]
 [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1186050:g2635875] [LN:BSUB0018]
 [AC:Z99121:AL009126] [GN:yvaK] [FN:unknown] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 18 of 21):
 from 3399551to 3609060.] [NT:similar to carboxylesterase] [LE:53733]
 [RE:54479] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000998_25422288_c2_277	2861	6633	153	50		
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Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000998_25442803_c2_306	2862	6634	261	86		
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Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000998_25586693_c3_346	2863	6635	333	110	374	1.7e-34

Description

sp:[LN:YAAK_BACSU] [AC:P24281] [GN:YAAK] [OR:BACILLUS SUBTILIS]
[DE:HYPOTHETICAL 11.8 KD PROTEIN IN DNAZ-RECR INTERGENIC REGION] [SP:P24281]
[DB:swissprot] >pir:[LN:S13787] [AC:S13787:S66050:C69737] [PN:conserved
hypothetical protein yaaK] [GN:yaaK] [OR:Bacillus subtilis] [DB:pir2]
>gp:[GI:d1005798:g467410] [LN:BAC180K] [AC:D26185] [PN:unknown] [OR:Bacillus
subtilis] [SR:Bacillus subtilis (sub_species:Marburg, strain:168) DNA]
[DB:genpept-bct1] [DE:B. subtilis DNA, 180 kilobase region of replication
origin.] [LE:92129] [RE:92452] [DI:direct] >gp:[GI:g40073] [LN:BSRECM]
[AC:X17014] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
dnaZX and recR genes and two unidentified readingframes.] [NT:ORF107]
[SP:P24281] [LE:1976] [RE:2299] [DI:direct] >gp:[GI:e1181953:g2632287]
[LN:BSUB0001] [AC:Z99104:AL009126] [GN:yaaK] [FN:unknown] [OR:Bacillus
subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 1
of 21): from 1 to213080.] [NT:similar to hypothetical proteins] [SP:P24281]
[LE:28527] [RE:28850] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000998_256468_c2_294	2864	6636	330	109		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000998_26460887_f1_34	2865	6637	1524	507	366	6.4e-32

Description

sp:[LN:TAGE_BACSU] [AC:P13484] [GN:TAGE:RODD:GTAA] [OR:BACILLUS SUBTILIS]
[EC:2.4.1.52] [DE:(EC 2.4.1.52) (TEICHOIC ACID BIOSYNTHESIS PROTEIN E)]
[SP:P13484] [DB:swissprot] >pir:[LN:S06048] [AC:S06048:F69720]
[PN:poly(glycerol-phosphate) alpha-glucosyltransferase, tagE:probable rodD
protein:UDP-glucose--polyglycerol phosphate glucosyltransferase tagE]
[GN:tagE:rodD] [OR:Bacillus subtilis] [EC: 2.4.1.52] [DB:pir2] [MP:310
degrees] >gp:[GI:g580920] [LN:BSRODC] [AC:X15200] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis rodC operon.] [NT:rodD (gtaA)
polypeptide (AA 1-673)] [SP:P13484] [LE:157] [RE:2178] [DI:direct]
>gp:[GI:e1184479:g2636099] [LN:BSUB0019] [AC:Z99122:AL009126]
[PN:UDP-glucose:polyglycerol phosphate] [GN:tagE] [FN:teichoic acid
biosynthesis] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:2.4.1.52]
[DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091to
3809700.] [NT:alternate gene name: rodD, gtaA, gtaD] [SP:P13484] [LE:80369]
[RE:82390] [DI:complement] >gp:[GI:e1184479:g2636099] [LN:BSUB0019]
[AC:Z99122:AL009126] [PN:UDP-glucose:polyglycerol phosphate] [GN:tagE]
[FN:teichoic acid biosynthesis] [OR:Bacillus subtilis] [DB:genpept]
[EC:2.4.1.52] [DE:Bacillus subtilis complete genome (section 19 of 21): from
3597091to 3809700.] [NT:alternate gene name: rodD, gtaA, gtaD] [SP:P13484]
[LE:80369] [RE:82390] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000998_26776562_c3_317	2866	6638	399	132		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000998_2769816_f3_206	2867	6639	135	44	135	2.5e-08

Description

gp:[GI:g2689564] [LN:U93688] [AC:U93688] [PN:integrase] [GN:int]
[OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus toxic
shock syndrome toxin-1 (tst), enterotoxin (ent), and integrase (int) genes,
complete cds.] [NT:similar to staphylococcal phage integrase] [LE:13871]
[RE:15091] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000998_30265952_c2_291	2868	6640	387	128	118	2.3e-07

Description

pir:[LN:H69029] [AC:H69029] [PN:mutator MutT related protein] [GN:MTH122]
[CL:mutT domain homology] [OR:Methanobacterium thermoautotrophicum]
[DB:pir2] >gp:[GI:g2621161] [LN:AE000801] [AC:AE000801:AE000666] [PN:mutator
MutT related protein] [GN:MTH122] [OR:Methanobacterium thermoautotrophicum]
[DB:genpept-bct1] [DE:Methanobacterium thermoautotrophicum from bases 68653
to 79584(section 7 of 148) of the complete genome.] [NT:Function Code:10.09
- Metabolism of Macromolecules,] [LE:9193] [RE:9660] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000998_30682802_c3_321	2869	6641	261	86		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000998_33399055_c2_273	2870	6642	393	130	419	3.0e-39

Description

pir:[LN:H69745] [AC:H69745] [PN:hypothetical protein ybcI] [GN:ybcI]
[OR:Bacillus subtilis] [DB:pir2] >gp:[GI:d1034047:g3599606] [LN:AB006424]
[AC:AB006424] [GN:ybcI] [OR:Bacillus subtilis] [SR:Bacillus subtilis
(strain:168) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis genomic DNA, 70 kb
region between 17 and 23degree.] [LE:13549] [RE:13923] [DI:direct]
>gp:[GI:e1182121:g2632455] [LN:BSUB0001] [AC:Z99104:AL009126] [GN:ybcI]
[FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
complete genome (section 1 of 21): from 1 to213080.] [LE:210558] [RE:210932]
[DI:direct] >gp:[GI:e1182139:g2632473] [LN:BSUB0002] [AC:Z99105:AL009126]
[GN:ybcI] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus
subtilis complete genome (section 2 of 21): from 194651 to415810.]
[LE:15908] [RE:16282] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000998_33756432_f1_7	2871	6643	141	46		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000998_34407625_c3_309	2872	6644	354	117	587	4.7e-57

Description

gp:[GI:g1658281] [LN:SLU74623] [AC:U74623] [PN:CadX] [FN:cadmium resistance]
[OR:Staphylococcus lugdunensis] [DB:genpept-bct1] [DE:Staphylococcus
lugdunensis strain 995 cadmium resistance plasmidpLUG10, complete sequence.]
[LE:2624] [RE:2971] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000998_34557262_c3_349	2873	6645	135	44		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000998_35431657_f2_114	2874	6646	135	44		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000998_36227142_c1_240	2875	6647	993	330	409	3.4e-38

Description

sp:[LN:LYTE_BACSU] [AC:P54421] [GN:LYTE:PAPQ] [OR:BACILLUS SUBTILIS]
[DE:PAPQ PRECURSOR] (CELL WALL-ASSOCIATED POLYPEPTIDE CWBP33)] [SP:P54421]
[DB:swissprot] >gp:[GI:g1488662] [LN:BSU38819] [AC:U38819]
[PN:phosphatase-associated protein] [GN:lytE] [OR:Bacillus subtilis]
[DB:genpept-bct2] [DE:Bacillus subtilis phosphatase-associated protein
(lytE) gene,complete cds.] [NT:Muralytic when cloned in E.coli; Iap60
homolog;] [LE:443] [RE:1447] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000998_36568828_c2_266	2876	6648	1050	349	984	4.0e-99

Description

pir:[LN:A43577] [AC:A43577] [PN:regulatory protein pfoR] [OR:Clostridium
perfringens] [DB:pir2]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000998_36593802_c2_282	2877	6649	867	288	454	5.8e-43

Description

sp:[LN:PLPA_PASHA] [AC:Q08868:Q07363] [GN:PLPA] [OR:PASTEURELLA HAEMOLYTICA] [DE:OUTER MEMBRANE LIPOPROTEIN 1 PRECURSOR (PLP1)] [SP:Q08868:Q07363] [DB:swissprot] >pir:[LN:JN0751] [AC:JN0751] [PN:Outer membrane 30K protein:ORF1] [CL:lipoprotein-28] [OR:Pasteurella haemolytica] [DB:pir2] >gp:[GI:g349530] [LN:PASLIPOPR] [AC:L11037] [PN:lipoprotein] [OR:Pasteurella haemolytica] [SR:Pasteurella haemolytica (strain A1) DNA] [DB:genpept-bct1] [DE:Pasteurella haemolytica lipoprotein gene, complete cds.] [NT:precursor] [LE:171] [RE:1004] [DI:direct] >gp:[GI:g150508] [LN:PASLIPOPRO] [AC:M91072] [PN:lipoprotein] [OR:Pasteurella haemolytica] [SR:Pasteurella haemolytica (strain A1) (library: pUC19 of R. Craven e] [DB:genpept-bct1] [DE:Pasteurella haemolytica (clones pGEB2830,pBRES2830) lipoproteingene, complete cds.] [LE:136] [RE:969] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000998_3944143_c3_308	2878	6650	627	208	971	9.5e-98

Description

gp:[GI:g1916729] [LN:AF134905] [AC:AF134905:U76550] [PN:CadD] [GN:cadD] [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus plasmid pRW001 CadD (cadD) gene, completecds.] [NT:confers low level cadmium resistance] [LE:2328] [RE:2957] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000998_3945253_f3_203	2879	6651	126	41		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000998_3954385_f1_32	2880	6652	123	40		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000998_4064818_c1_239	2881	6653	675	224	533	2.5e-51

Description

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sp:[LN:YAAE_ECOLI] [AC:P31547] [GN:YAAE] [OR:ESCHERICHIA COLI]
[DE:HYPOTHETICAL ABC TRANSPORTER PERMEASE PROTEIN YAAE] [SP:P31547]
[DB:swissprot] >pir:[LN:F64744] [AC:F64744 ] [PN:probable transport protein
yaeE] [GN:yaeE ] [CL:probable transport protein yaeE] [OR:Escherichia coli]
[DB:pir2] >gp:[GI:d1041643:g4902941]. [LN:ECOTSF] [AC:D83536]
[PN:Hypothetical 23.3 kd protein in rcsF-abc] [GN:yaeE] [OR:Escherichia
coli] [SR:Escherichia coli (strain:K12) DNA] [DB:genpept-bct1]
[DE:Escherichia coli genomic DNA. (4.1 - 6.1 min).] [NT:ORF_ID:o124#1;
similar to SwissProt Accession] [LE:30521] [RE:31174] [DI:complement]
>gp:[GI:g1552774] [LN:ECU70214] [AC:U70214] [GN:yaeE] [OR:Escherichia coli]
[DB:genpept-bct1] [DE:Escherichia coli chromosome minutes 4-6.]
[NT:hypothetical] [LE:52043] [RE:52696] [DI:complement] >gp:[GI:g1786397]
[LN:AE000129] [AC:AE000129:U00096] [PN:putative transport system permease
protein] [GN:yaeE] [FN:putative transport; Not classified] [OR:Escherichia
coli] [DB:genpept-bct2] [DE:Escherichia coli K-12 MG1655 section 19 of 400
of the completegenome.] [NT:f218; 100 pct identical to YAAE_ECOLI SW:
P31547] [LE:944] [RE:1597] [DI:complement]

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000998_4082828_c3_320	2882	6654	702	233	211	3.3e-17

Description

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pir:[LN:F71886] [AC:F71886 ] [PN:hypothetical protein jhp0787] [GN:jhp0787 ]
[OR:Helicobacter pylori] [SR:strain J99, , strain J99] [SR:strain J99, ]
[DB:pir2] >gp:[GI:g4155367] [LN:AE001509] [AC:AE001509:AE001439]
[PN:putative] [GN:jhp0787] [OR:Helicobacter pylori J99] [DB:genpept-bct2]
[DE:Helicobacter pylori, strain J99 section 70 of 132 of the
completegenome.] [NT:similar to H. pylori 26695 gene HP0851] [LE:2708]
[RE:3394] [DI:direct]
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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000998_4101525_f1_60	2883	6655	135	44		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000998_4328468_c2_298	2884	6656	1473	490	1279	2.2e-130

Description

pir:[LN:H69634] [AC:H69634] [PN:glutamate synthase (small subunit) gltB]
 [GN:gltB] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1183502:g2634227]
 [LN:BSUB0010] [AC:Z99113:AL009126] [PN:glutamate synthase (small subunit)]
 [GN:gltB] [FN:glutamate biosynthesis] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [EC:1.4.1.13] [DE:Bacillus subtilis complete genome
 (section 10 of 21): from 1781201to 2014980.] [LE:226628] [RE:228109]
 [DI:complement] >gp:[GI:e1185317:g2634238] [LN:BSUB0011]
 [AC:Z99114:AL009126] [PN:glutamate synthase (small subunit)] [GN:gltB]
 [FN:glutamate biosynthesis] [OR:Bacillus subtilis] [DB:genpept-bct1]
 [EC:1.4.1.13] [DE:Bacillus subtilis complete genome (section 11 of 21): from
 2000171to 2207900.] [LE:7658] [RE:9139] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000998_4335766_c1_261	2885	6657	141	46		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000998_4344011_f3_152	2886	6658	252	83	60	0.023

Description

gp:[GI:d1036760:g4062561] [LN:D90737] [AC:D90737:AB001340]
 [PN:4-hydroxyphenylacetate 3-monooxygenase (EC) [GN:nmoB] [OR:Escherichia
 coli] [SR:Escherichia coli(strain:K12) DNA, clone:Kohara clone #227]
 [DB:genpept-bct1] [DE:Escherichia coli genomic DNA. (22.8 - 23.1 min).]
 [NT:ORF_ID:o228#5; similar to PIR Accession Number] [LE:15357] [RE:15932]
 [DI:complement] >gp:[GI:d1036770:g4062570] [LN:D90738] [AC:D90738:AB001340]
 [PN:4-hydroxyphenylacetate 3-monooxygenase (EC) [GN:nmoB] [OR:Escherichia
 coli] [SR:Escherichia coli(strain:K12) DNA, clone:Kohara clone #228]
 [DB:genpept-bct1] [DE:Escherichia coli genomic DNA. (23.0 - 23.4 min).]
 [NT:ORF_ID:o228#5; similar to PIR Accession Number] [LE:3821] [RE:4396]
 [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000998_4485682_f3_159	2887	6659	264	87		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000998_4580132_f1_72	2888	6660	171	56	161	3.6e-11

Description

gp:[GI:g2689564] [LN:U93688] [AC:U93688] [PN:integrase] [GN:int]
 [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus toxic
 shock syndrome toxin-1 (tst), enterotoxin (ent), and integrase (int) genes,
 complete cds.] [NT:similar to staphylococcal phage integrase] [LE:13871]
 [RE:15091] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000998_4703167_f1_44	2889	6661	144	47		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000998_4703512_c3_315	2890	6662	486	161	335	2.4e-30

Description

pir:[LN:A70068] [AC:A70068] [PN:conserved hypothetical protein ywqN]
 [GN:ywqN] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1184521:g2636140]
 [LN:BSUB0019] [AC:Z99122:AL009126] [GN:ywqN] [FN:unknown] [OR:Bacillus
 subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section
 19 of 21): from 3597091to 3809700.] [NT:similar to hypothetical proteins]
 [LE:124753] [RE:125298] [DI:complement] >gp:[GI:e308071:g1894752]
 [LN:BSZ92952] [AC:Z92952] [PN:unknown] [GN:ywqN] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:B.subtilis ywq[A,B,C,D,E,F,G,H,I,J,K,L,M,N,O] genes.]
 [LE:13028] [RE:13573] [DI:direct] >gp:[GI:e1184521:g2636140] [LN:BSUB0019]
 [AC:Z99122:AL009126] [GN:ywqN] [FN:unknown] [OR:Bacillus subtilis]
 [DB:genpept] [DE:Bacillus subtilis complete genome (section 19 of 21): from
 3597091to 3809700.] [NT:similar to hypothetical proteins] [LE:124753]
 [RE:125298] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000998_47343_c1_219	2891	6663	132	43		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000998_5265643_f1_30	2892	6664	1122	373		
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Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000998_5343760_f2_129	2893	6665	267	88		
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Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000998_5860927_f2_138	2894	6666	189	62	75	0.023
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Description

gp:[GI:e1283542:g4455153] [LN:ATF6I18] [AC:AL022198] [PN:putative protein]
 [GN:F6I18.10] [OR:Arabidopsis thaliana] [SR:thale cress] [DB:genpept-pln1]
 [DE:Arabidopsis thaliana DNA chromosome 4, BAC clone F6I18 (ESSAIIproject).]
 [NT:contains EST gb:T22575, T22317] [LE:>199:404:631] [RE:347:548:921]
 [DI:complementJoin]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000998_6052175_f1_65	2895	6667	153	50		
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Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000998_6053437_c3_310	2896	6668	123	40		
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Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000998_6251262_f3_146	2897	6669	189	62	75	0.0084
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Description

gp:[GI:d1044717:g5105618] [LN:AP000062] [AC:AP000062] [PN:121aa long
 hypothetical protein] [GN:APE1925] [OR:Aeropyrum pernix] [SR:Aeropyrum
 pernix (strain:K1) DNA] [DB:genpept] [DE:Aeropyrum pernix genomic DNA,
 section 5/7.] [NT:similar to OWL:AB00947213 percent identity:62.500]
 [LE:233017] [RE:233382] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000998_657678_f3_208	2898	6670	135	44		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000998_6698526_c2_264	2899	6671	174	57		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000998_6743788_c2_272	2900	6672	132	43		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000998_6760887_f3_174	2901	6673	924	307	333	3.8e-30

Description

sp:[LN:GLTC_BACSU] [AC:P20668] [GN:GLTC] [OR:BACILLUS SUBTILIS]
 [DE:TRANSCRIPTIONAL REGULATORY PROTEIN GLTC] [SP:P20668] [DB:swissprot]
 >pir:[LN:A69635] [AC:A69635:A33951:A61642] [PN:transcription activator of
 glutamate synthase operon gltC:regulatory protein gltC] [GN:gltC]
 [CL:probable transcription regulator lsyR] [OR:Bacillus subtilis] [DB:pir2]
 >gp:[GI:e1183504:g2634229] [LN:BSUB0010] [AC:Z99113:AL009126]
 [PN:transcriptional regulator (LysR family)] [GN:gltC] [FN:positive
 regulation of the glutamate synthase] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 10 of 21):
 from 1781201to 2014980.] [SP:P20668] [LE:232835] [RE:233737] [DI:direct]
 >gp:[GI:e1185319:g2634240] [LN:BSUB0011] [AC:Z99114:AL009126]
 [PN:transcriptional regulator (LysR family)] [GN:gltC] [FN:positive
 regulation of the glutamate synthase] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 11 of 21):
 from 2000171to 2207900.] [SP:P20668] [LE:13865] [RE:14767] [DI:direct]
 >gp:[GI:g457514] [LN:M28509] [AC:M28509] [GN:gltC] [FN:positive
 transcriptional regulator] [OR:Bacillus subtilis] [DB:genpept-bct1]
 [DE:Bacillus subtilis (gltC) gene, complete cds and glutamate synthase,large
 subunit (gltA) gene, partial cds. gene.] [LE:34] [RE:936] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000998_6832950_c1_218	2902	6674	189	62		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000998_956312_f2_139	2903	6675	144	47		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000998_984703_c2_281	2904	6676	1026	341	763	1.0e-75

Description

sp:[LN:ABC_ECOLI] [AC:P30750:P77517] [GN:ABC] [OR:ESCHERICHIA COLI]
 [DE:ATP-BINDING PROTEIN ABC] [SP:P30750:P77517] [DB:swissprot]
 >pir:[LN:G64744] [AC:G64744:I41113] [PN:probable ABC-type transport protein
 abc] [GN:abc] [CL:unassigned ATP-binding cassette proteins: ATP-binding
 cassette homology] [OR:Escherichia coli] [DB:pir2] >gp:[GI:g1552775]
 [LN:ECU70214] [AC:U70214] [PN:ATP-binding protein] [GN:abc] [OR:Escherichia
 coli] [DB:genpept-bct1] [DE:Escherichia coli chromosome minutes 4-6.]
 [LE:52689] [RE:53720] [DI:complement] >gp:[GI:g1786398] [LN:AE000129]
 [AC:AE000129:U00096] [PN:ATP-binding component of a transporter] [GN:abc]
 [FN:transport; Not classified] [OR:Escherichia coli] [DB:genpept-bct2]
 [DE:Escherichia coli K-12 MG1655 section 19 of 400 of the completegenome.]
 [NT:f343; 98 pct identical to fragment (231) [LE:1590] [RE:2621]
 [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_10191427_c1_745	2905	6677	135	44		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_10320337_c3_1119	2906	6678	192	63		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000999_10359688_f3_663	2907	6679	198	65		
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Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000999_10546925_c3_1155	2908	6680	978	325	1246	6.8e-127
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Description

sp:[LN:DNAA_STAAU] [AC:P49994] [GN:DNAA] [OR:STAPHYLOCOCCUS AUREUS]
 [DE:CHROMOSOMAL REPLICATION INITIATOR PROTEIN DNAA] [SP:P49994]
 [DB:swissprot] >pir:[LN:JC5607] [AC:JC5607] [PN:replication initiation
 protein dnaA] [GN:dnaA] [CL:replication initiation protein dnaA]
 [OR:Staphylococcus aureus] [DB:pir2] >gp:[GI:d1014451:g1694677] [LN:D89066]
 [AC:D89066] [PN:DnaA] [GN:dnaA] [OR:Staphylococcus aureus]
 [SR:Staphylococcus aureus DNA] [DB:genpept-bct1] [DE:Staphylococcus aureus
 DNA for DnaA, complete cds.] [LE:456] [RE:1817] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000999_10556300_f2_428	2909	6681	174	57		
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Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000999_10556712_c3_1187	2910	6682	990	329	1667	1.7e-171
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Description

gp:[GI:g1408063] [LN:STAMECRA] [AC:L14017] [PN:methicillin-resistance
 protein] [GN:mecR] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus
 (strain COL) DNA] [DB:genpept-bct1] [DE:Staphylococcus aureus
 methicillin-resistance protein (mecR) geneand unknown ORF, complete cds.]
 [NT:putative] [LE:125] [RE:1111] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000999_10582782_f3_549	2911	6683	141	46		
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Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000999_10629385_f1_185	2912	6684	153	50		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000999_10634800_c1_819	2913	6685	966	321	143	2.4e-07

Description

pir:[LN:D69900] [AC:D69900] [PN:conserved hypothetical protein yobV]
 [GN:yobV] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:g2619048] [LN:AF027868]
 [AC:AF027868] [PN:transcription regulator] [GN:yobV] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:Bacillus subtilis chromosome region between terC and
 odhAB.] [NT:similar to Mycobacterium tuberculosis hypothetical] [LE:63061]
 [RE:64002] [DI:complement] >gp:[GI:e1185382:g2634303] [LN:BSUB0011]
 [AC:Z99114:AL009126] [GN:yobV] [FN:unknown] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 11 of 21):
 from 2000171to 2207900.] [NT:similar to hypothetical proteins] [LE:82152]
 [RE:83093] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000999_1071002_f3_616	2914	6686	411	136	71	0.026

Description

gp:[GI:g142964] [LN:BACGERD] [AC:M27259] [OR:Bacillus subtilis]
 [SR:B.subtilis (strain 168) DNA, clone lambda-EMBL-3-2H] [DB:genpept-bct1]
 [DE:B.subtilis gerD gene, complete cds.] [NT:unknown ORF] [LE:<1] [RE:282]
 [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000999_10727217_f1_212	2915	6687	270	89	212	2.5e-17

Description

pir:[LN:B69770] [AC:B69770] [PN:conserved hypothetical protein ydaS]
 [GN:ydaS] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:d1020027:g1881247]
 [LN:AB001488] [AC:AB001488] [GN:ydaS] [OR:Bacillus subtilis] [SR:Bacillus
 subtilis (strain:168) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis genome
 sequence, 148 kb sequence of the regionbetween 35 and 47 degree.]
 [NT:FUNCTION UNKNOWN.] [LE:25711] [RE:25968] [DI:complement]
 >gp:[GI:e1182403:g2632737] [LN:BSUB0003] [AC:Z99106:AL009126] [GN:ydaS]
 [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
 complete genome (section 3 of 21): from 402751 to611850.] [NT:similar to
 hypothetical proteins from B. subtilis] [LE:89455] [RE:89712]
 [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_10928_c2_1083	2916	6688	1242	413	240	8.2e-18

Description

pir:[LN:T03492] [AC:T03492] [PN:hypothetical protein] [OR:Rhodobacter capsulatus] [DB:pir2] [MP:1] >gp:[GI:g3128293] [LN:AF010496] [AC:AF010496] [PN:hypothetical protein] [OR:Rhodobacter capsulatus] [DB:genpept-bct2] [DE:Rhodobacter capsulatus strain SB1003, partial genome.] [LE:54291] [RE:55613] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_10928_f1_226	2917	6689	1017	338	175	1.3e-10

Description

pir:[LN:T03492] [AC:T03492] [PN:hypothetical protein] [OR:Rhodobacter capsulatus] [DB:pir2] [MP:1] >gp:[GI:g3128293] [LN:AF010496] [AC:AF010496] [PN:hypothetical protein] [OR:Rhodobacter capsulatus] [DB:genpept-bct2] [DE:Rhodobacter capsulatus strain SB1003, partial genome.] [LE:54291] [RE:55613] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_111500_c3_1239	2918	6690	546	181	101	1.9e-05

Description

gp:[GI:g940735] [LN:LMIAP1270] [AC:X85869] [PN:invasive associated protein] [GN:iap] [OR:Listeria monocytogenes] [DB:genpept-bct1] [DE:L.monocytogenes type 1 partial iap gene (strain 12705/89).] [NT:invades nonprofessional phagocytic cells] [LE:<1] [RE:>260] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_111592_c2_931	2919	6691	243	80	83	0.0083

Description

gp:[GI:e1349691:g3880163] [LN:CET24A11] [AC:Z49072] [GN:T24A11.2] [OR:Caenorhabditis elegans] [DB:genpept-inv1] [DE:Caenorhabditis elegans cosmid T24A11, complete sequence.] [LE:22751:23187:23506] [RE:23145:23464:23646] [DI:complementJoin]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_115627_f2_344	2920	6692	168	55		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_1205000_f1_183	2921	6693	555	184	314	4.0e-28

Description

pir:[LN:F69768] [AC:F69768] [PN:acetyltransferase homolog ydaF] [GN:ydaF]
 [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:d1020012:g1881232] [LN:AB001488]
 [AC:AB001488] [GN:ydaF] [OR:Bacillus subtilis] [SR:Bacillus subtilis
 (strain:168) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis genome sequence,
 148 kb sequence of the regionbetween 35 and 47 degree.] [NT:PROBABLE
 ACETYLTRANSFERASE.] [LE:6233] [RE:6784] [DI:direct]
 >gp:[GI:e1182387:g2632721] [LN:BSUB0003] [AC:Z99106:AL009126] [GN:ydaF]
 [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
 complete genome (section 3 of 21): from 402751 to611850.] [NT:similar to
 acetyltransferase] [LE:69977] [RE:70528] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_12536337_f2_405	2922	6694	327	108		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_12588250_c1_671	2923	6695	198	65		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_1259387_f2_250	2924	6696	126	41		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_1261078_f1_223	2925	6697	579	192	471	9.1e-45

Description

sp:[LN:XPT_BACSU] [AC:P42085] [GN:XPT] [OR:BACILLUS SUBTILIS] [EC:2.4.2.-]
[DE:XANTHINE PHOSPHORIBOSYLTRANSFERASE,] [SP:P42085] [DB:swissprot]
>pir:[LN:S51309] [AC:S51309:E69734] [PN:xanthine phosphoribosyltransferase
xpt] [GN:xpt] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:g1256617]
[LN:BACYACA] [AC:L77246] [PN:adenine phosphoribosyltransferase] [GN:xpt]
[FN:purine biosynthesis] [OR:Bacillus subtilis] [DB:genpept-bct1]
[EC:2.4.2.7] [DE:Bacillus subtilis (YAC10-9 clone) DNA region between the
serA andkdg loci.] [NT:27% identity with E.coli adenine] [LE:1426] [RE:2010]
[DI:direct] >gp:[GI:e1183653:g2634626] [LN:BSUB0012] [AC:Z99115:AL009126]
[PN:xanthine phosphoribosyltransferase] [GN:xpt] [FN:purine biosynthesis]
[OR:Bacillus subtilis] [DB:genpept-bct1] [EC:2.4.2.7] [DE:Bacillus subtilis
complete genome (section 12 of 21): from 2195541to 2409220.] [SP:P42085]
[LE:123142] [RE:123726] [DI:complement] >gp:[GI:g633169] [LN:BSXPTPBUX]
[AC:X83878] [PN:xanthine phosphoribosyltransferase] [GN:xpt] [OR:Bacillus
subtilis] [DB:genpept-bct1] [DE:B.subtilis xpt and pbuX genes.] [SP:P42085]
[LE:357] [RE:941] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_1301_f3_471	2926	6698	123	40		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_13089052_f1_2	2927	6699	123	40		

Description

NO-HIT

AI7503000999_13089052_f1_2

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_134677_f2_417	2928	6700	1101	366	1373	2.4e-140

Description

sp:[LN:YYAF_BACSU] [AC:P37518] [GN:YYAF] [OR:BACILLUS SUBTILIS] [DE:REGION]
[SP:P37518] [DB:swissprot] >pir:[LN:S66016] [AC:S66016:E70084] [PN:probable
GTP-binding protein yyaF] [GN:yyaF] [CL:yeast probable purine
nucleotide-binding protein YBR025c] [OR:Bacillus subtilis] [DB:pir2]
>gp:[GI:d1005764:g467376] [LN:BAC180K] [AC:D26185] [PN:unknown] [OR:Bacillus
subtilis] [SR:Bacillus subtilis (sub_species:Marburg, strain:168) DNA]
[DB:genpept-bct1] [DE:B. subtilis DNA, 180 kilobase region of replication
origin.] [LE:47839] [RE:48939] [DI:complement] >gp:[GI:e1184818:g2636639]
[LN:BSUB0021] [AC:Z99124:AL009126] [GN:yyaF] [FN:unknown] [OR:Bacillus
subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section
21 of 21): from 3999281to 4214814.] [NT:similar to hypothetical proteins]
[SP:P37518] [LE:199771] [RE:200871] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_13704191_c1_811	2929	6701	171	56		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_13750258_f1_41	2930	6702	162	53		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_1379132_c1_806	2931	6703	564	187	589	2.9e-57

Description

gp:[GI:d1045999:g5360823] [LN:D86934] [AC:D86934] [PN:IS150-like
transposase] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus
(strain:N315) DNA, clone_lib:library of N31] [DB:genpept] [DE:Staphylococcus
aureus genes, mec region, partial and complete cds.] [NT:ORF N028; putative]
[LE:<20180] [RE:20578] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_13828575_f1_31	2932	6704	444	147	617	3.1e-60

Description

sp:[LN:ARSC_STAAU] [AC:P30330] [GN:ARSC] [OR:STAPHYLOCOCCUS AUREUS]
 [DE:ARSENATE REDUCTASE (ARSENICAL PUMP MODIFIER)] [SP:P30330] [DB:swissprot]
 >pir:[LN:D41903] [AC:D41903] [PN:arsenate reductase,] [GN:arsC]
 [CL:protein-tyrosine-phosphatase, low molecular weight] [OR:Staphylococcus
 aureus] [EC:1.-.-.-] [DB:pir1] >gp:[GI:g150729] [LN:PI2ARSRBC] [AC:M86824]
 [PN:arsenate reductase] [GN:arsC] [FN:Reduction of arsenate to arsenite]
 [OR:Plasmid pI258] [SR:Plasmid pI258 DNA] [DB:genpept-bct1] [DE:Plasmid
 pI258 arsenic resistance operon (arsRBC) genes, completecds.] [LE:1894]
 [RE:2289] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_1384628_f2_290	2933	6705	1278	425	251	4.3e-19

Description

pir:[LN:H64514] [AC:H64514] [PN:hypothetical protein MJECL41]
 [OR:Methanococcus jannaschii] [DB:pir2] [MP:ECLREV53908-52610]
 >gp:[GI:g1522674] [LN:MII2CG] [AC:L77118] [PN:M. jannaschii predicted coding
 region MJECL41] [GN:MJECL41] [OR:Methanococcus jannaschii] [DB:genpept-bct2]
 [DE:Methanococcus jannaschii large extra-chromosomal element,
 completesequence.] [NT:identified by GeneMark; putative] [LE:52610]
 [RE:53908] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000999_13864680_c2_1056	2934	6706	384	127	247	5.0e-21

Description

sp:[LN:YQCJ_BACSU] [AC:P45949] [GN:YQCJ] [OR:BACILLUS SUBTILIS]
[DE:HYPOTHETICAL 12.3 KD PROTEIN IN CWLA-CISA INTERGENIC REGION] [SP:P45949]
[DB:swissprot] >pir:[LN:H69949] [AC:H69949] [PN:transcription regulator
ArsR family homolog yqcJ] [GN:yqcJ] [CL:arsenical resistance operon
repressor] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:d1013110:g1303775]
[LN:BACJH642] [AC:D84432:D82370] [PN:YqcJ] [OR:Bacillus subtilis]
[SR:Bacillus subtilis (strain:JH642(trpC2 PheA1)) DNA] [DB:genpept-bct1]
[DE:Bacillus subtilis DNA, 283 Kb region containing skin element.]
[LE:61977] [RE:62294] [DI:direct] >gp:[GI:d1007542:g1217882] [LN:BACSKIN]
[AC:D32216] [PN:ORF3] [OR:Bacillus subtilis] [SR:Bacillus subtilis
(strain:JH642 (trpC2 pheA1)) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis 48
kb region including a skin element which is located between spoIVCB and
spoIIIC.] [NT:similarity to arsenical resistance operon] [LE:43732]
[RE:44049] [DI:direct] >gp:[GI:e1183810:g2635026] [LN:BSUB0014]
[AC:Z99117:AL009126] [GN:yqcJ] [FN:unknown] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 14 of 21):
from 2599451 to 2812870.] [NT:similar to transcriptional regulator (ArsR
family)] [SP:P45949] [LE:57136] [RE:57453] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000999_13912551_c1_827	2935	6707	1695	564	156	6.7e-08

Description

gp:[GI:g4530172] [LN:AF085222] [AC:AF085222] [PN:putative primase]
[OR:Streptococcus thermophilus bacteriophage DT1] [DB:genpept-phg]
[DE:Streptococcus thermophilus bacteriophage DT1, complete genome.]
[NT:Orf36] [LE:28549] [RE:30063] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_14111687_f3_529	2936	6708	225	74	104	3.3e-05

Description

sp:[LN:Y4IQ_RHISN] [AC:P55500] [GN:Y4IQ,Y4ND,Y4SD] [OR:RHIZOBIUM SP]
[SR:NGR234,] [DE:PUTATIVE INSERTION SEQUENCE ATP-BINDING PROTEIN
Y4IQ/Y4ND/Y4SD] [SP:P55500] [DB:swissprot] >gp:[GI:g2182455] [LN:AE000079]
[AC:AE000079:U00090] [PN:Y4iQ] [GN:y4iQ] [OR:Rhizobium sp. NGR234]
[DB:genpept-bct2] [DE:Rhizobium sp. NGR234 plasmid pNGR234a, section 16 of
46 of thecomplete plasmid sequence.] [NT:putative insertion sequence
ATP-binding protein;] [LE:1883] [RE:2779] [DI:complement] >gp:[GI:g2182539]
[LN:AE000086] [AC:AE000086:U00090] [PN:Y4nD] [GN:y4nD] [OR:Rhizobium sp.
NGR234] [DB:genpept-bct2] [DE:Rhizobium sp. NGR234 plasmid pNGR234a, section
23 of 46 of thecomplete plasmid sequence.] [NT:putative insertion sequence
ATP-binding protein;] [LE:8640] [RE:9536] [DI:complement] >gp:[GI:g2182618]
[LN:AE000095] [AC:AE000095:U00090] [PN:Y4sD] [GN:y4sD] [OR:Rhizobium sp.
NGR234] [DB:genpept-bct2] [DE:Rhizobium sp. NGR234 plasmid pNGR234a, section
32 of 46 of thecomplete plasmid sequence.] [NT:putative insertion sequence
ATP-binding protein;] [LE:7675] [RE:8571] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_14220027_f3_618	2937	6709	1143	380	190	3.0e-12

Description

gp:[GI:d1025733:g2879913] [LN:D85752] [AC:D85752] [GN:bacG] [OR:Enterococcus
faecalis] [SR:Enterococcus faecalis plasmid:pPD1 DNA] [DB:genpept-bct1]
[DE:Enterococcus faecalis plasmid pPD1 bacA, bacB, bacC, bacD, bacE,bacF,
bacG, bacH and bacI genes, complete cds.] [LE:5832] [RE:7055] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_14460882_c3_1296	2938	6710	342	114	484	3.8e-46

Description

gp:[GI:g1022726] [LN:SHU35635] [AC:U35635] [PN:unknown] [OR:Staphylococcus
haemolyticus] [SR:Staphylococcus haemolyticus strain=Y176] [DB:genpept-bct1]
[DE:Staphylococcus haemolyticus IS1272 ORF1 and ORF2 genes, completecds.]
[NT:ORF1] [LE:1101] [RE:1922] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_14532058_c3_1228	2939	6711	273	90	452	9.4e-43

Description

sp:[LN:TRAI_STAAU] [AC:P14506] [OR:STAPHYLOCOCCUS AUREUS] [DE:TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS257 IN TRANSPOSON TN4003] [SP:P14506] [DB:swissprot] >pir:[LN:S04162] [AC:S04162] [PN:transposase 1] [OR:Staphylococcus aureus] [DB:pir2] >gp:[GI:g46748] [LN:SATN4003] [AC:X13290] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:Staphylococcus aureus multi-resistance plasmid pSK1 DNA containingtransposon Tn4003.] [NT:transposase (AA 1-224)] [SP:P14506] [LE:89] [RE:763] [DI:complement] >gp:[GI:g46753] [LN:SATN4003] [AC:X13290] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:Staphylococcus aureus multi-resistance plasmid pSK1 DNA containingtransposon Tn4003.] [NT:transposase (AA 1-224)] [SP:P14506] [LE:4017] [RE:4691] [DI:complement] >gp:[GI:g1762092] [LN:SEU40381] [AC:U40381] [PN:transposase] [GN:tnp] [OR:Staphylococcus epidermidis] [DB:genpept-bct1] [DE:Staphylococcus epidermidis plasmid pSK697 insertion sequenceIS257(697A) putative transposase gene, complete cds.] [NT:Tnp; putative transposase] [LE:57] [RE:731] [DI:direct] >gp:[GI:g1762098] [LN:SEU40384] [AC:U40384] [PN:transposase] [GN:tnp] [OR:Staphylococcus epidermidis] [DB:genpept-bct1] [DE:Staphylococcus epidermidis plasmid pSK818 insertion sequenceIS257(818A) putative transposase gene, complete cds.] [NT:Tnp; putative transposase] [LE:57] [RE:731] [DI:direct] >gp:[GI:g3676405] [LN:AF051916] [AC:AF051916] [PN:putative transposase TnpC] [GN:tnpC] [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus plasmid pJE1 remnant of replication proteinRep (rep), trimethoprim resistance protein DfrA (dfrA), thymidylatesynthetase ThyE (thyE), and putative transposase Tnp (tnp) genes,complete cds; and unknown gene.] [LE:65] [RE:739] [DI:direct] >gp:[GI:g3676411] [LN:AF051916] [AC:AF051916] [PN:putative transposase TnpE] [GN:tnpE] [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus plasmid pJE1 remnant of replication proteinRep (rep), trimethoprim resistance protein DfrA (dfrA), thymidylatesynthetase ThyE (thyE), and putative transposase Tnp (tnp) genes,complete cds; and unknown gene.] [LE:4409] [RE:5083] [DI:direct] >gp:[GI:g3676433] [LN:AF051917] [AC:AF051917:L19570] [PN:putative transposase TnpC] [GN:tnpC] [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus plasmid pSK41, complete sequence.] [LE:22981]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_14578382_f1_27	2940	6712	192	63		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_14625031_f3_489	2941	6713	132	43		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_14719827_c3_1275	2942	6714	330	109	85	0.0070

Description

gp:[GI:g4049891] [LN:AF063866] [AC:AF063866] [PN:ORF MSV019 hypothetical protein] [GN:MSV019] [OR:Melanoplus sanguinipes entomopoxvirus] [DB:genpept-vrl] [DE:Melanoplus sanguinipes entomopoxvirus, complete genome.] [LE:21761] [RE:23074] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_14728382_f1_210	2943	6715	300	99	336	1.8e-30

Description

sp:[LN:RS6_BACSU] [AC:P21468] [GN:RPSF] [OR:BACILLUS SUBTILIS] [DE:30S RIBOSOMAL PROTEIN S6 (BS9)] [SP:P21468] [DB:swissprot] >pir:[LN:S66015] [AC:S66015:S11356:E69699] [PN:ribosomal protein S6 (BS9) rpsF:ribosomal protein BS9] [GN:rpsF] [CL:Escherichia coli ribosomal protein S6] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:d1005763:g467375] [LN:BAC180K] [AC:D26185] [PN:ribosomal protein S6] [GN:rpsF] [OR:Bacillus subtilis] [SR:Bacillus subtilis (sub_species:Marburg, strain:168) DNA] [DB:genpept-bct1] [DE:B. subtilis DNA, 180 kilobase region of replication origin.] [LE:47441] [RE:47728] [DI:complement] >gp:[GI:e1184817:g2636638] [LN:BSUB0021] [AC:Z99124:AL009126] [PN:ribosomal protein S6 (BS9)] [GN:rpsF] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.] [SP:P21468] [LE:199373] [RE:199660] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_14881552_f1_187	2944	6716	216	71		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000999_15033181_c3_1093	2945	6717	444	147	90	0.0071

Description

gp:[GI:g4176374] [LN:AC004953] [AC:AC004953] [GN:WUGSC:H_DJ1059M17.2]
[OR:Homo sapiens] [SR:INFORMATION] [DB:genpept-pri3] [DE:Homo sapiens PAC
clone DJ1059M17 from 7q21-q31.1, complete sequence.] [NT:myosin regulatory
light chain 2; similar to S22715] [LE:67137:67324:69882]
[RE:67235:67372:69960] [DI:complementJoin]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000999_15052318_f2_391	2946	6718	1395	464	1606	4.9e-165

Description

sp:[LN:THDF_BACSU] [AC:P25811] [GN:THDF] [OR:BACILLUS SUBTILIS] [DE:POSSIBLE
THIOPHENE AND FURAN OXIDATION PROTEIN THDF] [SP:P25811] [DB:swissprot]
>pir:[LN:JQ1215] [AC:I40439:S66026:C69722:JQ1215:S18075] [PN:thiophen /
furan oxidation protein thdF:50K protein homolog] [GN:thdF] [CL:thiophen /
furan oxidation protein:translation elongation factor Tu homology]
[OR:Bacillus subtilis] [DB:pir2] >gp:[GI:d1005774:g467386] [LN:BAC180K]
[AC:D26185] [PN:thiophen and furan oxidation] [GN:tdhF] [OR:Bacillus
subtilis] [SR:Bacillus subtilis (sub_species:Marburg, strain:168) DNA]
[DB:genpept-bct1] [DE:B. subtilis DNA, 180 kilobase region of replication
origin.] [LE:59506] [RE:60885] [DI:complement] >gp:[GI:g40025] [LN:BSORIGS]
[AC:X62539] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis genes
rpmH, rnpA, 50kd, gidA and gidB.] [NT:homologous to E.coli 50K] [SP:P25811]
[LE:2515] [RE:3894] [DI:direct] >gp:[GI:e1184828:g2636649] [LN:BSUB0021]
[AC:Z99124:AL009126] [GN:thdF] [FN:thiophen and furan oxidation]
[OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete
genome (section 21 of 21): from 3999281to 4214814.] [SP:P25811] [LE:211438]
[RE:212817] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000999_15055313_c3_1183	2947	6719	444	147	753	1.2e-74

Description

gp:[GI:d1046028:g5360852] [LN:D86934] [AC:D86934] [OR:Staphylococcus aureus]
[SR:Staphylococcus aureus (strain:N315) DNA, clone_lib:library of N31]
[DB:genpept] [DE:Staphylococcus aureus genes, mec region, partial and
complete cds.] [NT:ORF CN038] [LE:45523] [RE:>45966] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000999_15632952_c1_833	2948	6720	489	162		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000999_157500_c1_771	2949	6721	729	242	253	1.2e-21

Description

sp:[LN:YD31_HELPY] [AC:O25889] [GN:HP1331] [OR:HELICOBACTER PYLORI] [SR:,CAMPYLOBACTER PYLORI] [DE:HYPOTHETICAL PROTEIN HP1331] [SP:O25889] [DB:swissprot] >pir:[LN:C64686] [AC:C64686] [PN:conserved hypothetical integral membrane protein HP1331] [CL:hypothetical protein b2682] [OR:Helicobacter pylori] [DB:pir2] >gp:[GI:g2314496] [LN:AE000634] [AC:AE000634:AE000511] [PN:conserved hypothetical integral membrane] [GN:HP1331] [OR:Helicobacter pylori 26695] [DB:genpept-bct2] [DE:Helicobacter pylori 26695 section 112 of 134 of the completegenome.] [NT:similar to GB:L42023 SP:P44302 PID:1008819] [LE:10600] [RE:11286] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000999_15752213_f1_167	2950	6722	270	89	74	0.034

Description

gp:[GI:g2645365] [LN:SHU83823] [AC:U83823] [PN:NADH dehydrogenase subunit 4] [GN:ND4] [OR:Mitochondrion Sigmodon hispidus] [SR:Sigmodon hispidus] [DB:genpept-rod] [DE:Sigmodon hispidus NADH dehydrogenase subunit 3 (ND3) and NADHdehydrogenase subunit 4L (ND4L) genes, complete cds, NADHdehydrogenase subunit 4 (ND4) gene, partial cds, and tRNA-Arg gene,complete sequence, mitochondrial genes encoding mitochondrialproducts.] [LE:709] [RE:>1332] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000999_15788276_f3_494	2951	6723	198	65	56	0.028

Description

gp:[GI:g452394] [LN:BMFLC3] [AC:Z26886] [PN:Nd-sD mutant fibroin light chain] [OR:Bombyx mori] [SR:domestic silkworm] [DB:genpept-inv1] [DE:B.mori gene for Nd-sD mutant fibroin light chain.] [LE:<1:1275:1732] [RE:125:1447:2074] [DI:directJoin]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_15893843_f2_246	2952	6724	135	44		
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_161661_f3_507	2953	6725	147	48		
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_16222092_f1_44	2954	6726	141	46		
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_162812_c2_1058	2955	6727	147	48		
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_16432963_c1_709	2956	6728	1116	371	972	7.4e-98
<u>Description</u>						

pir:[LN:A69847] [AC:A69847] [PN:cystathionine gamma-synthase homolog yjcI]
 [GN:yjcI] [CL:O-succinylhomoserine (thiol)-lyase] [OR:Bacillus subtilis]
 [DB:pir2] >gp:[GI:e1183207:g2633541] [LN:BSUB0007] [AC:Z99110:AL009126]
 [GN:yjcI] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus
 subtilis complete genome (section 7 of 21): from 1194391to 1411140.]
 [NT:similar to cystathionine gamma-synthase] [LE:63573] [RE:64694]
 [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000999_16601512_c1_834	2957	6729	510	169	98	0.0027

Description

gp:[GI:e1346924:g3877219] [LN:CEF46F3] [AC:Z81085] [GN:F46F3.3]
 [OR:Caenorhabditis elegans] [DB:genpept-inv1] [DE:Caenorhabditis elegans
 cosmid F46F3, complete sequence.] [LE:12629:13473:14592:14734]
 [RE:12740:13771:14687:14877] [DI:directJoin]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000999_16688_c2_1062	2958	6730	216	71	95	6.4e-05

Description

gp:[GI:g5230679] [LN:AF036485] [AC:AF036485:AF036486:AF036487:U93364]
 [PN:hypothetical protein] [OR:Plasmid pNZ4000] [DB:genpept] [DE:Plasmid
 pNZ4000, complete sequence.] [NT:Orf-100] [LE:42675:1] [RE:42810:167]
 [DI:complementJoin]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000999_16695311_f2_259	2959	6731	693	230	1184	2.5e-120

Description

sp:[LN:TRA2_STAAU] [AC:P19380] [OR:STAPHYLOCOCCUS AUREUS] [DE:TRANSPOSASE
 FOR INSERTION SEQUENCE-LIKE ELEMENT IS431MEC] [SP:P19380] [DB:swissprot]
 >pir:[LN:S12093] [AC:S12093:JU0116] [PN:probable transposase]
 [OR:Staphylococcus aureus] [DB:pir2] >gp:[GI:g46602] [LN:SAIS431M]
 [AC:X53818:M18438] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:S.
 aureus IS431mec gene associated with methicillin resistance.] [NT:putative
 transposase (AA 1 - 224)] [SP:P19380] [LE:272] [RE:946] [DI:direct]
 >gp:[GI:e1237900:g2791991] [LN:SAMECAR1I] [AC:Y14051] [PN:putative
 transposase] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:Staphylococcus
 aureus mecA, mecR1, mecI genes and ORF168, ORF142,ORF44, ORF145 and ORF224.]
 [NT:ORF224] [LE:8096] [RE:8770] [DI:direct] >gp:[GI:d1046034:g5360858]
 [LN:D86934] [AC:D86934] [PN:transposase for insertion sequence-like element]
 [OR:Staphylococcus aureus] [SR:Staphylococcus aureus (strain:N315) DNA,
 clone_lib:library of N31] [DB:genpept] [DE:Staphylococcus aureus genes, mec
 region, partial and complete cds.] [NT:ORF N062] [LE:48054] [RE:48728]
 [DI:direct] >gp:[GI:d1046044:g5360868] [LN:D86934] [AC:D86934]
 [PN:transposase for insertion sequence-like element] [OR:Staphylococcus
 aureus] [SR:Staphylococcus aureus (strain:N315) DNA, clone_lib:library of
 N31] [DB:genpept] [DE:Staphylococcus aureus genes, mec region, partial and
 complete cds.] [NT:ORF N070] [LE:53400] [RE:54074] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_16695311_f2_282	2960	6732	693	230	1191	4.6e-121

sp:[LN:TRA2_STAAU] [AC:P19380] [OR:STAPHYLOCOCCUS AUREUS] [DE:TRANSPOSASE FOR INSERTION SEQUENCE-LIKE ELEMENT IS431MEC] [SP:P19380] [DB:swissprot] >pir:[LN:S12093] [AC:S12093:JU0116] [PN:probable transposase] [OR:Staphylococcus aureus] [DB:pir2] >gp:[GI:g46602] [LN:SAIS431M] [AC:X53818:M18438] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:S. aureus IS431mec gene associated with methicillin resistance.] [NT:putative transposase (AA 1 - 224)] [SP:P19380] [LE:272] [RE:946] [DI:direct] >gp:[GI:e1237900:g2791991] [LN:SAMECAR1I] [AC:Y14051] [PN:putative transposase] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:Staphylococcus aureus mecA, mecR1, mecI genes and ORF168, ORF142, ORF44, ORF145 and ORF224.] [NT:ORF224] [LE:8096] [RE:8770] [DI:direct] >gp:[GI:d1046034:g5360858] [LN:D86934] [AC:D86934] [PN:transposase for insertion sequence-like element] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus (strain:N315) DNA, clone_lib:library of N31] [DB:genpept] [DE:Staphylococcus aureus genes, mec region, partial and complete cds.] [NT:ORF N062] [LE:48054] [RE:48728] [DI:direct] >gp:[GI:d1046044:g5360868] [LN:D86934] [AC:D86934] [PN:transposase for insertion sequence-like element] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus (strain:N315) DNA, clone_lib:library of N31] [DB:genpept] [DE:Staphylococcus aureus genes, mec region, partial and complete cds.] [NT:ORF N070] [LE:53400] [RE:54074] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_16975082_c1_860	2961	6733	306	101		

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_17004551_f1_11	2962	6734	144	47		

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_193812_c1_810	2963	6735	129	42		

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000999_19720462_f2_314	2970	6742	1203	400	370	4.6e-34

Description

sp:[LN:YJIJ_ECOLI] [AC:P39381] [GN:YJIJ] [OR:ESCHERICHIA COLI]
 [DE:HYPOTHETICAL 41.4 KD PROTEIN IN IADA-MCRD INTERGENIC REGION (F392)]
 [SP:P39381] [DB:swissprot] >pir:[LN:S56557] [AC:S56557:F65247]
 [PN:hypothetical 41.4K protein (iadA-mcrD intergenic region):hypothetical
 protein f392] [GN:yjiJ] [OR:Escherichia coli] [DB:pir2] >gp:[GI:g537173]
 [LN:ECOUW93] [AC:U14003] [OR:Escherichia coli] [DB:genpept-bct1]
 [DE:Escherichia coli K-12 chromosomal region from 92.8 to 00.1 minutes.]
 [NT:ORF_f392] [LE:252329] [RE:253507] [DI:complement] >gp:[GI:g1790788]
 [LN:AE000503] [AC:AE000503:U00096] [PN:putative transport protein] [GN:yjiJ]
 [FN:putative transport; Not classified] [OR:Escherichia coli]
 [DB:genpept-bct2] [DE:Escherichia coli K-12 MG1655 section 393 of 400 of the
 completegenome.] [NT:f392; 100 pct identical amino acid sequence and]
 [LE:10037] [RE:11215] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000999_19767150_c3_1177	2971	6743	567	188	746	6.6e-74

Description

gp:[GI:d1046049:g5360873] [LN:D86934] [AC:D86934] [PN:orfX]
 [OR:Staphylococcus aureus] [SR:Staphylococcus aureus (strain:N315) DNA,
 clone_lib:library of N31] [DB:genpept] [DE:Staphylococcus aureus genes, mec
 region, partial and complete cds.] [NT:ORF CN051] [LE:56338] [RE:>56817]
 [DI:complement] >gp:[GI:d1046058:g5391439] [LN:AB014440] [AC:AB014440]
 [PN:orfX] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus
 (strain:NCTC8325) DNA] [DB:genpept] [DE:Staphylococcus aureus genes for
 orf1, orfX, orf2, orf3, partial andcomplete cds.] [NT:integration site of
 mecDNA was predicted to locate] [LE:1396] [RE:1875] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000999_19803150_f2_421	2972	6744	129	42		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000999_20194532_c1_732	2973	6745	156	51		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000999_20523253_c3_1227	2977	6749	252	83	447	3.2e-42

Description

sp:[LN:TRAI_STAAU] [AC:P14506] [OR:STAPHYLOCOCCUS AUREUS] [DE:TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS257 IN TRANSPOSON TN4003] [SP:P14506] [DB:swissprot] >pir:[LN:S04162] [AC:S04162] [PN:transposase 1] [OR:Staphylococcus aureus] [DB:pir2] >gp:[GI:g46748] [LN:SATN4003] [AC:X13290] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:Staphylococcus aureus multi-resistance plasmid pSK1 DNA containingtransposon Tn4003.] [NT:transposase (AA 1-224)] [SP:P14506] [LE:89] [RE:763] [DI:complement] >gp:[GI:g46753] [LN:SATN4003] [AC:X13290] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:Staphylococcus aureus multi-resistance plasmid pSK1 DNA containingtransposon Tn4003.] [NT:transposase (AA 1-224)] [SP:P14506] [LE:4017] [RE:4691] [DI:complement] >gp:[GI:g1762092] [LN:SEU40381] [AC:U40381] [PN:transposase] [GN:tnp] [OR:Staphylococcus epidermidis] [DB:genpept-bct1] [DE:Staphylococcus epidermidis plasmid pSK697 insertion sequenceIS257(697A) putative transposase gene, complete cds.] [NT:Tnp; putative transposase] [LE:57] [RE:731] [DI:direct] >gp:[GI:g1762098] [LN:SEU40384] [AC:U40384] [PN:transposase] [GN:tnp] [OR:Staphylococcus epidermidis] [DB:genpept-bct1] [DE:Staphylococcus epidermidis plasmid pSK818 insertion sequenceIS257(818A) putative transposase gene, complete cds.] [NT:Tnp; putative transposase] [LE:57] [RE:731] [DI:direct] >gp:[GI:g3676405] [LN:AF051916] [AC:AF051916] [PN:putative transposase TnpC] [GN:tnpC] [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus plasmid pJE1 remnant of replication proteinRep (rep), trimethoprim resistance protein DfrA (dfrA), thymidylatesynthetase ThyE (thyE), and putative transposase Tnp (tnp) genes,complete cds; and unknown gene.] [LE:65] [RE:739] [DI:direct] >gp:[GI:g3676411] [LN:AF051916] [AC:AF051916] [PN:putative transposase TnpE] [GN:tnpE] [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus plasmid pJE1 remnant of replication proteinRep (rep), trimethoprim resistance protein DfrA (dfrA), thymidylatesynthetase ThyE (thyE), and putative transposase Tnp (tnp) genes,complete cds; and unknown gene.] [LE:4409] [RE:5083] [DI:direct] >gp:[GI:g3676433] [LN:AF051917] [AC:AF051917:L19570] [PN:putative transposase TnpC] [GN:tnpC] [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus plasmid pSK41, complete sequence.] [LE:22981]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000999_20585963_c3_1206	2978	6750	348	115	478	1.7e-45

Description

gp:[GI:d1045998:g5360822] [LN:D86934] [AC:D86934] [PN:IS150-like transposase] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus (strain:N315) DNA, clone_lib:library of N31] [DB:genpept] [DE:Staphylococcus aureus genes, mec region, partial and complete cds.] [NT:ORF N027; putative] [LE:19826] [RE:20179] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000999_2120265_c3_1214	2982	6754	870	289	151	6.1e-08

Description

pir:[LN:S76167] [AC:S76167] [PN:hypothetical protein] [OR:Synechocystis sp.] [SR:PCC 6803, , PCC 6803] [SR:PCC 6803,] [DB:pir2]
>gp:[GI:d1019159:g1653513] [LN:D90914] [AC:D90914:AB001339] [PN:hypothetical protein] [OR:Synechocystis sp.] [SR:Synechocystis sp. (strain:PCC6803) DNA] [DB:genpept-bct1] [DE:Synechocystis sp. PCC6803 complete genome, 16/27, 1991550-2137258.] [NT:ORF_ID:slr0959] [LE:37283] [RE:38872] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000999_2128400_f1_188	2983	6755	138	45		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000999_2148468_f2_400	2984	6756	2073	690	1718	6.6e-177

Description

gp:[GI:g3789932] [LN:AF090142] [AC:AF090142] [PN:lipase precursor] [GN:gehD] [OR:Staphylococcus epidermidis] [DB:genpept-bct2] [EC:3.1.1.3] [DE:Staphylococcus epidermidis lipase precursor (gehD) gene, completecds.] [NT:GehD] [LE:293] [RE:2224] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000999_21506575_c1_702	2985	6757	897	298	331	6.2e-30

Description

pir:[LN:JC5911] [AC:JC5911] [PN:lysin] [GN:lys] [OR:Lactobacillus phage phi-gle] [DB:pir2]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000999_21521878_c1_795	2986	6758	354	117	181	1.2e-12

Description

pir:[LN:F64114] [AC:F64114] [PN:type I site-specific deoxyribonuclease, chain hsdR] [GN:hsdR] [CL:DEAD/H box helicase homology] [OR:Haemophilus influenzae] [EC:3.1.21.3] [DB:pir2] >gp:[GI:g1574743] [LN:U32808] [AC:U32808:L42023] [PN:type I restriction enzyme (hsdR)] [GN:HI1285] [OR:Haemophilus influenzae Rd] [DB:genpept-bct2] [DE:Haemophilus influenzae Rd section 123 of 163 of the completegenome.] [NT:similar to PID:1685100 percent identity: 59.01;} [LE:5702] [RE:8869] [DI:complement]

NO-HIT

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gp:[GI:d1046045:g5360869] [LN:D86934] [AC:D86934] [OR:Staphylococcus aureus]
[SR:Staphylococcus aureus (strain:N315) DNA, clone_lib:library of N31]
[DB:genpept] [DE:Staphylococcus aureus genes, mec region, partial and
complete cds.] [NT:ORF CN049] [LE:54106] [RE:>54378] [DI:complement]
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gp:[GI:g30444072] [LN:AF055713] [AC:AF055713] [PN:beta-hemolysin] [GN:hlb]
[OR:Staphylococcus schleiferi] [DB:genpept-bct2] [DE:Staphylococcus
schleiferi beta-hemolysin (hlb) gene, partial cds.] [LE:1] [RE:>987]
[DI:direct]
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NO-HIT

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000999_2209675_f1_61	2992	6764	1470	489	465	3.9e-44

Description

sp:[LN:TYD2_PETCR] [AC:Q06086] [GN:TYRDC-2] [OR:PETROSELINUM CRISPUM]
[SR:,PARSLEY:PETROSELINUM HORTENSE] [EC:4.1.1.25] [DE:TYROSINE DECARBOXYLASE
2,] [SP:Q06086] [DB:swissprot] >pir:[LN:A44405] [AC:A44405] [PN:tyrosine
decarboxylase,] [GN:tyrCD] [CL:aromatic-L-amino-acid decarboxylase:animal
histidine decarboxylase homology] [OR:Petroselinum crispum] [SR:,parsley]
[EC:4.1.1.25] [DB:pir2] >gp:[GI:g169671] [LN:PUMTRYDC2X] [AC:M96070]
[PN:tyrosine decarboxylase] [GN:TryDC-2] [OR:Petroselinum crispum]
[SR:Petroselinum crispum (library: lambda gt11) cDNA to mRNA]
[DB:genpept-pln1] [EC:4.1.1.25] [DE:Parsley tyrosine decarboxylase (TryDC-2)
mRNA, complete cds.] [LE:4] [RE:1548] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000999_2214217_c2_984	2993	6765	1845	614	2888	6.9e-301

Description

gp:[GI:g5114231] [LN:AF136709] [AC:AF136709] [PN:histidine kinase YycG]
[GN:yycG] [OR:Staphylococcus aureus] [DB:genpept] [DE:Staphylococcus aureus
response regulator YycF (yycF) and histidinekinase YycG (yycG) genes,
complete cds.] [LE:1363] [RE:3189] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000999_22275082_f2_264	2994	6766	135	44		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000999_22291327_c2_908	2995	6767	141	46		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000999_22383437_f2_293	2996	6768	321	106	80	0.0091

Description

pir:[LN:S29577] [AC:I51043:S29577] [PN:Ig light chain] [GN:IgL]
[OR:Oncorhynchus mykiss] [SR:,rainbow trout] [DB:pir2]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000999_22475037_c3_1209	2997	6769	126	41	114	2.3e-06

Description

gp:[GI:g2605928] [LN:AF029727] [AC:AF029727] [OR:Enterococcus faecium]
[DB:genpept-bct2] [DE:Enterococcus faecium insertion sequence IS1485,
complete sequence.] [NT:putative; orfB] [LE:402] [RE:1238] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000999_22537563_c1_840	2998	6770	231	76		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000999_22679825_f1_84	2999	6771	168	55	111	7.6e-06

Description

pir:[LN:B69978] [AC:B69978] [PN:2-nitropropane dioxygenase homolog yrpB]
[GN:yrpB] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:g1934639] [LN:BSU93875]
[AC:U93875] [PN:2-nitropropane dioxygenase] [GN:yrpB] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis alcohol dehydrogenase (adhB) gene,
partial cds,hypothetical spore coat protein (yraF), hypothetical spore
coatprotein (yraG), YraH (yraH), YraI (yraI), YraJ (yraJ), YraK (yraK),YraL
(yraL), chitosanase precursor (csn), YraM (yram), LysR-familytranscription
regulator (yraN), YraO (yraO), YrpG (yrpG), RNAPolymerase sigma factor SigZ
(sigZ), YrpE (yrpE), YrpD (yrpD), YrpC(yrpC) and 2-nitropropane dioxygenase
(yrpB) genes, complete cds,and aminoglycoside 6-adenylyltransferase (aadK)
gene, partial cds.] [NT:similar to 2-nitropropane dioxigenase of Williopsis]
[LE:16473] [RE:17516] [DI:complement] >gp:[GI:e1183909:g2635125]
[LN:BSUB0014] [AC:Z99117:AL009126] [GN:yrpB] [FN:unknown] [OR:Bacillus
subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section
14 of 21): from 2599451to 2812870.] [NT:similar to 2-nitropropane
dioxygenase] [LE:136734] [RE:137777] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000999_22900337_c2_906	3000	6772	135	44		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_22902302_c1_767	3001	6773	1407	468	2010	7.5e-208

Description

sp:[LN:SYS_STAAU] [AC:P95689] [GN:SERS] [OR:STAPHYLOCOCCUS AUREUS]
 [EC:6.1.1.11] [DE:SERYL-TRNA SYNTHETASE, (SERINE--TRNA LIGASE) (SERRS)]
 [SP:P95689] [DB:swissprot] >gp:[GI:e291101:g1835218] [LN:SASERS] [AC:Y09924]
 [PN:seryl-trna synthetase] [GN:sers] [OR:Staphylococcus aureus]
 [DB:genpept-bct1] [EC:6.1.1.11] [DE:S.aureus serS gene.] [SP:P95689] [LE:1]
 [RE:1287] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_23437803_f3_452	3002	6774	714	237	129	7.7e-07

Description

gp:[GI:g4981720] [LN:AE001774] [AC:AE001774:AE000512] [PN:transcriptional
 regulator, crp family] [GN:TM1171] [OR:Thermotoga maritima]
 [DB:genpept-bct2] [DE:Thermotoga maritima section 86 of 136 of the complete
 genome.] [NT:similar to GB:Z26044 SP:P47200 PID:398391 percent] [LE:5164]
 [RE:5769] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_23438301_f1_87	3003	6775	255	84		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_23438876_f3_528	3004	6776	258	85		

Description

NO-HIT

GenBank: E05476

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_23439193_c3_1263	3005	6777	495	164	453	7.4e-43

Description

pir:[LN:G69784] [AC:G69784] [PN:hypothetical protein ydhK] [GN:ydhK]
[OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1182558:g2632892] [LN:BSUB0004]
[AC:Z99107:AL009126] [GN:ydhK] [FN:unknown] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 4 of 21):
from 600701 to813890.] [LE:23509] [RE:24126] [DI:direct]
>gp:[GI:d1020482:g1945095] [LN:D88802] [AC:D88802] [GN:ydhK] [OR:Bacillus
subtilis] [SR:Bacillus subtilis (sub_species:Marburg, strain:168,
isolate:JH642] [DB:genpept-bct1] [DE:Bacillus subtilis DNA for
phoB-rrnE-groESL region, complete cds.] [NT:membrane protein] [LE:10511]
[RE:11128] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_2345025_c2_913	3006	6778	144	47		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_23462762_c3_1097	3007	6779	1527	508	2298	2.3e-238

Description

sp:[LN:AHPF_STAAU] [AC:O05204] [GN:AHPF] [OR:STAPHYLOCOCCUS AUREUS]
[EC:1.6.4.-] [DE:ALKYL HYDROPEROXIDE REDUCTASE SUBUNIT F,] [SP:O05204]
[DB:swissprot] >gp:[GI:g1916317] [LN:SAU92441] [AC:U92441:X85029] [PN:alkyl
hydroperoxide reductase subunit F] [GN:ahpF] [OR:Staphylococcus aureus]
[DB:genpept-bct1] [DE:Staphylococcus aureus alkyl hydroperoxide reductase
subunit C(aphC) and subunit F (aphF) genes, complete cds.] [NT:AhpF]
[LE:1376] [RE:2899] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_23468762_f3_521	3008	6780	132	43		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_23507_c1_765	3009	6781	2709	902	3998	0.0

Description

gp:[GI:d1001842:g540542] [LN:STAGYRABA] [AC:D10489] [PN:DNA gyrase A]
[GN:gyrA] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus
(strain:ATCC12600) DNA]. [DB:genpept-bct1] [EC:5.99.1.3] [DE:Staphylococcus
aureus genes for DNA gyrase A and B, complete cds.] [LE:2152] [RE:4815]
[DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_23537785_f2_233	3010	6782	138	45		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_23538427_c2_887	3011	6783	309	102	132	8.3e-09

Description

pir:[LN:F71456] [AC:F71456] [PN:hypothetical protein PH0308] [GN:PH0308]
[OR:Pyrococcus horikoshii] [DB:pir2] >gp:[GI:d1030324:g3256698]
[LN:AP000001]
[AC:AP000001:AB009465:AB009464:AB009466:AB009467:AB009468:AB009469]
[PN:215aa long hypothetical protein] [GN:PH0308] [OR:Pyrococcus horikoshii]
[SR:Pyrococcus horikoshii (strain:OT3) DNA] [DB:genpept-bct1] [DE:Pyrococcus
horikoshii OT3 genomic DNA, 1-287000 nt. position (1/7).]
[NT:motif=prokaryotic membrane lipoprotein lipid] [LE:271764] [RE:272411]
[DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_23556577_f1_99	3012	6784	324	107		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_23563500_c1_706	3013	6785	156	51		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000999_235678_f2_239	3014	6786	216	71	203	2.3e-16

Description

pir:[LN:F69903] [AC:F69903] [PN:D-alanyl-D-alanine carboxypeptidase homolog yodJ] [GN:yodJ] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:g2415396] [LN:AF015775] [AC:AF015775] [PN:carboxypeptidase] [GN:yodJ] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis YodA (yodA), YodB (yodB), YodC (yodC), YodD (yodD), ABC-transporter (yodE), permease (yodF), proteinase (ctpA), YodH (yodH), YodI (yodI), carboxypeptidase (yodJ), purinenucleoside phosphorylase (deoD), YodL (yodL), YodM (yodM), YodN (yodN), YodO (yodO), YodP (yodP), acetylornithine deacetylase (argE), butirate-acetoacetate CoA transferase (yodR), butyrateacetoacetate-CoA transferase (yodS), YodT (yodT), CgeE (cgeE), CgeD (cgeD), CgeC (cgeC), CgeA (cgeA), CgeB (cgeB), YzxA (yzxA), UDP-glucose epimerase (yodU), YodV (yodV), and YodW (yodW) genes, complete cds; and YodZ (yodZ) gene, partial cds.] [NT:similar to Enterococcus faecium D-alanyl-D-alanine] [LE:8510] [RE:9331] [DI:complement] >gp:[GI:e1185433:g2634354] [LN:BSUB0011] [AC:Z99114:AL009126] [GN:yodJ] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 11 of 21): from 2000171 to 2207900.] [NT:similar to D-alanyl-D-alanine carboxypeptidase] [LE:133640] [RE:134461] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000999_23610885_c1_820	3015	6787	126	41		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000999_23610952_c2_1082	3016	6788	855	284	305	3.6e-27

Description

pir:[LN:H69468] [AC:H69468] [PN:lysophospholipase homolog] [OR:Archaeoglobus fulgidus] [DB:pir2] >gp:[GI:g2648798] [LN:AE000982] [AC:AE000982:AE000782] [PN:lysophospholipase] [GN:AF1753] [OR:Archaeoglobus fulgidus] [DB:genpept-bct2] [DE:Archaeoglobus fulgidus section 125 of 172 of the complete genome.] [NT:similar to GP:1763011 percent identity: 33.46;] [LE:10776] [RE:11576] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000999_23612907_c1_696	3017	6789	144	47		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_23631512_c3_1178	3018	6790	1323	440	2289	2.0e-237

Description

gp:[GI:d1046046:g5360870] [LN:D86934] [AC:D86934] [OR:Staphylococcus aureus]
 [SR:Staphylococcus aureus (strain:N315) DNA, clone_lib:library of N31]
 [DB:genpept] [DE:Staphylococcus aureus genes, mec region, partial and
 complete cds.] [NT:ORF CN050] [LE:54760] [RE:>56082] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_23632883_c1_844	3019	6791	183	60		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_23634682_c2_1013	3020	6792	375	124		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_23634786_f3_619	3021	6793	1200	399	692	3.5e-68

Description

gp:[GI:d1025735:g2879915] [LN:D85752] [AC:D85752] [GN:bacI] [OR:Enterococcus
 faecalis] [SR:Enterococcus faecalis plasmid:ppd1 DNA] [DB:genpept-bct1]
 [DE:Enterococcus faecalis plasmid pPD1 bacA, bacB, bacC, bacD, bacE, bacF,
 bacG, bacH and bacI genes, complete cds.] [LE:7732] [RE:8931] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_23635302_c1_867	3022	6794	138	45		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_23635931_c1_854	3023	6795	375	124	637	2.3e-62

Description

sp:[LN:MERT_STAAU] [AC:P08656] [GN:MERT] [OR:STAPHYLOCOCCUS AUREUS]
 [DE:MERCURIC TRANSPORT PROTEIN (MERCURY ION TRANSPORT PROTEIN)] [SP:P08656]
 [DB:swissprot] >pir:[LN:D29504] [AC:D29504] [PN:hypothetical 14K protein
 (mer operon)] [OR:Staphylococcus aureus] [DB:pir2] >gp:[GI:g459906]
 [LN:L29436] [AC:L29436:M15048:N00048] [GN:mert] [OR:Plasmid pI258]
 [SR:Plasmid pI258 DNA] [DB:genpept-bct1] [DE:Plasmid pI258 (from S.aureus
 strain RN23 8325) mercury resistance(mer) operon encoding mercuric reductase
 (merA), organomercuriallyase (merB), regulatory protein (merR) and membrane
 transportprotein (merT), complete cds.] [LE:2704] [RE:3090] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_23679765_f3_449	3024	6796	1269	422	1274	7.4e-130

Description

gp:[GI:e1299582:g3687416] [LN:BLY17554] [AC:Y17554] [PN:arginine deiminase]
 [GN:arcA] [OR:Bacillus licheniformis] [DB:genpept-bct1] [EC:3.5.3.6]
 [DE:Bacillus licheniformis arcA, arcB, arcC and arcD genes.] [LE:248]
 [RE:1489] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_23703175_c3_1103	3025	6797	135	44		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_23704502_f1_158	3026	6798	267	88		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_23834461_f3_588	3027	6799	162	53		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_23860812_f2_403	3028	6800	603	200	540	4.5e-52

Description

gp:[GI:g4185302] [LN:AF089862] [AC:AF089862] [PN:type-I signal peptidase SipB] [GN:sipB] [OR:Staphylococcus carnosus] [DB:genpept-bct2]
[DE:Staphylococcus carnosus type-I signal peptidase SipA (sipA) and type-I signal peptidase SipB (sipB) genes, complete cds; and unknown gene.]
[NT:leader peptidase] [LE:1502] [RE:2071] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_23866566_c2_1067	3029	6801	159	52		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_23959802_c1_787	3030	6802	171	56		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_23959802_c3_1250	3031	6803	153	50		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_23959802_c3_1261	3032	6804	132	43		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_23959802_f2_313	3033	6805	210	69		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_23959802_f3_447	3034	6806	141	46		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_24016062_f1_168	3035	6807	129	42		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_24023300_c2_964	3036	6808	516	171	760	2.2e-75

Description

sp:[LN:DNAA_STAAU] [AC:P49994] [GN:DNAA] [OR:STAPHYLOCOCCUS AUREUS]
[DE:CHROMOSOMAL REPLICATION INITIATOR PROTEIN DNAA] [SP:P49994]
[DB:swissprot] >pir:[LN:JC5607] [AC:JC5607] [PN:replication initiation
protein dnaA] [GN:dnaA] [CL:replication initiation protein dnaA]
[OR:Staphylococcus aureus] [DB:pir2] >gp:[GI:d1014451:g1694677] [LN:D89066]
[AC:D89066] [PN:DnaA] [GN:dnaA] [OR:Staphylococcus aureus]
[SR:Staphylococcus aureus DNA] [DB:genpept-bct1] [DE:Staphylococcus aureus
DNA for DnaA, complete cds.] [LE:456] [RE:1817] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_24101587_f3_455	3037	6809	339	112	79	0.0098

Description

pir:[LN:S42040] [AC:S42040] [PN:hypothetical protein 3] [OR:Leuconostoc
oenos] [DB:pir2] >gp:[GI:g515739] [LN:LEUORF15X] [AC:L28806] [FN:unknown]
[OR:Oenococcus oeni] [DB:genpept-bct1] [DE:Leuconostoc oenos complete
ORF1-ORF5.] [NT:ORF3; putative] [LE:2571] [RE:2975] [DI:direct]
>gp:[GI:g454968] [LN:LOPLORFG] [AC:Z29976] [OR:Oenococcus oeni]
[DB:genpept-bct1] [DE:L.oenos plasmid p4028 ORF1, ORF2, ORF3, ORF4, ORF5
genes.] [NT:ORF3] [LE:2571] [RE:2975] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_24110635_c3_1231	3038	6810	132	43		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_24220062_c3_1104	3039	6811	285	94	68	0.045

Description

gp:[GI:g4731269] [LN:AF110706] [AC:AF110706] [PN:cytochrome oxidase I]
 [OR:Mitochondrion Bemisia tabaci] [SR:sweet potato whitefly]
 [DB:genpept-inv2] [DE:Bemisia tabaci cytochrome oxidase I gene, partial
 cds;mitochondrial gene for mitochondrial product.] [NT:premature stop
 codon.] [LE:<1] [RE:330] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_24234562_c2_890	3040	6812	222	73	64	0.026

Description

gp:[GI:g4808591] [LN:AF093829] [AC:AF093829]
 [PN:alpha-1,2-fucosyltransferase long form] [OR:Helicobacter pylori]
 [DB:genpept-bct2] [DE:Helicobacter pylori strain UA1182
 alpha-1,2-fucosyltransferasegene, alternative products, complete cds.]
 [NT:ribosomal slippage] [LE:141:573] [RE:573:1042] [DI:directJoin]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_24250010_c3_1271	3041	6813	225	74		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_24255312_f1_128	3042	6814	159	52		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_24256437_c1_717	3043	6815	141	46		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000999_24273442_f1_22	3044	6816	384	127	144	4.1e-10

Description

pir:[LN:C70043] [AC:C70043] [PN:hypothetical protein yv1A] [GN:yv1A]
[OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1186201:g2636026] [LN:BSUB0018]
[AC:Z99121:AL009126] [GN:yv1A] [FN:unknown] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 18 of 21):
from 3399551to 3609060.] [LE:207957] [RE:208283] [DI:complement]
>gp:[GI:e1184419:g2636039] [LN:BSUB0019] [AC:Z99122:AL009126] [GN:yv1A]
[FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
complete genome (section 19 of 21): from 3597091to 3809700.] [LE:10417]
[RE:10743] [DI:complement] >gp:[GI:g2618844] [LN:AF017113] [AC:AF017113]
[PN:Yv1A] [GN:yv1A] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus
subtilis 300-304 degree genomic sequence.] [LE:19550] [RE:19876] [DI:direct]
>gp:[GI:e1184419:g2636039] [LN:BSUB0019] [AC:Z99122:AL009126] [GN:yv1A]
[FN:unknown] [OR:Bacillus subtilis] [DB:genpept] [DE:Bacillus subtilis
complete genome (section 19 of 21): from 3597091to 3809700.] [LE:10417]
[RE:10743] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000999_24273442_f1_85	3045	6817	384	127	142	6.7e-10

Description

pir:[LN:C70043] [AC:C70043] [PN:hypothetical protein yv1A] [GN:yv1A]
[OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1186201:g2636026] [LN:BSUB0018]
[AC:Z99121:AL009126] [GN:yv1A] [FN:unknown] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 18 of 21):
from 3399551to 3609060.] [LE:207957] [RE:208283] [DI:complement]
>gp:[GI:e1184419:g2636039] [LN:BSUB0019] [AC:Z99122:AL009126] [GN:yv1A]
[FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
complete genome (section 19 of 21): from 3597091to 3809700.] [LE:10417]
[RE:10743] [DI:complement] >gp:[GI:g2618844] [LN:AF017113] [AC:AF017113]
[PN:Yv1A] [GN:yv1A] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus
subtilis 300-304 degree genomic sequence.] [LE:19550] [RE:19876] [DI:direct]
>gp:[GI:e1184419:g2636039] [LN:BSUB0019] [AC:Z99122:AL009126] [GN:yv1A]
[FN:unknown] [OR:Bacillus subtilis] [DB:genpept] [DE:Bacillus subtilis
complete genome (section 19 of 21): from 3597091to 3809700.] [LE:10417]
[RE:10743] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000999_24297050_c2_904	3046	6818	141	46		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_24299037_c3_1238	3047	6819	255	84	68	0.045

Description

gp:[GI:g4049677] [LN:AF063866] [AC:AF063866] [PN:ORF MSV084 hypothetical protein] [GN:MSV084] [OR:Melanoplus sanguinipes entomopoxvirus] [DB:genpept-vrl] [DE:Melanoplus sanguinipes entomopoxvirus, complete genome.] [LE:80206] [RE:80577] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_24329192_c2_986	3048	6820	180	59		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_24332641_c1_768	3049	6821	129	42		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_24401712_c1_826	3050	6822	1125	374	117	0.0014

Description

pir:[LN:C70168] [AC:C70168] [PN:DNA polymerase I (polA) homolog] [OR:Borrelia burgdorferi] [SR:, Lyme disease spirochete] [DB:pir2]
>gp:[GI:g2688462] [LN:AE001156] [AC:AE001156:AE000783] [PN:DNA polymerase I (polA)] [GN:BB0548] [OR:Borrelia burgdorferi] [SR:Lyme disease spirochete] [DB:genpept-bct2] [DE:Borrelia burgdorferi (section 42 of 70) of the complete genome.] [NT:similar to GB:L42023 SP:P43741 PID:1005915] [LE:6171] [RE:8897] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_24406311_c3_1111	3051	6823	135	44		

Description

NO-HIT

AI7503000999_24406338_c3_1122	3052	6824	186	61
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NO-HIT

AI7503000999_24407313_c2_880	3053	6825	126	41
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NO-HIT

AI7503000999_24407812_c3_1182	3054	6826	771	256	1062	2.2e-107
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gp:[GI:d1046030:g5360854] [LN:D86934] [AC:D86934]
[PN:glycerophosphoryldiester phosphodiesterase] [OR:Staphylococcus aureus]
[SR:Staphylococcus aureus (strain:N315) DNA, clone_lib:library of N31]
[DB:genpept] [DE:Staphylococcus aureus genes, mec region, partial and
complete cds.] [NT:ORF N039; putative] [LE:46160] [RE:>46792]
[DI:complement]
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AI7503000999_24407828_c3_1230	3055	6827	2013	670	157	2.1e-07
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gp:[GI:g4049717] [LN:AF063866] [AC:AF063866] [PN:ORF MSV156 hypothetical protein] [GN:MSV156] [OR:Melanoplus sanguinipes entomopoxvirus] [DB:genpept-vrl] [DE:Melanoplus sanguinipes entomopoxvirus, complete genome.] [LE:140126] [RE:143509] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_24409452_c3_1294	3056	6828	432	143	132	7.6e-09

Description

sp:[LN:Y577_METJA] [AC:Q57997] [GN:MJ0577] [OR:METHANOCOCCUS JANNASCHII]
 [DE:PROTEIN MJ0577] [SP:Q57997] [DB:swissprot] >pir:[LN:A64372] [AC:A64372]
 [PN:hypothetical protein homolog MJ0577] [CL:Escherichia coli ybdQ protein]
 [OR:Methanococcus jannaschii] [DB:pir2] [MP:FOR512975-513463]
 >gp:[GI:g1591284] [LN:U67506] [AC:U67506:L77117] [PN:conserved hypothetical
 protein] [GN:MJ0577] [OR:Methanococcus jannaschii] [DB:genpept-bct2]
 [DE:Methanococcus jannaschii section 48 of 150 of the complete genome.]
 [NT:similar to SP:P42297 PID:603780 PID:849027] [LE:8204] [RE:8692]
 [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_24411262_f1_37	3057	6829	180	59		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_24412507_f2_339	3058	6830	135	44		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_24414680_c1_843	3059	6831	1287	428	141	1.3e-05

Description

gp:[GI:g1041785] [LN:PYU36927] [AC:U36927] [PN:rhopty protein]
 [FN:erythrocyte invasion and possible binding] [OR:Plasmodium yoelii]
 [DB:genpept-inv1] [DE:Plasmodium yoelii rhopty protein gene, partial cds.]
 [LE:<1] [RE:7206] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000999_24414818_f3_516	3060	6832	441	146	94	0.00083

Description

sp:[LN:PHNB_ECOLI] [AC:P16681] [GN:PHNB] [OR:ESCHERICHIA COLI] [DE:PHNB PROTEIN] [SP:P16681] [DB:swissprot] >pir:[LN:C35718] [AC:C35718:S56335:B65220] [PN:phnB protein] [GN:phnB] [OR:Escherichia coli] [DB:pir2] >gp:[GI:g147195] [LN:ECOPHNAQ] [AC:J05260] [OR:Escherichia coli] [SR:E.coli (strain B) DNA] [DB:genpept-bct1] [DE:E.coli psiD locus containing alkylphosphonate uptake (phn) genes Athrough Q, complete cds.] [NT:phnB protein] [LE:3767] [RE:4210] [DI:direct] >gp:[GI:g536951] [LN:ECOUW93] [AC:U14003] [GN:phnB] [OR:Escherichia coli] [DB:genpept-bct1] [DE:Escherichia coli K-12 chromosomal region from 92.8 to 00.1 minutes.] [LE:16226] [RE:16669] [DI:complement] >gp:[GI:g1790546] [LN:AE000483] [AC:AE000483:U00096] [PN:orf, hypothetical protein] [GN:phnB] [FN:orf; Unknown] [OR:Escherichia coli] [DB:genpept-bct2] [DE:Escherichia coli K-12 MG1655 section 373 of 400 of the completegenome.] [NT:f147; 100 pct identical amino acid sequence and] [LE:97] [RE:540] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000999_24424092_c2_1017	3061	6833	522	173	104	0.00027

Description

gp:[GI:e1488089:g5051453] [LN:NME242841] [AC:AJ242841] [PN:hypothetical protein] [OR:Neisseria meningitidis] [DB:genpept-bct1] [DE:Neisseria meningitidis DNA for opcA region, strain Z2491.] [NT:ORFA] [LE:10162] [RE:10707] [DI:direct] >gp:[GI:e1488089:g5051453] [LN:NME242841] [AC:AJ242841] [PN:hypothetical protein] [OR:Neisseria meningitidis] [DB:genpept] [DE:Neisseria meningitidis DNA for opcA region, strain Z2491.] [NT:orfA] [LE:10162] [RE:10707] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000999_24430392_c1_856	3062	6834	681	226	1116	4.1e-113

Description

sp:[LN:MERB_STAAU] [AC:P08653] [GN:MERB] [OR:STAPHYLOCOCCUS AUREUS] [EC:4.99.1.2] [DE:ALKYLMERCURY LYASE, (ORGANOMERCURIAL LYASE)] [SP:P08653] [DB:swissprot] >pir:[LN:F29504] [AC:F29504] [PN:alkylmercury lyase,] [CL:alkylmercury lyase] [OR:Staphylococcus aureus] [EC:4.99.1.2] [DB:pir2] >gp:[GI:g459908] [LN:L29436] [AC:L29436:M15048:N00048] [PN:organomercurial lyase] [GN:merB] [OR:Plasmid pI258] [SR:Plasmid pI258 DNA] [DB:genpept-bct1] [DE:Plasmid pI258 (from S.aureus strain RN23 8325) mercury resistance(mer) operon encoding mercuric reductase (merA), organomercuriallyase (merB), regulatory protein (merR) and membrane transportprotein (merT), complete cds.] [LE:4873] [RE:5523] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_24431502_c3_1121	3063	6835	846	281	347	1.3e-31

Description

gp:[GI:g3818562] [LN:AF076529] [AC:AF076529] [PN:ATP binding protein BviA] [GN:bviA] [OR:Butyrivibrio fibrisolvens] [DB:genpept-bct2] [DE:Butyrivibrio fibrisolvens response regulator homolog gene, partialcds; histidine kinase homolog, butyrivibriocin AR10 operon,complete sequence; and unknown gene.] [LE:2342] [RE:3187] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_24432662_c2_1052	3064	6836	969	322	301	2.3e-47

Description

sp:[LN:YACK_ECOLI] [AC:P36649:P75655] [GN:YACK] [OR:ESCHERICHIA COLI] [DE:PROBABLE 53.4 KD BLUE-COPPER PROTEIN YACQ PRECURSOR] [SP:P36649:P75655] [DB:swissprot] >pir:[LN:C64735] [AC:C64735:S45200] [PN:probable copper-binding protein yack] [GN:yack] [OR:Escherichia coli] [DB:pir2] >gp:[GI:g1786314] [LN:AE000121] [AC:AE000121:U00096] [PN:orf, hypothetical protein] [GN:yack] [FN:orf; Unknown] [OR:Escherichia coli] [DB:genpept-bct2] [DE:Escherichia coli K-12 MG1655 section 11 of 400 of the completegenome.] [NT:o516; 100 pct identical to 463 residues] [LE:9364] [RE:10914] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_24475252_f1_1	3065	6837	159	52		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_24486008_c2_1059	3066	6838	978	325	136	1.6e-06

Description

gp:[GI:g4378164] [LN:AF102543] [AC:AF102543] [PN:unknown] [OR:Zymomonas mobilis] [DB:genpept-bct2] [DE:Zymomonas mobilis 5,10-methylenetetrahydrofolate reductase (metF)gene, partial cds; lipoprotein precursor (vacJ), ferredoxin-NADP+reductase (fpr), succinic semialdehyde dehydrogenase (gabD),thymidylate synthetase (thyA), gluconate permease (gntP),UTP-glucose-1-phosphate uridyltransferase, diaminopimelatedecarboxylase (lysA), arginosuccinate lyase (argH), NADH-dependentbutanol dehydrogenase (yugJ), and morphine 6-dehydrogenase (mdh)genes, complete cds; tRNA-Ala gene, complete sequence;aminopeptidase N (pepN) gene, complete cds; and unknown genes.] [NT:zm4orf2] [LE:12502] [RE:13458] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000999_24641941_f3_456	3067	6839	510	169		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000999_24645817_c2_979	3068	6840	453	150	461	1.0e-43

Description

gp:[GI:g143421] [LN:BACRGC] [AC:M57623:J05723] [PN:ribosomal protein L9]
[GN:ribosomal protein L9] [OR:Bacillus stearothermophilus]
[SR:B.stearothermophilus DNA] [DB:genpept-bct1] [DE:B.stearothermophilus
ribosomal protein L9 gene, complete cds.] [LE:1] [RE:450] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000999_24647142_c2_930	3069	6841	645	214	575	8.7e-56

Description

gp:[GI:e352094:g2462707] [LN:SXLACRPH] [AC:Y14599] [PN:hypothetical protein]
[GN:orf5] [OR:Staphylococcus xylosus] [DB:genpept-bct1] [DE:Staphylococcus
xylosus lacR, lacP, lacH genes and 2 ORF's.] [LE:6476] [RE:7105]
[DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000999_24647292_f3_668	3070	6842	1275	424	1180	6.7e-120

Description

sp:[LN:PBUX_BACSU] [AC:P42086] [GN:PBUX] [OR:BACILLUS SUBTILIS] [DE:XANTHINE
PERMEASE] [SP:P42086] [DB:swissprot] >pir:[LN:S51310] [AC:S51310:E69673]
[PN:xanthine permease pbuX] [GN:pbuX] [CL:xanthine permease pbuX]
[OR:Bacillus subtilis] [DB:pir2] >gp:[GI:g1256618] [LN:BACYACA] [AC:L77246]
[PN:transport protein] [GN:ypaQ] [FN:pyrimidine salvage] [OR:Bacillus
subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis (YAC10-9 clone) DNA region
between the serA andkdg loci.] [NT:26% of identity to the Bacillus
caldolyticus uracil] [LE:2007] [RE:3323] [DI:direct]
>gp:[GI:e1183652:g2634625] [LN:BSUB0012] [AC:Z99115:AL009126] [PN:xanthine
permease] [GN:pbuX] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus
subtilis complete genome (section 12 of 21): from 2195541to 2409220.]
[NT:alternate gene name: ypaQ] [SP:P42086] [LE:121829] [RE:123145]
[DI:complement] >gp:[GI:g633170] [LN:BSXPTPBUX] [AC:X83878] [PN:xanthine
permease] [GN:pbuX] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis
xpt and pbuX genes.] [SP:P42086] [LE:938] [RE:2254] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000999_24650427_f3_493	3071	6843	3126	1041	1653	2.3e-220

Description

pir:[LN:F64114] [AC:F64114] [PN:type I site-specific deoxyribonuclease, chain hsdR] [GN:hsdR] [CL:DEAD/H box helicase homology] [OR:Haemophilus influenzae] [EC:3.1.21.3] [DB:pir2] >gp:[GI:g1574743] [LN:U32808] [AC:U32808:L42023] [PN:type I restriction enzyme (hsdR)] [GN:HI1285] [OR:Haemophilus influenzae Rd] [DB:genpept-bct2] [DE:Haemophilus influenzae Rd section 123 of 163 of the completegenome.] [NT:similar to PID:1685100 percent identity: 59.01;] [LE:5702] [RE:8869] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000999_24783462_c2_1016	3072	6844	339	112	77	0.0086

Description

gp:[GI:g2772544] [LN:STREMM40G] [AC:L46817] [PN:M-40 protein] [GN:emm40] [FN:antiphagocytic] [OR:Streptococcus pyogenes] [DB:genpept-bct2] [DE:Streptococcus pyogenes M-40 protein (emm40) gene, partial cds.] [LE:<1] [RE:>341] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000999_24797126_f1_88	3073	6845	249	82	69	0.036

Description

gp:[GI:g2772603] [LN:DMU85764] [AC:U85764] [PN:accessory gland protein Acp32CD] [GN:Acp32CD] [FN:responsible for physiological and behavioral] [OR:Drosophila melanogaster] [SR:fruit fly] [DB:genpept-inv1] [DE:Drosophila melanogaster accessory gland protein Acp32CD (Acp32CD)gene, partial cds.] [LE:74] [RE:>377] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000999_24800412_c2_981	3074	6846	147	48		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000999_24812927_f2_227	3075	6847	183	60		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_24817142_c1_764	3076	6848	1947	648	3147	0.0

Description

pir:[LN:A40585] [AC:A40585:A35406:S54711:A42295:S36024] [PN:DNA
topoisomerase (ATP-hydrolyzing), chain B] [GN:gyrB] [CL:DNA topoisomerase
(ATP-hydrolyzing) chain B] [OR:Staphylococcus aureus] [EC:5.99.1.3]
[DB:pir1] >gp:[GI:g296395] [LN:SAGYRREC] [AC:X71437] [PN:DNA gyrase]
[GN:gyrB] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:S.aureus genes
gyrB, gyrA and recF (partial).] [SP:P20832] [LE:282] [RE:2216] [DI:direct]
>gp:[GI:d1001841:g540541] [LN:STAGYRABA] [AC:D10489] [PN:DNA gyrase B]
[GN:gyrB] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus
(strain:ATCC12600) DNA] [DB:genpept-bct1] [EC:5.99.1.3] [DE:Staphylococcus
aureus genes for DNA gyrase A and B, complete cds.] [LE:181] [RE:2115]
[DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_24847250_f2_320	3077	6849	153	50		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_24848452_c3_1175	3078	6850	792	263	223	1.7e-18

Description

pir:[LN:H70089] [AC:H70089] [PN:hypothetical protein yycI] [GN:yycI]
[OR:Bacillus subtilis] [DB:pir2] >gp:[GI:d1011959:g1064811] [LN:BACGNTZA]
[AC:D78193] [GN:yycI] [OR:Bacillus subtilis] [SR:Bacillus subtilis
(strain:168) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis 36kb sequence
between gntZ and trnY genes encoding 34 ORFs.] [LE:31210] [RE:32052]
[DI:complement] >gp:[GI:e1184764:g2636585] [LN:BSUB0021]
[AC:Z99124:AL009126] [GN:yycI] [FN:unknown] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 21 of 21):
from 3999281 to 4214814.] [LE:149594] [RE:150436] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_254527_c2_1038	3079	6851	186	61		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_25548452_f1_207	3080	6852	915	304	354	2.3e-32

Description

pir:[LN:A69867] [AC:A69867] [PN:conserved hypothetical protein ykuT]
 [GN:ykuT] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1181925:g2632241]
 [LN:BS16829KB] [AC:AJ222587] [PN:YkuT protein] [GN:ykuT] [OR:Bacillus
 subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis 29kB DNA fragment from
 ykwC gene to cse15 gene.] [LE:25580] [RE:26383] [DI:complement]
 >gp:[GI:e1185011:g2633792] [LN:BSUB0008] [AC:Z99111:AL009126] [GN:ykuT]
 [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
 complete genome (section 8 of 21): from 1394791to 1603020.] [NT:similar to
 hypothetical proteins] [LE:95836] [RE:96639] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_25554012_c2_912	3081	6853	213	70		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_25554675_c3_1094	3082	6854	927	308	179	2.5e-11

Description

sp:[LN:SR40_YEAST] [AC:P32583] [GN:SRP40:YKR092C:YKR412A] [OR:SACCHAROMYCES
 CEREVISIAE] [SR:,BAKER'S YEAST] [DE:SUPPRESSOR PROTEIN SRP40] [SP:P32583]
 [DB:swissprot] >pir:[LN:S38170] [AC:S38170:S40645:S37702] [PN:SRP40
 protein:protein YKR092c:protein YKR412a] [GN:SRP40] [OR:Saccharomyces
 cerevisiae] [DB:pir2] [MP:11R] >gp:[GI:g450552] [LN:SCDNACHXI] [AC:X73541]
 [OR:Saccharomyces cerevisiae] [SR:baker's yeast] [DB:genpept-pln1]
 [DE:S.cerevisiae DNA of chromosome XI, right arm.] [NT:ORF YKR412]
 [SP:P32583] [LE:1952] [RE:3172] [DI:complement] >gp:[GI:g486581]
 [LN:SCYKR092C] [AC:Z28317:Y13137] [GN:SRP40] [OR:Saccharomyces cerevisiae]
 [SR:baker's yeast] [DB:genpept-pln1] [DE:S.cerevisiae chromosome XI reading
 frame ORF YKR092c.] [NT:ORF YKR092c] [SP:P32583] [LE:400] [RE:1620]
 [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_25565637_f2_257	3083	6855	126	41		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_25583568_f1_12	3084	6856	363	120	71	0.022

Description

pir:[LN:T03326] [AC:T03326] [PN:gene 119 protein] [GN:119] [OR:Lactococcus phage bIL170] [DB:pir2] >gp:[GI:g3282279] [LN:AF009630] [AC:AF009630] [PN:119] [GN:119] [OR:bacteriophage bIL170] [DB:genpept-phg] [DE:Bacteriophage bIL170, complete genome.] [LE:15351] [RE:15644] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_25587802_c1_809	3085	6857	777	258	114	0.00010

Description

sp:[LN:FLIZ_BORBU] [AC:Q44904:Q44764] [GN:FLIZ:BB0276] [OR:BORRELIA BURGDORFERI] [SR:,LYME DISEASE SPIROCHETE] [DE:FLAGELLAR PROTEIN FLIZ] [SP:Q44904:Q44764] [DB:swissprot] >pir:[LN:D70134] [AC:D70134] [PN:flagellar biosynthesis protein (fliZ) homolog] [OR:Borrelia burgdorferi] [SR:, Lyme disease spirochete] [DB:pir2] >gp:[GI:g1165261] [LN:BBU43739] [AC:U43739] [PN:FliZ] [GN:fliZ] [OR:Borrelia burgdorferi] [SR:Lyme disease spirochete strain=B31] [DB:genpept-bct1] [DE:Borrelia burgdorferi fesmid clone 31, complete sequence.] [NT:flagellar protein required for flagella formation] [LE:9847] [RE:10473] [DI:complement] >gp:[GI:g2688190] [LN:AE001137] [AC:AE001137:AE000783] [PN:flagellar biosynthesis protein (fliZ)] [GN:BB0276] [OR:Borrelia burgdorferi] [SR:Lyme disease spirochete] [DB:genpept-bct2] [DE:Borrelia burgdorferi (section 23 of 70) of the complete genome.] [NT:similar to PID:1165261 PID:1185058 SP:Q44904] [LE:15237] [RE:15863] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_25642038_f3_481	3086	6858	138	45		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_25660880_c2_975	3087	6859	177	58		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_25667767_c3_1114	3088	6860	1191	396	907	5.7e-91

Description

pir:[LN:B69847] [AC:B69847] [PN:cystathionine beta-lyase homolog yjcJ]
 [GN:yjcJ] [CL:O-succinylhomoserine (thiol)-lyase] [OR:Bacillus subtilis]
 [DB:pir2] >gp:[GI:e1183208:g2633542] [LN:BSUB0007] [AC:Z99110:AL009126]
 [GN:yjcJ] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus
 subtilis complete genome (section 7 of 21): from 1194391to 1411140.]
 [NT:similar to cystathionine beta-lyase] [LE:64687] [RE:65859] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_25679712_f3_626	3089	6861	660	219	153	2.0e-09

Description

gp:[GI:e1315386:g3417427] [LN:SPBC30B4] [AC:AL031262] [PN:hypothetical
 protein] [GN:SPBC30B4.01c] [OR:Schizosaccharomyces pombe] [SR:fission yeast]
 [DB:genpept-pln1] [DE:S.pombe chromosome II cosmid c30B4.] [NT:SPBC30B4.01c,
 len:344aa, similarity, YNL283C,] [LE:<1] [RE:1034] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_25792911_c1_777	3090	6862	129	42		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_25831512_c3_1105	3091	6863	129	42		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_26172675_f1_124	3092	6864	129	42		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_26181512_c2_1003	3093	6865	126	41		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000999_26198535_c3_1116	3094	6866	765	254	136	5.4e-07

Description

pir:[LN:D70817] [AC:D70817] [PN:hypothetical protein Rv1716] [GN:Rv1716]
 [OR:Mycobacterium tuberculosis] [DB:pir2] >gp:[GI:e1299966:g3261548]
 [LN:MTV048] [AC:AL022003:AL123456] [PN:hypothetical protein Rv1716]
 [GN:Rv1716] [OR:Mycobacterium tuberculosis] [DB:genpept-bct1]
 [DE:Mycobacterium tuberculosis H37Rv complete genome; segment 77/162.]
 [NT:Rv1716, (MTV048.03,MTCY04C12.01) len: 276. Unknown] [LE:1750] [RE:2580]
 [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000999_26214002_f3_647	3095	6867	870	289	627	2.7e-61

Description

sp:[LN:SPOJ_BACSU] [AC:P26497] [GN:SPO0J] [OR:BACILLUS SUBTILIS] [DE:STAGE 0
 SPORULATION PROTEIN J] [SP:P26497] [DB:swissprot] >pir:[LN:A38536]
 [AC:I40445:A38536:S66020:E69710:S18081] [PN:Soj antagonist / chromosome
 positioning and transport protein spo0J:spo0J93 protein:stage 0 sporulation
 protein J93] [GN:spo0J:spo0J93] [CL:Bacillus subtilis transport protein
 spo0J] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:d1005768:g467380]
 [LN:BAC180K] [AC:D26185] [PN:stage 0 sporulation] [GN:spo0J] [OR:Bacillus
 subtilis] [SR:Bacillus subtilis (sub_species:Marburg, strain:168) DNA]
 [DB:genpept-bct1] [DE:B. subtilis DNA, 180 kilobase region of replication
 origin.] [LE:53552] [RE:54400] [DI:complement] >gp:[GI:g40031] [LN:BSORIGS]
 [AC:X62539] [GN:spo0J93] [OR:Bacillus subtilis] [DB:genpept-bct1]
 [DE:B.subtilis genes rpmH, rnpA, 50kd, gidA and gidB.] [SP:P26497] [LE:9000]
 [RE:9848] [DI:direct] >gp:[GI:e1184822:g2636643] [LN:BSUB0021]
 [AC:Z99124:AL009126] [PN:antagonist of Soj] [GN:spo0J] [FN:involved in
 positionning part of the chromosome] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 21 of 21):
 from 3999281to 4214814.] [SP:P26497] [LE:205484] [RE:206332] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000999_26261512_f2_275	3096	6868	162	53		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000999_26351510_f2_375	3097	6869	138	45		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000999_26365911_f1_165	3098	6870	561	186	203	2.3e-16

Description

pir:[LN:E69779] [AC:E69779] [PN:transcription regulator TetR/AcrR family homolog ydeS] [GN:ydeS] [OR:Bacillus subtilis] [DB:pir2]
>gp:[GI:d1020119:g1881339] [LN:AB001488] [AC:AB001488] [GN:ydeS]
[OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:168) DNA]
[DB:genpept-bct1] [DE:Bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.] [NT:PROBABLE TRANSCRIPTIONAL REGULATOR, SIMILAR TO] [LE:111555] [RE:112151] [DI:direct] >gp:[GI:e1182498:g2632832]
[LN:BSUB0003] [AC:Z99106:AL009126] [GN:ydeS] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.] [NT:similar to transcriptional regulator (TetR/AcrR)] [LE:175301] [RE:175897] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000999_26597010_f3_530	3099	6871	186	61	103	2.9e-05

Description

sp:[LN:Y4UH_RHISN] [AC:Q53200] [GN:Y4UH] [OR:RHIZOBIUM SP] [SR:NGR234,]
[DE:PUTATIVE INSERTION SEQUENCE ATP-BINDING PROTEIN Y4UH] [SP:Q53200]
[DB:swissprot] >gp:[GI:e213893:g1486429] [LN:RSPNGR234] [AC:Z68203]
[PN:transposase homologue] [GN:orf10] [OR:Rhizobium sp.] [SR:Rhizobium sp]
[DB:genpept-bct1] [DE:Rhizobium sp. plasmid NGR234a DNA.] [NT:putative]
[SP:Q53200] [LE:13370] [RE:14116] [DI:complement] >gp:[GI:g2182658]
[LN:AE000099] [AC:AE000099:U00090] [PN:Y4uH] [GN:y4uH] [OR:Rhizobium sp.
NGR234] [DB:genpept-bct2] [DE:Rhizobium sp. NGR234 plasmid pNGR234a, section 36 of 46 of thecomplete plasmid sequence.] [NT:putative insertion sequence ATP-binding protein] [LE:8181] [RE:8927] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_26600015_f1_162	3100	6872	354	117	280	1.6e-24

Description

sp:[LN:RNPA_BACSU] [AC:P25814] [GN:RNPA] [OR:BACILLUS SUBTILIS]
[EC:3.1.26.5] [DE:RIBONUCLEASE P PROTEIN COMPONENT, (PROTEIN C5) (RNASE P)]
[SP:P25814] [DB:swissprot] >pir:[LN:S66029] [AC:S66029:D69693]
[PN:ribonuclease P protein component rnpA] [GN:rnpA] [CL:ribonuclease P,
protein component] [OR:Bacillus subtilis] [DB:pir2]
>gp:[GI:d1005777:g467389] [LN:BAC180K] [AC:D26185] [PN:protein component of
ribonuclease P] [GN:rnpA] [OR:Bacillus subtilis] [SR:Bacillus subtilis
(sub_species:Marburg, strain:168) DNA] [DB:genpept-bct1] [DE:B. subtilis
DNA, 180 kilobase region of replication origin.] [LE:62749] [RE:63099]
[DI:complement] >gp:[GI:e1184831:g2636652] [LN:BSUB0021]
[AC:Z99124:AL009126] [PN:ribonuclease P (protein component)] [GN:rnpA]
[OR:Bacillus subtilis] [DB:genpept-bct1] [EC:3.1.26.5] [DE:Bacillus subtilis
complete genome (section 21 of 21): from 3999281to 4214814.] [SP:P25814]
[LE:214681] [RE:215031] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_26604502_f2_390	3101	6873	159	52	205	1.4e-16

Description

sp:[LN:RL34_BACST] [AC:P23376] [GN:RPMH] [OR:BACILLUS STEAROTHERMOPHILUS]
[DE:50S RIBOSOMAL PROTEIN L34] [SP:P23376] [DB:swissprot] >pir:[LN:C48396]
[AC:C48396] [PN:ribosomal protein L34] [CL:Escherichia coli ribosomal
protein L34] [OR:Bacillus stearothermophilus] [DB:pir2]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_26615636_f1_194	3102	6874	144	47		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000999_26756660_c2_950	3103	6875	651	216	109	0.00035

Description

pir:[LN:B69858] [AC:B69858] [PN:hypothetical protein yknW] [GN:yknW]
 [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1185024:g2633805] [LN:BSUB0008]
 [AC:Z99111:AL009126] [GN:yknW] [FN:unknown] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 8 of 21):
 from 1394791to 1603020.] [LE:108197] [RE:108892] [DI:direct]
 >gp:[GI:g3282118] [LN:AF012285] [AC:AF012285:AF012284:U51911] [PN:YknW]
 [GN:yknW] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis
 mobA-nprE gene region.] [LE:8685] [RE:9380] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000999_26759707_c1_830	3104	6876	450	149	504	2.9e-48

Description

gp:[GI:d1046006:g5360830] [LN:D86934] [AC:D86934] [OR:Staphylococcus aureus]
 [SR:Staphylococcus aureus (strain:N315) DNA, clone_lib:library of N31]
 [DB:genpept] [DE:Staphylococcus aureus genes, mec region, partial and
 complete cds.] [NT:ORF N044] [LE:28947] [RE:29264] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000999_270890_c3_1162	3105	6877	186	61		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000999_2745462_c1_691	3106	6878	642	213	116	0.00066

Description

gp:[GI:e1407824:g4493894] [LN:PFMAL3P2] [AC:AL034558] [GN:MAL3P2.16]
 [OR:Plasmodium falciparum] [SR:malaria parasite P. falciparum]
 [DB:genpept-inv1] [DE:Plasmodium falciparum MAL3P2, complete sequence.]
 [NT:predicted using hexExon; MAL3P2.16 (PF0235w),] [LE:73132:73647]
 [RE:73149:77270] [DI:directJoin]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000999_2782563_c3_1129	3107	6879	153	50		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_2819632_f1_105	3108	6880	387	128		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_2867812_c2_1060	3109	6881	213	70		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_2921941_c1_680	3110	6882	159	52		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_2925292_f2_325	3111	6883	123	40		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_2931557_c3_1158	3112	6884	1119	372	1692	3.7e-174

Description

sp:[LN:RECF_STAAU] [AC:P29232] [GN:RECF] [OR:STAPHYLOCOCCUS AUREUS] [DE:RECF PROTEIN] [SP:P29232] [DB:swissprot] >pir:[LN:C40585]
[AC:S54710:C40585:C42295:S36023] [PN:recF protein] [CL:recF protein]
[OR:Staphylococcus aureus] [DB:pir2]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_29320127_c3_1181	3113	6885	390	129	677	1.4e-66

Description

gp:[GI:d1046033:g5360857] [LN:D86934] [AC:D86934] [OR:Staphylococcus aureus]
[SR:Staphylococcus aureus (strain:N315) DNA, clone_lib:library of N31]
[DB:genpept] [DE:Staphylococcus aureus genes, mec region, partial and
complete cds.] [NT:ORF CN041] [LE:47629] [RE:>48018] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_2946092_c2_1006	3114	6886	435	144	97	0.00051

Description

pir:[LN:F71224] [AC:F71224] [PN:hypothetical protein PH0057] [GN:PH0057]
[CL:protein kinase C inhibitor:histidine triad homology] [OR:Pyrococcus
horikoshii] [DB:pir2] >gp:[GI:d1030068:g3256442] [LN:AP000001]
[AC:AP000001:AB009465:AB009464:AB009466:AB009467:AB009468:AB009469]
[PN:168aa long hypothetical protein] [GN:PH0057] [OR:Pyrococcus horikoshii]
[SR:Pyrococcus horikoshii (strain:OT3) DNA] [DB:genpept-bct1] [DE:Pyrococcus
horikoshii OT3 genomic DNA, 1-287000 nt. position (1/7).] [NT:similar to
owl:HPAE00058613 percent identity:] [LE:49752] [RE:50258] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_29532926_c3_1128	3115	6887	156	51		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_29860902_c3_1115	3116	6888	2277	758	1816	2.7e-187

Description

pir:[LN:C69657] [AC:C69657] [PN:cobalamin-independent methionine synthase
metC] [GN:metC] [CL:cobalamin-independent methionine synthase] [OR:Bacillus
subtilis] [DB:pir2] >gp:[GI:e1181518:g2632038] [LN:BSAJ2571] [AC:AJ002571]
[PN:MetC] [GN:metC] [FN:involved in methionine metabolism] [OR:Bacillus
subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis 168 56 kb DNA fragment
between xlyA and ykoR.] [SP:P80877] [LE:35445] [RE:37733] [DI:complement]
>gp:[GI:e1183338:g2633672] [LN:BSUB0007] [AC:Z99110:AL009126]
[PN:cobalamin-independent methionine synthase] [GN:metC] [FN:methionine
biosynthesis] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
complete genome (section 7 of 21): from 1194391to 1411140.] [SP:P80877]
[LE:188394] [RE:190682] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_3007887_f1_113	3117	6889	129	42		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000999_30080255_f1_172	3118	6890	384	127		
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Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000999_30084637_f3_567	3119	6891	156	51		
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Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000999_30086682_c2_1041	3120	6892	732	243	1134	5.1e-115
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Description

pir:[LN:C29504] [AC:C29504] [PN:hypothetical 24K protein (mer operon)]
 [OR:Staphylococcus aureus] [DB:pir2] >gp:[GI:g459905] [LN:L29436]
 [AC:L29436:M15048:N00048] [OR:Plasmid pI258] [SR:Plasmid pI258 DNA]
 [DB:genpept-bct1] [DE:Plasmid pI258 (from S.aureus strain RN23 8325) mercury
 resistance(mer) operon encoding mercuric reductase (merA),
 organomercuriallyase (merB), regulatory protein (merR) and membrane
 transportprotein (merT), complete cds.] [NT:ORF4] [LE:1936] [RE:2616]
 [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000999_30111718_c2_1051	3121	6893	2124	707	1980	7.5e-211
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Description

sp:[LN:COPB_ENTHR] [AC:P05425] [GN:COPB] [OR:ENTEROCOCCUS HIRAE]
 [EC:3.6.1.36] [DE:COPPER/POTASSIUM-TRANSPORTING ATPASE B,] [SP:P05425]
 [DB:swissprot] >pir:[LN:B45995] [AC:B45995] [PN:copper-transporting ATPase,
 copB] [GN:copB] [CL:Enterococcus copper-transporting ATPase copB: ATPase
 nucleotide-binding domain homology:ATPase transduction domain homology]
 [OR:Enterococcus hirae] [EC:3.6.1.-] [DB:pir1] >gp:[GI:g290643]
 [LN:ENECOPPUMP] [AC:L13292:J02729] [PN:ATPase] [GN:copB] [FN:copper pump]
 [OR:Enterococcus hirae] [SR:Enterococcus hirae DNA] [DB:genpept-bct1]
 [DE:Enterococcus hirae ATPase (copA) gene, complete cds; ATPase (copB)gene,
 complete cds.] [NT:putative] [LE:2273] [RE:4510] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_30516552_f1_160	3122	6894	144	47		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_31267125_c3_1216	3123	6895	132	43		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_31443827_f2_419	3124	6896	510	169	563	1.6e-54

Description

sp:[LN:SSB_BACSU] [AC:P37455] [GN:SSB] [OR:BACILLUS SUBTILIS]
 [DE:SINGLE-STRAND BINDING PROTEIN (SSB) (HELIX-DESTABILIZING PROTEIN)]
 [SP:P37455] [DB:swissprot] >pir:[LN:S66014] [AC:S66014:F69718] [PN:single
 strand DNA binding protein ssb] [GN:ssb] [CL:single-stranded DNA-binding
 protein: single-stranded DNA-binding protein homology] [OR:Bacillus
 subtilis] [DB:pir2] >gp:[GI:d1005762:g467374] [LN:BAC180K] [AC:D26185]
 [PN:single strand DNA binding protein] [GN:ssb] [OR:Bacillus subtilis]
 [SR:Bacillus subtilis (sub_species:Marburg, strain:168) DNA]
 [DB:genpept-bct1] [DE:B. subtilis DNA, 180 kilobase region of replication
 origin.] [LE:46882] [RE:47400] [DI:complement] >gp:[GI:e1184816:g2636637]
 [LN:BSUB0021] [AC:Z99124:AL009126] [PN:single-strand DNA-binding protein]
 [GN:ssb] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
 complete genome (section 21 of 21): from 3999281to 4214814.] [SP:P37455]
 [LE:198814] [RE:199332] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_31535626_f3_569	3125	6897	153	50		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_3158177_f2_232	3126	6898	123	40		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000999_32062762_c2_954	3127	6899	183	60		
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Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000999_32226577_c3_1254	3128	6900	354	117	596	5.2e-58
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Description

pir:[LN:B29504] [AC:B29504] [PN:hypothetical 18K protein (mer operon)]
 [OR:Staphylococcus aureus] [DB:pir2] >gp:[GI:g459904] [LN:L29436]
 [AC:L29436:M15048:N00048] [OR:Plasmid pI258] [SR:Plasmid pI258 DNA]
 [DB:genpept-bct1] [DE:Plasmid pI258 (from S.aureus strain RN23 8325) mercury
 resistance(mer) operon encoding mercuric reductase (merA),
 organomercuriallyase (merB), regulatory protein (merR) and membrane
 transportprotein (merT), complete cds.] [NT:ORF3] [LE:1454] [RE:1939]
 [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000999_32423410_c1_718	3129	6901	210	69	167	1.5e-12
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Description

sp:[LN:YG27 ARCFU] [AC:O28646] [GN:AF1627] [OR:ARCHAEOGLOBUS FULGIDUS]
 [DE:HYPOTHETICAL TRANSCRIPTIONAL REGULATOR AF1627] [SP:O28646]
 [DB:swissprot] >pir:[LN:B69453] [AC:B69453] [PN:repressor protein homolog]
 [OR:Archaeoglobus fulgidus] [DB:pir2] >gp:[GI:g2648932] [LN:AE000990]
 [AC:AE000990:AE000782] [PN:repressor protein] [GN:AF1627] [OR:Archaeoglobus
 fulgidus] [DB:genpept-bct2] [DE:Archaeoglobus fulgidus section 117 of 172 of
 the complete genome.] [NT:similar to GB:L77117 PID:1590997 percent
 identity:] [LE:7667] [RE:7882] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000999_32577_f3_495	3130	6902	138	45		
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Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000999_3320317_f3_648	3131	6903	237	78	150	9.5e-11

Description

gp:[GI:g2109447] [LN:SPDNAARG] [AC:AF000658] [FN:unknown] [OR:Streptococcus pneumoniae] [DB:genpept-bct2] [DE:Streptococcus pneumoniae R801 tRNA-Arg gene, partial sequence, and putative serine protease (sphtra), SPspoJ (spspoJ), initiator protein (spdnaa) and beta subunit of DNA polymerase III (spdnan) genes, complete cds.] [NT:ORFX] [LE:5708] [RE:5902] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000999_33228180_f1_192	3132	6904	243	80		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000999_33244187_c3_1168	3133	6905	1989	662	1592	1.5e-163

Description

sp:[LN:YYBT_BACSU] [AC:P37484] [GN:YYBT] [OR:BACILLUS SUBTILIS] [DE:HYPOTHETICAL 74.3 KD PROTEIN IN RPLI-COTF INTERGENIC REGION] [SP:P37484] [DB:swissprot] >pir:[LN:S65976] [AC:S65976:G70088] [PN:hypothetical protein yybT] [GN:yybT] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:d1005724:g467336] [LN:BAC180K] [AC:D26185] [PN:unknown] [OR:Bacillus subtilis] [SR:Bacillus subtilis (sub_species:Marburg, strain:168) DNA] [DB:genpept-bct1] [DE:B. subtilis DNA, 180 kilobase region of replication origin.] [LE:11639] [RE:13618] [DI:complement] >gp:[GI:e1184777:g2636598] [LN:BSUB0021] [AC:Z99124:AL009126] [GN:yybT] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 21 of 21): from 3999281 to 4214814.] [SP:P37484] [LE:163571] [RE:165550] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000999_33261588_c2_1004	3134	6906	690	229		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_33261637_c3_1237	3135	6907	543	180	79	0.0068

Description

gp:[GI:g765070] [LN:STAATL] [AC:L41499] [OR:Staphylococcus aureus]
[SR:Staphylococcus aureus (strain 8325/4) DNA] [DB:genpept-bct1]
[DE:Staphylococcus aureus ORF1, partial cds, ORF2, ORF3, autolysin(atl)
genes, complete cds.] [NT:ORF1] [LE:<1] [RE:249] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_33337760_c2_983	3136	6908	705	234	1191	4.6e-121

Description

gp:[GI:g5114230] [LN:AF136709] [AC:AF136709] [PN:response regulator YycF]
[GN:yycF] [OR:Staphylococcus aureus] [DB:genpept] [DE:Staphylococcus aureus
response regulator YycF (yycF) and histidinekinase YycG (yycG) genes,
complete cds.] [LE:649] [RE:1350] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_33720053_c1_808	3137	6909	126	41		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_33790702_f3_612	3138	6910	150	49		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_33867212_f3_548	3139	6911	339	112		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000999_33994126_f3_633	3140	6912	144	47	47	0.045

Description

gp:[GI:g1204027] [LN:UREUREASEA] [AC:L40489] [OR:Ureaplasma urealyticum] [SR:Ureaplasma urealyticum (strain 7) DNA] [DB:genpept-bct1] [DE:Ureaplasma urealyticum strain 7 urease operon encoding ORF1, ureA, ureB, ureC, ureE, ureF, and ureG, complete cds, and ureD genes, 5'end of cds.] [NT:ORF1; Protein sequence is in conflict with the] [LE:136] [RE:468] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000999_34016880_f2_333	3141	6913	2028	675	3474	0.0

Description

pir:[LN:JQ0774] [AC:JQ0774] [PN:penicillin-binding protein mecA, low-affinity:penicillin-binding protein 2'] [GN:mecA] [OR:Staphylococcus epidermidis] [DB:pir2] >gp:[GI:g46994] [LN:SEMECAPB] [AC:X52592] [OR:Staphylococcus epidermidis] [DB:genpept-bct1] [DE:S. epidermidis mecA gene for PBP2' (penicillin binding protein 2').] [NT:PBP2' (AA 1 - 668)] [LE:141] [RE:2147] [DI:direct] >gp:[GI:d1046026:g5360850] [LN:D86934] [AC:D86934] [PN:penicillin binding protein 2] [GN:mecA] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus (strain:N315) DNA, clone_lib:library of N31] [DB:genpept] [DE:Staphylococcus aureus genes, mec region, partial and complete cds.] [NT:ORF N058] [LE:43471] [RE:45477] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000999_3401887_f1_225	3142	6914	1485	494	1969	1.7e-203

Description

pir:[LN:DEBSMP] [AC:S66039:S12623:D69638] [PN:IMP dehydrogenase,:inositol-monophosphate dehydrogenase guaB] [GN:guaB] [CL:IMP dehydrogenase:CBS homology] [OR:Bacillus subtilis] [EC:1.1.1.205] [DB:pir1] >gp:[GI:d1005787:g467399] [LN:BAC180K] [AC:D26185] [PN:IMP dehydrogenase] [GN:guaB] [OR:Bacillus subtilis] [SR:Bacillus subtilis (sub_species:Marburg, strain:168) DNA] [DB:genpept-bct1] [DE:B. subtilis DNA, 180 kilobase region of replication origin.] [LE:79515] [RE:80981] [DI:direct] >gp:[GI:e1181942:g2632276] [LN:BSUB0001] [AC:Z99104:AL009126] [PN:inositol-monophosphate dehydrogenase] [GN:guaB] [FN:GMP biosynthesis] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:1.1.1.205] [DE:Bacillus subtilis complete genome (section 1 of 21): from 1 to213080.] [NT:alternate gene name: guaA] [SP:P21879] [LE:15913] [RE:17379] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_34023251_f2_389	3143	6915	198	65	68	0.045

Description

gp:[GI:g205733] [LN:RATNKBNT4] [AC:M21187:J03185:M18622] [OR:Rattus norvegicus] [SR:Rat testis DNA, clone rNT19] [DB:genpept-rod] [DE:Rat neurotensin/neuromedin N gene, exon 4.] [NT:preproneurotensin/neuromedin N] [LE:M21218.1:8:11] [RE:232:163] [DI:directJoin]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_34160260_f2_322	3144	6916	138	45		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_34178401_f3_462	3145	6917	150	49		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_34179761_c2_903	3146	6918	147	48		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_34180340_f2_398	3147	6919	711	236	609	2.2e-59

Description

gp:[GI:d1025734:g2879914] [LN:D85752] [AC:D85752] [GN:bacH] [OR:Enterococcus faecalis] [SR:Enterococcus faecalis plasmid:pPD1 DNA] [DB:genpept-bct1] [DE:Enterococcus faecalis plasmid pPD1 bacA, bacB, bacC, bacD, bacE,bacF, bacG, bacH and bacI genes, complete cds.] [LE:7148] [RE:7735] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000999_34182952_f3_625	3148	6920	402	133	88	0.013

Description

pir:[LN:G69850] [AC:G69850] [PN:hypothetical protein yjha] [GN:yjha]
[OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1183238:g2633572] [LN:BSUB0007]
[AC:Z99110:AL009126] [GN:yjha] [FN:unknown] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 7 of 21):
from 1194391to 1411140.] [LE:94377] [RE:95018] [DI:direct] >gp:[GI:g2612890]
[LN:AF015825] [AC:AF015825] [PN:putative lipoprotein] [GN:yjha] [OR:Bacillus
subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis 168 cotT-rapA region
sequence.] [LE:8537] [RE:9178] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000999_34266582_c2_965	3149	6921	1158	385	1796	3.6e-185

Description

sp:[LN:DP3B_STAAU] [AC:P50029] [GN:DNAN] [OR:STAPHYLOCOCCUS AUREUS]
[EC:2.7.7.7] [DE:DNA POLYMERASE III, BETA CHAIN,] [SP:P50029] [DB:swissprot]
>pir:[LN:S54708] [AC:S54708] [PN:DNA-directed DNA polymerase, III beta
chain:dnaN] [GN:dnaN] [CL:DNA-directed DNA polymerase III beta chain]
[OR:Staphylococcus aureus] [EC:2.7.7.7] [DB:pir1]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000999_34414012_f1_211	3150	6922	273	90	336	1.8e-30

Description

pir:[LN:S66013] [AC:S66013:S11368:A69701] [PN:ribosomal protein S18
(rpsR):ribosomal protein BS21] [GN:rpsR] [CL:Escherichia coli ribosomal
protein S18] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:d1005761:g467373]
[LN:BAC180K] [AC:D26185] [PN:ribosomal protein S18] [GN:rpsR] [OR:Bacillus
subtilis] [SR:Bacillus subtilis (sub_species:Marburg, strain:168) DNA]
[DB:genpept-bct1] [DE:B. subtilis DNA, 180 kilobase region of replication
origin.] [LE:46599] [RE:46844] [DI:complement] >gp:[GI:e1184815:g2636636]
[LN:BSUB0021] [AC:Z99124:AL009126] [PN:ribosomal protein S18] [GN:rpsR]
[OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete
genome (section 21 of 21): from 3999281to 4214814.] [SP:P21475] [LE:198531]
[RE:198776] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_34414187_c1_692	3151	6923	399	132	152	5.8e-11

Description

pir:[LN:B69778] [AC:B69778] [PN:hypothetical protein ydeH] [GN:ydeH]
[OR:Bacillus subtilis] [DB:pir2] >gp:[GI:d1020108:g1881328] [LN:AB001488]
[AC:AB001488] [GN:ydeH] [OR:Bacillus subtilis] [SR:Bacillus subtilis
(strain:168) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis genome sequence,
148 kb sequence of the regionbetween 35 and 47 degree.] [NT:FUNCTION
UNKNOWN.] [LE:100881] [RE:101327] [DI:direct] >gp:[GI:e1182486:g2632820]
[LN:BSUB0003] [AC:Z99106:AL009126] [GN:ydeH] [FN:unknown] [OR:Bacillus
subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 3
of 21): from 402751 to611850.] [LE:164626] [RE:165072] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_34417552_f3_615	3152	6924	381	126		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_34417813_c2_985	3153	6925	807	268	851	4.9e-85

Description

pir:[LN:A70090] [AC:A70090] [PN:hypothetical protein yycJ] [GN:yycJ]
[OR:Bacillus subtilis] [DB:pir2] >gp:[GI:d1011958:g1064810] [LN:BACGNTZA]
[AC:D78193] [GN:yycJ] [OR:Bacillus subtilis] [SR:Bacillus subtilis
(strain:168) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis 36kb sequence
between gntZ and trnY genesencoding 34 ORFs.] [LE:30382] [RE:31188]
[DI:complement] >gp:[GI:e1184763:g2636584] [LN:BSUB0021]
[AC:Z99124:AL009126] [GN:yycJ] [FN:unknown] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 21 of 21):
from 3999281to 4214814.] [LE:148766] [RE:149572] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_34580342_c1_730	3154	6926	771	256	802	7.7e-80

Description

pir:[LN:A70001] [AC:A70001] [PN:ABC transporter (ATP-binding protein) homolog ytsC] [GN:ytsC] [CL:ATP-binding cassette homology] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1185911:g2635522] [LN:BSUB0016] [AC:Z99119:AL009126] [GN:ytsC] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.] [NT:similar to ABC transporter (ATP-binding protein)] [LE:112638] [RE:113399] [DI:complement] >gp:[GI:g2293177] [LN:AF008220] [AC:AF008220] [PN:transporter] [GN:ytsC] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis rrnB-dnaB genomic region.] [LE:67028] [RE:67789] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_34631527_f1_20	3155	6927	834	277	609	2.2e-59

Description

gp:[GI:d1045999:g5360823] [LN:D86934] [AC:D86934] [PN:IS150-like transposase] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus (strain:N315) DNA, clone_lib:library of N31] [DB:genpept] [DE:Staphylococcus aureus genes, mec region, partial and complete cds.] [NT:ORF N028; putative] [LE:<20180] [RE:20578] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_34643751_c1_688	3156	6928	591	196	910	2.8e-91

Description

gp:[GI:g1916316] [LN:SAU92441] [AC:U92441:X85029] [PN:alkyl hydroperoxide reductase subunit C] [GN:ahpC] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:Staphylococcus aureus alkyl hydroperoxide reductase subunit C(aphC) and subunit F (aphF) genes, complete cds.] [NT:AhpC] [LE:791] [RE:1360] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000999_34664700_f2_393	3157	6929	861	286	617	3.1e-60

Description

sp:[LN:YYAA_BACSU] [AC:P37524] [GN:YYAA] [OR:BACILLUS SUBTILIS]
[DE:HYPOTHETICAL 32.8 KD PROTEIN IN SPO0J-GIDB INTERGENIC REGION]
[SP:P37524] [DB:swissprot] >pir:[LN:I40442] [AC:I40442:S66023:H70083:S18078]
] [PN:DNA-binding protein Spo0J-like homolog yyaA:probable DNA binding
protein (replication origin region)] [GN:yyaA] [CL:Bacillus subtilis
transport protein spo0J] [OR:Bacillus subtilis] [DB:pir2]
>gp:[GI:d1005771:g467383] [LN:BAC180K] [AC:D26185] [PN:DNA binding protein
(probable)] [OR:Bacillus subtilis] [SR:Bacillus subtilis
(sub_species:Marburg, strain:168) DNA] [DB:genpept-bct1] [DE:B. subtilis
DNA, 180 kilobase region of replication origin.] [LE:55893] [RE:56744]
[DI:complement] >gp:[GI:g40028] [LN:BSORIGS] [AC:X62539] [OR:Bacillus
subtilis] [DB:genpept-bct1] [DE:B.subtilis genes rpmH, rnpA, 50kd, gidA and
gidB.] [NT:unnamed protein product] [SP:P37524] [LE:6656] [RE:7507]
[DI:direct] >gp:[GI:e1184825:g2636646] [LN:BSUB0021] [AC:Z99124:AL009126]
[GN:yyaA] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus
subtilis complete genome (section 21 of 21): from 3999281to 4214814.]
[NT:similar to DNA-binding protein Spo0J-like] [SP:P37524] [LE:207825]
[RE:208676] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000999_35157813_f2_244	3158	6930	519	172	473	5.6e-45

Description

sp:[LN:ATDA_ECOLI] [AC:P37354] [GN:SPEG] [OR:ESCHERICHIA COLI] [EC:2.3.1.57]
[DE:ACETYLTRANSFERASE) (SAT)] [SP:P37354] [DB:swissprot]
>gp:[GI:d1016007:g1742583] [LN:D90799] [AC:D90799:AB001340] [PN:Spermidine
N1-acetyltransferase (EC 2.3.1.57)] [GN:speG] [OR:Escherichia coli]
[SR:Escherichia coli (strain:K12) DNA, clone_lib:Kohara lambda minise]
[DB:genpept-bct1] [DE:E.coli genomic DNA, Kohara clone #308(35.3-35.7
min.)] [NT:ORF_ID:o309#16; similar to [SwissProt Accession] [LE:<18154]
[RE:18711] [DI:direct] >gp:[GI:d1016029:g1742606] [LN:D90800]
[AC:D90800:AB001340] [PN:Spermidine N1-acetyltransferase (EC 2.3.1.57)]
[GN:speG] [OR:Escherichia coli] [SR:Escherichia coli (strain:K12) DNA,
clone_lib:Kohara lambda minise] [DB:genpept-bct1] [DE:E.coli genomic DNA,
Kohara clone #309(35.4-35.7 min.)] [NT:ORF_ID:o309#16; similar to
[SwissProt Accession] [LE:<14930] [RE:15487] [DI:direct]
>gp:[GI:d1016031:g1742609] [LN:D90801] [AC:D90801:AB001340] [PN:Spermidine
N1-acetyltransferase (EC 2.3.1.57)] [GN:speG] [OR:Escherichia coli]
[SR:Escherichia coli (strain:K12) DNA, clone_lib:Kohara lambda minise]
[DB:genpept-bct1] [DE:E.coli genomic DNA, Kohara clone #310(35.7-36.0
min.)] [NT:ORF_ID:o309#16; similar to [SwissProt Accession] [LE:<814]
[RE:1371] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_35324092_c1_772	3159	6931	987	328	219	9.3e-28

Description

sp:[LN:MET2_YEAST] [AC:P08465] [GN:MET2:YNL277W:N0615] [OR:SACCHAROMYCES CEREVISIAE] [SR:,BAKER'S YEAST] [EC:2.3.1.31] [DE:ACETYLASE)] [SP:P08465] [DB:swissprot] >pir:[LN:S63251] [AC:S63251:A27163] [PN:homoserine O-acetyltransferase,:protein N0615:protein YNL277w] [GN:MET2] [CL:homoserine acetyltransferase] [OR:Saccharomyces cerevisiae] [EC:2.3.1.31] [DB:pir2] [MP:14L] >gp:[GI:e239735:g1302344] [LN:SCYNL277W] [AC:Z71553:Y13139] [GN:MET2] [OR:Saccharomyces cerevisiae] [SR:baker's yeast] [DB:genpept-plnl] [DE:S.cerevisiae chromosome XIV reading frame ORF YNL277w.] [NT:ORF YNL277w] [SP:P08465] [LE:896] [RE:2356] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_35334686_f2_331	3160	6932	1659	552	1253	1.2e-127

Description

gp:[GI:g1022726] [LN:SHU35635] [AC:U35635] [PN:unknown] [OR:Staphylococcus haemolyticus] [SR:Staphylococcus haemolyticus strain=Y176] [DB:genpept-bct1] [DE:Staphylococcus haemolyticus IS1272 ORF1 and ORF2 genes, completecds.] [NT:ORF1] [LE:1101] [RE:1922] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_35343807_f1_220	3161	6933	237	78		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_35369052_c1_774	3162	6934	1404	467	1261	1.8e-128

Description

gp:[GI:g4416322] [LN:AF106032] [AC:AF106032] [PN:replicative helicase] [GN:dnaB] [OR:Bacillus stearothermophilus] [DB:genpept-bct2] [DE:Bacillus stearothermophilus replicative helicase (dnaB) gene,complete cds.] [NT:5'-3' helicase; similar to Bacillus subtilis DnaC;] [LE:1] [RE:1365] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_35554635_c2_1001	3163	6935	132	43		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000999_35944052_c1_682	3164	6936	690	229		
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Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000999_35978127_f3_661	3165	6937	777	258	559	4.3e-54
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Description

sp:[LN:YWC_G_BACSU] [AC:P39605] [GN:YWC_G_IPA-43D] [OR:BACILLUS SUBTILIS]
[DE:HYPOTHETICAL 28.3 KD PROTEIN IN QOXD-VPR INTERGENIC REGION] [SP:P39605]
[DB:swissprot] >pir:[LN:S39698] [AC:S39698:B70053] [PN:NADPH-flavin
oxidoreductase homolog ywcG:protein ipa-43d] [GN:ywcG] [CL:NADPH-flavin
oxidoreductase homolog] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:g413967]
[LN:BSGENR] [AC:X73124] [GN:ipa-43d] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:B.subtilis genomic region (325 to 333).] [SP:P39605]
[LE:45340] [RE:46089] [DI:direct] >gp:[GI:e1186310:g2636346] [LN:BSUB0020]
[AC:Z99123:AL009126] [GN:ywcG] [FN:unknown] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 20 of 21):
from 3798401to 4010550.] [NT:alternate gene name: ipa-43d; similar to]
[SP:P39605] [LE:111873] [RE:112622] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000999_35984430_f2_444	3166	6938	126	41		
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Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000999_35991677_c2_973	3167	6939	177	58		
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Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000999_36135952_f2_327	3168	6940	1650	549	2777	4.0e-289
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Description

gp:[GI:d1046002:g5360826] [LN:D86934] [AC:D86934] [PN:site-specific
recombinase] [GN:ccrB] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus
(strain:N315) DNA, clone_lib:library of N31] [DB:genpept] [DE:Staphylococcus
aureus genes, mec region, partial and complete cds.] [NT:ORF N037; cassette
chromosome recombinase B] [LE:25508] [RE:27136] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000999_36147301_f3_670	3169	6941	237	78	78	0.0090

Description

sp:[LN:COTE_BACSU] [AC:P14016] [GN:COTE] [OR:BACILLUS SUBTILIS] [DE:SPORE COAT PROTEIN E] [SP:P14016] [DB:swissprot] >pir:[LN:A31245] [AC:A31245:B69605] [PN:outer spore coat protein cote] [GN:cote] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:g1200225] [LN:BSCOTE] [AC:X13009] [PN:coat protein] [GN:cote] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis cote gene for 21kD coat protein.] [SP:P14016] [LE:390] [RE:935] [DI:direct] >gp:[GI:e1185294:g2634075] [LN:BSUB0009] [AC:Z99112:AL009126] [PN:morphogenic protein] [GN:cote] [FN:outer coat assembly] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.] [SP:P14016] [LE:176015] [RE:176560] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000999_36211052_c1_855	3170	6942	1662	553	2755	8.5e-287

Description

sp:[LN:NERA STAAU] [AC:P08663] [GN:NERA] [OR:STAPHYLOCOCCUS AUREUS] [EC:1.16.1.1] [DE:MERCURIC REDUCTASE, (HG(II) REDUCTASE)] [SP:P08663] [DB:swissprot] >pir:[LN:E29504] [AC:E29504] [PN:mercury(II) reductase, :Hg(II) reductase:mercuric reductase] [GN:merA] [CL:Bacillus mercury(II) reductase:dihydrolipoamide dehydrogenase homology:heavy-metal-associated homology] [OR:Staphylococcus aureus] [EC:1.16.1.1] [DB:pir2] >gp:[GI:g459907] [LN:L29436] [AC:L29436:M15048:N00048] [PN:mercuric reductase] [GN:merA] [OR:Plasmid pI258] [SR:Plasmid pI258 DNA] [DB:genpept-bct1] [DE:Plasmid pI258 (from S.aureus strain RN23 8325) mercury resistance(mer) operon encoding mercuric reductase (merA), organomercuriallyase (merB), regulatory protein (merR) and membrane transportprotein (merT), complete cds.] [LE:3148] [RE:4791] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000999_36225427_f2_319	3171	6943	615	204		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000999_36226501_c2_1018	3172	6944	891	296		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_36228126_f2_392	3173	6945	1896	631	2407	6.4e-250

Description

sp:[LN:GIDA_BACSU] [AC:P25812] [GN:GIDA] [OR:BACILLUS SUBTILIS] [DE:GLUCOSE INHIBITED DIVISION PROTEIN A] [SP:P25812] [DB:swissprot] >pir:[LN:BWBSGA] [AC:I40440:S66025:G69631:JQ1216:S18076] [PN:glucose-inhibited division protein gidA] [GN:gidA] [CL:gidA protein] [OR:Bacillus subtilis] [DB:pir1] >gp:[GI:d1005773:g467385] [LN:BAC180K] [AC:D26185] [PN:unknown] [GN:gidA] [OR:Bacillus subtilis] [SR:Bacillus subtilis (sub_species:Marburg, strain:168) DNA] [DB:genpept-bct1] [DE:B. subtilis DNA, 180 kilobase region of replication origin.] [LE:57599] [RE:59485] [DI:complement] >gp:[GI:g40026] [LN:BSORIGS] [AC:X62539] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis genes rpmH, rnpA, 50kd, gidA and gidB.] [NT:homologous to E.coli gidA] [SP:P25812] [LE:3915] [RE:5801] [DI:direct] >gp:[GI:e1184827:g2636648] [LN:BSUB0021] [AC:Z99124:AL009126] [PN:glucose-inhibited division protein] [GN:gidA] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.] [SP:P25812] [LE:209531] [RE:211417] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_36359761_f3_604	3174	6946	840	279	581	2.0e-56

Description

sp:[LN:YFOL_STRTR] [AC:P96051] [OR:STREPTOCOCCUS THERMOPHILUS] [DE:(ORF1091)] [SP:P96051] [DB:swissprot] >gp:[GI:g1685111] [LN:STU58210] [AC:U58210] [OR:Streptococcus thermophilus] [SR:Streptococcus thermophilus strain=Sfi6] [DB:genpept-bct2] [DE:Streptococcus thermophilus tetrahydrofolatedehydrogenase/cyclohydrolase (fold), penicillin-binding protein 2b(pbp2b) and DNA repair and recombination protein (recM) genes,complete cds.] [NT:orf1091] [LE:1091] [RE:1927] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_36522507_f1_163	3175	6947	741	246	740	2.9e-73

Description

sp:[LN:GIDB_BACSU] [AC:P25813] [GN:GIDB] [OR:BACILLUS SUBTILIS] [DE:GLUCOSE INHIBITED DIVISION PROTEIN B] [SP:P25813] [DB:swissprot] >pir:[LN:BWBSGB] [AC:I40441:S66024:H69631:JQ1217:S18077] [PN:glucose-inhibited division protein gidB] [GN:gidB] [CL:gidB protein] [OR:Bacillus subtilis] [DB:pir1] >gp:[GI:d1005772:g467384] [LN:BAC180K] [AC:D26185] [PN:unknown] [GN:gidB] [OR:Bacillus subtilis] [SR:Bacillus subtilis (sub_species:Marburg, strain:168) DNA] [DB:genpept-bct1] [DE:B. subtilis DNA, 180 kilobase region of replication origin.] [LE:56866] [RE:57585] [DI:complement] >gp:[GI:g40027] [LN:BSORIGS] [AC:X62539] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis genes rpmH, rnpA, 50kd, gidA and gidB.] [NT:homologous to E.coli gidB] [SP:P25813] [LE:5815] [RE:6534] [DI:direct] >gp:[GI:e1184826:g2636647] [LN:BSUB0021] [AC:Z99124:AL009126] [PN:glucose-inhibited division protein] [GN:gidB] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.] [SP:P25813] [LE:208798] [RE:209517] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_36584652_c1_805	3176	6948	339	112	380	4.0e-35

Description

gp:[GI:d1045996:g5360820] [LN:D86934] [AC:D86934] [PN:transposase] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus (strain:N315) DNA, clone_lib:library of N31] [DB:genpept] [DE:Staphylococcus aureus genes, mec region, partial and complete cds.] [NT:ORF N026; putative] [LE:19527] [RE:19751] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_37892_f1_217	3177	6949	162	53		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_3906578_f1_8	3178	6950	123	40		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_3913137_f2_262	3179	6951	570	189	982	6.5e-99

Description

gp:[GI:g459909] [LN:L29436] [AC:L29436:M15048:N00048] [OR:Plasmid pI258] [SR:Plasmid pI258 DNA] [DB:genpept-bct1] [DE:Plasmid pI258 (from S.aureus strain RN23 8325) mercury resistance(mer) operon encoding mercuric reductase (merA), organomercuriallyase (merB), regulatory protein (merR) and membrane transportprotein (merT), complete cds.] [NT:ORF1] [LE:5718] [RE:6266] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_3937713_c3_1215	3180	6952	174	57		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_3938802_f2_326	3181	6953	1383	460	2306	3.2e-239

Description

gp:[GI:d1046000:g5360824] [LN:D86934] [AC:D86934] [PN:site-specific recombinase] [GN:ccrA] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus (strain:N315) DNA, clone_lib:library of N31] [DB:genpept] [DE:Staphylococcus aureus genes, mec region, partial and complete cds.] [NT:ORF N034; cassette chromosome recombinase A] [LE:24137] [RE:25486] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_3954450_c3_1101	3182	6954	129	42		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_4016887_f1_6	3183	6955	174	57	157	2.6e-10

Description

sp:[LN:CADA_LISMO] [AC:Q60048] [GN:CADA] [OR:LISTERIA MONOCYTOGENES] [EC:3.6.1.-] [DE:ATPASE] [SP:Q60048] [DB:swissprot] >gp:[GI:g495646] [LN:LISCADTNP] [AC:L28104] [PN:ATPase] [GN:cadA] [FN:cadmium resistance] [OR:Transposon Tn5422] [SR:Listeria monocytogenes (individual_isolate Lm74) DNA; Transposo] [DB:genpept-una] [DE:Listeria monocytogenes ATPase (cadA) gene; accessory protein (cadC)gene; resolvase (tnpR) gene and transposase (tnpA) gene.] [LE:158] [RE:2293] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000999_4022952_f1_64	3184	6956	1515	504	1186	3.9e-140

Description

pir:[LN:C70880] [AC:C70880] [PN:probable hsdM protein] [GN:hsdM]
[OR:Mycobacterium tuberculosis] [DB:pir2] >gp:[GI:e1173886:g2624278]
[LN:MTV002] [AC:AL008967:AL123456] [PN:hsdM] [GN:hsdM] [OR:Mycobacterium
tuberculosis] [DB:genpept-bct1] [DE:Mycobacterium tuberculosis H37Rv
complete genome; segment 122/162.] [NT:Rv2756c, (MTV002.21c), len: 540 aa.
hsdM, type I] [LE:19902] [RE:21524] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000999_4025302_f3_464	3185	6957	1293	430	1892	2.4e-195

Description

sp:[LN:ARSB_STAAU] [AC:P30329] [GN:ARSB] [OR:STAPHYLOCOCCUS AUREUS]
[DE:ARSENICAL PUMP MEMBRANE PROTEIN] [SP:P30329] [DB:swissprot]
>pir:[LN:C41903] [AC:C41903] [PN:arsenical pump membrane protein] [GN:arsB
] [CL:arsenical pump membrane protein] [OR:Staphylococcus aureus] [DB:pir1]
>gp:[GI:g150728] [LN:PI2ARSRBC] [AC:M86824] [PN:arsenic efflux pump protein]
[GN:arsB] [FN:arsenic efflux pump component (membrane) [OR:Plasmid pI258]
[SR:Plasmid pI258 DNA] [DB:genpept-bct1] [DE:Plasmid pI258 arsenic
resistance operon (arsRBC) genes, completecds.] [LE:587] [RE:1876]
[DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000999_4093937_c3_1172	3186	6958	192	63		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000999_4098518_c2_1040	3187	6959	417	138	682	4.0e-67

Description

sp:[LN:MERR_STAAU] [AC:P22874] [GN:MERR] [OR:STAPHYLOCOCCUS AUREUS]
[DE:MERCURIC RESISTANCE OPERON REGULATORY PROTEIN] [SP:P22874]
[DB:swissprot] >pir:[LN:A29504] [AC:A29504] [PN:hypothetical 16K protein
(mer operon)] [CL:transcription repressor glrR] [OR:Staphylococcus aureus]
[DB:pir2] >gp:[GI:g459903] [LN:L29436] [AC:L29436:M15048:N00048] [OR:Plasmid
pI258] [SR:Plasmid pI258 DNA] [DB:genpept-bct1] [DE:Plasmid pI258 (from
S.aureus strain RN23 8325) mercury resistance(mer) operon encoding mercuric
reductase (merA), organomercuriallyase (merB), regulatory protein (merR) and
membrane transportprotein (merT), complete cds.] [NT:ORF2] [LE:1030]
[RE:1437] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_4120462_f2_235	3188	6960	945	314	791	1.1e-78

Description

sp:[LN:ARCL_ECOLI] [AC:Q46807] [GN:YQEA] [OR:ESCHERICHIA COLI] [DE:CARBAMATE KINASE-LIKE PROTEIN 1] [SP:Q46807] [DB:swissprot] >pir:[LN:B65071] [AC:B65071] [PN:hypothetical protein b2874] [CL:carbamate kinase] [OR:Escherichia coli] [DB:pir2] >gp:[GI:g887824] [LN:ECU28375] [AC:U28375] [OR:Escherichia coli] [DB:genpept-bct1] [DE:Escherichia coli K-12 genome; approximately 64 to 65 minutes.] [NT:ORF_o310] [LE:21276] [RE:22208] [DI:direct] >gp:[GI:g1789238] [LN:AE000370] [AC:AE000370:U00096] [PN:putative kinase] [GN:yqeA] [FN:putative enzyme; Not classified] [OR:Escherichia coli] [DB:genpept-bct2] [DE:Escherichia coli K-12 MG1655 section 260 of 400 of the completegenome.] [NT:o310; This 310 aa ORF is 45 pct identical (21 gaps)] [LE:11360] [RE:12292] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_41265_c3_1170	3189	6961	1365	454	1593	1.2e-163

Description

pir:[LN:A42280] [AC:S65968:A42280:H69683] [PN:adenylosuccinate synthase, purA:IMP--aspartate ligase] [GN:purA] [CL:adenylosuccinate synthase] [OR:Bacillus subtilis] [EC:6.3.4.4] [DB:pir2] >gp:[GI:d1005716:g467328] [LN:BAC180K] [AC:D26185] [PN:adenylosuccinate synthetase] [GN:purA] [OR:Bacillus subtilis] [SR:Bacillus subtilis (sub_species:Marburg, strain:168) DNA] [DB:genpept-bct1] [DE:B. subtilis DNA, 180 kilobase region of replication origin.] [LE:3429] [RE:4721] [DI:complement] >gp:[GI:e1184768:g2636589] [LN:BSUB0021] [AC:Z99124:AL009126] [PN:adenylosuccinate synthetase] [GN:purA] [FN:AMP biosynthesis] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:6.3.4.4] [DE:Bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.] [SP:P29726] [LE:155361] [RE:156653] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_4179680_c2_977	3190	6962	936	311	214	1.7e-16

Description

sp:[LN:YYBS_BACSU] [AC:P37485] [GN:YYBS] [OR:BACILLUS SUBTILIS]
[DE:HYPOTHETICAL 34.5 KD PROTEIN IN RPLI-COTF INTERGENIC REGION] [SP:P37485]
[DB:swissprot] >pir:[LN:S65977] [AC:S65977:F70088] [PN:hypothetical protein
yybS] [GN:yybS] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:d1005725:g467337]
[LN:BAC180K] [AC:D26185] [PN:unknown] [OR:Bacillus subtilis] [SR:Bacillus
subtilis (sub_species:Marburg, strain:168) DNA] [DB:genpept-bct1] [DE:B.
subtilis DNA, 180 kilobase region of replication origin.] [LE:13655]
[RE:14584] [DI:complement] >gp:[GI:e1184778:g2636599] [LN:BSUB0021]
[AC:Z99124:AL009126] [GN:yybS] [FN:unknown] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 21 of 21):
from 3999281to 4214814.] [SP:P37485] [LE:165587] [RE:166516] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_4196051_f1_29	3191	6963	333	110	424	8.7e-40

Description

pir:[LN:A41902] [AC:A41902] [PN:arsenical resistance operon repressor]
[GN:arsR] [CL:arsenical resistance operon repressor] [OR:Staphylococcus
xylosus] [DB:pir1]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_42162_c3_1124	3192	6964	126	41		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000999_4305342_f2_445	3193	6965	1557	518	2015	2.2e-208

Description

sp:[LN:GUAA_BACSU] [AC:P29727:O34531] [GN:GUAA] [OR:BACILLUS SUBTILIS] [EC:6.3.5.2] [DE:AMIDOTRANSFERASE) (GMP SYNTHETASE)] [SP:P29727:O34531] [DB:swissprot] >pir:[LN:C69638] [AC:C69638:B42280] [PN:GMP synthase (glutamine-hydrolyzing), guaA] [GN:guaA] [CL:GMP synthase (glutamine-hydrolyzing):trpG homology] [OR:Bacillus subtilis] [EC:6.3.5.2] [DB:pir2] >gp:[GI:g2239288] [LN:BSU51115] [AC:U51115] [PN:GMP synthetase] [GN:guaA] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis CotA (cotA), GabP (gabP), YeaB (yeaB), YeaC(yeaC), YebA (yebA), GMP synthetase (guaA) genes, complete cds, andAIR carboxylase I (purE) gene, partial cds.] [LE:9970] [RE:11511] [DI:direct] >gp:[GI:e1182615:g2632949] [LN:BSUB0004] [AC:Z99107:AL009126] [PN:GMP synthetase] [GN:guaA] [FN:GMP biosynthesis] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:6.3.5.2] [DE:Bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.] [NT:alternate gene name: guaB] [SP:P29727] [LE:91559] [RE:93100] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000999_4335750_f1_166	3194	6966	600	199	158	2.0e-11

Description

pir:[LN:I40868] [AC:I40868] [PN:hypothetical protein 3] [OR:Clostridium perfringens] [DB:pir2] >gp:[GI:g853809] [LN:CPNANH] [AC:X87369] [OR:Clostridium perfringens] [DB:genpept-bct1] [DE:C.perfringens nanH gene & ORF1,2,3 & 4.] [NT:ORF3] [LE:4957] [RE:5754] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000999_4453165_c1_862	3195	6967	537	178	202	1.8e-15

Description

gp:[GI:d1006123:g473790] [LN:ECO82K] [AC:D26562] [PN:'ORF'] [OR:Escherichia coli] [SR:Escherichia coli (sub_strain W3110, strain K-12) (library: Kohara')] [DB:genpept-bct1] [DE:Escherichia coli genome, 2.4-4.1 min region (110,917-193,643 bpfrom 0 min).] [NT:'copper resistance protein copA homology'] [LE:25693] [RE:27117] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000999_446062_c3_1226	3196	6968	159	52	231	2.5e-19

Description

pir:[LN:A60634] [AC:A60634:C30471:S26349] [PN:probable transposase]
 [OR:Staphylococcus aureus] [DB:pir2] >gp:[GI:g46597] [LN:SAIS2571]
 [AC:X53952] [PN:transposase] [OR:Staphylococcus aureus] [DB:genpept-bct1]
 [DE:S.aureus plasmid pSH6 DNA for insertion sequences IS257-1 andIS256.]
 [LE:188] [RE:862] [DI:direct] >gp:[GI:g3676452] [LN:AF051917]
 [AC:AF051917:L19570] [PN:putative transposase TnpE] [GN:tnpE]
 [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus
 plasmid pSK41, complete sequence.] [LE:40946] [RE:41620] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000999_4475050_f2_341	3197	6969	162	53	68	0.045

Description

pir:[LN:F71007] [AC:F71007] [PN:hypothetical protein PH1356] [GN:PH1356]
 [OR:Pyrococcus horikoshii] [DB:pir2] >gp:[GI:d1031405:g3257779]
 [LN:AP000006]
 [AC:AP000006:AB005215:AB009510:AB009511:AB009512:AB009513:AB009514]
 [PN:111aa long hypothetical protein] [GN:PH1356] [OR:Pyrococcus horikoshii]
 [SR:Pyrococcus horikoshii (strain:OT3) DNA, clone:Pyrococcus horikoshi]
 [DB:genpept-bct1] [DE:Pyrococcus horikoshii OT3 genomic DNA, 1166001-1485000
 nt. position(6/7).] [LE:56557] [RE:56892] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000999_4485937_f1_10	3198	6970	1044	347	1060	3.5e-107

Description

sp:[LN:OTCC_HAEIN] [AC:P44770] [GN:ARCB:HI0596] [OR:HAEMOPHILUS INFLUENZAE]
 [EC:2.1.3.3] [DE:ORNITHINE CARBAMOYLTRANSFERASE, CATABOLIC, (OTCASE)]
 [SP:P44770] [DB:swissprot] >pir:[LN:H64079] [AC:H64079] [PN:ornithine
 carbamoyltransferase,] [CL:ornithine carbamoyltransferase:
 aspartate/ornithine carbamoyltransferase homology] [OR:Haemophilus
 influenzae] [EC:2.1.3.3] [DB:pir2] >gp:[GI:g1573585] [LN:U32741]
 [AC:U32741:L42023] [PN:ornithine carbamoyltransferase (arcB)] [GN:HI0596]
 [OR:Haemophilus influenzae Rd] [DB:genpept-bct2] [DE:Haemophilus influenzae
 Rd section 56 of 163 of the complete genome.] [NT:similar to GB:X05637
 SP:P08308 PID:45288 percent] [LE:3467] [RE:4471] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000999_448785_f3_518	3199	6971	927	308	408	4.3e-38

Description

sp:[LN:SOXR_ARTSP] [AC:Q44311] [GN:SOXR] [OR:ARTHROBACTER SP] [SR:TE1826,]
 [DE:TRANSCRIPTIONAL REGULATOR SOXR] [SP:Q44311] [DB:swissprot]
 >gp:[GI:d1026865:g3116220] [LN:AB007122] [AC:AB007122] [PN:negative
 regulator] [OR:Arthrobacter sp.] [SR:Arthrobacter sp. (strain:TE1826) DNA]
 [DB:genpept-bct1] [DE:Arthrobacter sp. gene for negative regulator,
 sarcosine oxidase, transporter, creatinase, creatininase and
 transporter, complete cds.] [LE:321] [RE:1190] [DI:complement]
 >gp:[GI:d1010363:g1333651] [LN:ARGTE1826] [AC:D63413] [PN:regulator]
 [GN:soxR] [OR:Arthrobacter sp.] [SR:Arthrobacter sp. (strain:TE1826) DNA]
 [DB:genpept-bct1] [DE:Arthrobacter sp. gene for sarcosine oxidase, complete
 cds.] [LE:1539] [RE:2408] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000999_4694677_c1_832	3200	6972	324	107		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000999_4697337_f3_519	3201	6973	549	182	255	7.1e-22

Description

pir:[LN:B69978] [AC:B69978] [PN:2-nitropropane dioxygenase homolog yrpB]
 [GN:yrpB] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:g1934639] [LN:BSU93875]
 [AC:U93875] [PN:2-nitropropane dioxygenase] [GN:yrpB] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:Bacillus subtilis alcohol dehydrogenase (adhB) gene,
 partial cds, hypothetical spore coat protein (yraF), hypothetical spore
 coatprotein (yraG), YraH (yraH), YraI (yraI), YraJ (yraJ), YraK (yraK), YraL
 (yraL), chitosanase precursor (csn), YraM (yraM), LysR-family transcription
 regulator (yraN), YraO (yraO), YrpG (yrpG), RNAPolymerase sigma factor SigZ
 (sigZ), YrpE (yrpE), YrpD (yrpD), YrpC (yrpC) and 2-nitropropane dioxygenase
 (yrpB) genes, complete cds, and aminoglycoside 6-adenylyltransferase (aadK)
 gene, partial cds.] [NT:similar to 2-nitropropane dioxigenase of Williopsis]
 [LE:16473] [RE:17516] [DI:complement] >gp:[GI:e1183909:g2635125]
 [LN:BSUB0014] [AC:Z99117:AL009126] [GN:yrpB] [FN:unknown] [OR:Bacillus
 subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section
 14 of 21): from 2599451 to 2812870.] [NT:similar to 2-nitropropane
 dioxygenase] [LE:136734] [RE:137777] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_4714062_c1_759	3202	6974	135	44		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_4722338_c3_1233	3203	6975	234	77	57	0.047

Description

gp:[GI:g1354131] [LN:EhU48386] [AC:U48386] [PN:pEhS4] [GN:EhS4]
[OR:Entamoeba histolytica] [DB:genpept-inv2] [DE:Entamoeba histolytica
putative serine/threonine protein kinase(EhS4) gene, complete cds.]
[NT:putative serine/threonine protein kinase] [LE:243:510] [RE:463:1791]
[DI:directJoin]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_4725385_f1_213	3204	6976	675	224	366	1.2e-33

Description

sp:[LN:YRHP_BACSU] [AC:O05406] [GN:YRHP] [OR:BACILLUS SUBTILIS]
[DE:HYPOTHETICAL 23.4 KD PROTEIN IN AAPA-SIGV INTERGENIC REGION] [SP:O05406]
[DB:swissprot] >pir:[LN:F69975] [AC:F69975] [PN:dihydrodipicolinate
reductase homolog yrhP] [GN:yrhP] [CL:hypothetical protein b1798]
[OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1183940:g2635156] [LN:BSUB0014]
[AC:Z99117:AL009126] [GN:yrhP] [FN:unknown] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 14 of 21):
from 2599451to 2812870.] [NT:similar to dihydrodipicolinate reductase]
[SP:O05406] [LE:167862] [RE:168494] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_4726555_f2_234	3205	6977	474	157	203	2.3e-16

Description

gp:[GI:g4980875] [LN:AE001717] [AC:AE001717:AE000512] [PN:arginine
repressor] [GN:TM0371] [OR:Thermotoga maritima] [DB:genpept-bct2]
[DE:Thermotoga maritima section 29 of 136 of the complete genome.]
[NT:similar to GB:M27869 SP:P17893 PID:142450] [LE:2550] [RE:3008]
[DI:direct] >gp:[GI:e1489641:g5102818] [LN:TMA132286] [AC:AJ132286]
[PN:arginine repressor] [GN:argR] [FN:regulation of arginine biosynthesis
genes] [OR:Thermotoga maritima] [DB:genpept] [DE:Thermotoga maritima argR
gene, strain MSB8.] [LE:1] [RE:459] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_4971051_c2_1028	3214	6986	825	274	196	1.3e-15

Description

gp:[GI:g1405404] [LN:LLU60336] [AC:U60336] [PN:AbiGi] [GN:abiGi] [FN:with AbiGii, causes abortive infection of phage] [OR:Lactococcus lactis subsp. cremoris] [DB:genpept-bct1] [DE:Lactococcus lactis cremoris abortive infection proteins (abiGi andabiGii) genes, complete cds.] [LE:4376] [RE:5125] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_5133462_f3_538	3215	6987	1530	509	146	1.2e-06

Description

pir:[LN:G71620] [AC:G71620] [PN:hypothetical protein PFB0195c] [GN:PFB0195c] [OR:Plasmodium falciparum] [DB:pir2] >gp:[GI:g3845121] [LN:AE001380] [AC:AE001380:AE001362] [PN:hypothetical protein] [GN:PFB0195c] [OR:Plasmodium falciparum] [SR:malaria parasite P. falciparum] [DB:genpept-inv2] [DE:Plasmodium falciparum chromosome 2, section 17 of 73 of thecomplete sequence.] [NT:predicted by GlimmerM] [LE:1011] [RE:3101] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_5190938_c3_1167	3216	6988	471	156	77	0.031

Description

sp:[LN:YH37_HAEIN] [AC:P44301] [GN:HI1737] [OR:HAEMOPHILUS INFLUENZAE] [DE:HYPOTHETICAL PROTEIN HI1737] [SP:P44301] [DB:swissprot] >pir:[LN:E64041] [AC:E64041] [PN:branched-chain amino acid transport protein azlD homolog HI1737] [CL:branched-chain amino acid transport protein azlD] [OR:Haemophilus influenzae] [DB:pir2] >gp:[GI:g1574595] [LN:U32846] [AC:U32846:L42023] [PN:conserved hypothetical protein] [GN:HI1737] [OR:Haemophilus influenzae Rd] [DB:genpept-bct2] [DE:Haemophilus influenzae Rd section 161 of 163 of the completegenome.] [NT:similar to GB:AL009126 percent identity: 53.70;] [LE:9500] [RE:9829] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_5275393_f1_18	3217	6989	132	43		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_5292300_c2_1002	3218	6990	342	113	83	0.029

Description

pir:[LN:A71655] [AC:A71655] [PN:hypothetical protein RP511] [GN:RP511]
 [OR:Rickettsia prowazekii] [DB:pir2] >gp:[GI:e1342807:g3861063] [LN:RPXX03]
 [AC:AJ235272:AJ235269] [PN:unknown] [GN:RP511] [OR:Rickettsia prowazekii]
 [DB:genpept-bct1] [DE:Rickettsia prowazekii strain Madrid E, complete
 genome; segment3/4.] [LE:35291] [RE:38143] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_5313316_c2_936	3219	6991	1413	470	245	8.3e-38

Description

pir:[LN:S74046] [AC:S74046] [PN:probable sugar transport protein c0110]
 [OR:Sulfolobus solfataricus] [DB:pir2] >gp:[GI:e283949:g1707740]
 [LN:SS100KBFR] [AC:Y08256] [PN:sugar transporter] [GN:orf c01010]
 [OR:Sulfolobus solfataricus] [DB:genpept-bct1] [DE:S.solfataricus 100 kbp
 DNA fragment.] [LE:71310] [RE:72581] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_5367337_c3_1274	3220	6992	138	45		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_57217_c1_735	3221	6993	207	68		

Description

NO-HIT

ORF = 6990-6993

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_582777_c2_892	3222	6994	1476	491	1405	9.7e-144

Description

sp:[LN:YHCL_BACSU] [AC:P54596] [GN:YHCL] [OR:BACILLUS SUBTILIS]
 [DE:HYPOTHETICAL 49.0 KD PROTEIN IN CSPB-GLPP INTERGENIC REGION] [SP:P54596]
 [DB:swissprot] >pir:[LN:H69822] [AC:H69822] [PN:sodium-glutamate symporter
 homolog yhcL] [GN:yhcL] [CL:Bacillus subtilis sodium-glutamate symporter
 homolog yhcL] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e233874:g1239988]
 [LN:BS75DGREG] [AC:X96983] [PN:hypothetical protein] [GN:yhcL] [OR:Bacillus
 subtilis] [DB:genpept-bct1] [DE:B.subtilis chromosomal DNA (region 75
 degrees: cspB upstream ofglpPFDK operon).] [NT:similarity to the
 proton/sodium-glutamate symport] [SP:P54596] [LE:7868] [RE:9259] [DI:direct]
 >gp:[GI:e1182902:g2633236] [LN:BSUB0005] [AC:Z99108:AL009126] [GN:yhcL]
 [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
 complete genome (section 5 of 21): from 802821 to1011250.] [NT:similar to
 sodium-glutamate symporter] [SP:P54596] [LE:183674] [RE:185065] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_595937_f2_394	3223	6995	177	58		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_6016063_f3_662	3224	6996	123	40		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_6054512_f3_600	3225	6997	207	68		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_6095000_f2_425	3226	6998	147	48		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_649141_f2_330	3227	6999	567	188		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_6521882_f1_32	3228	7000	195	64	81	0.0019

Description

gp:[GI:g5306165] [LN:AF160864] [AC:AF160864] [PN:orf98] [GN:orf98]
 [OR:Mitochondrion Tetrahymena pyriformis] [SR:Tetrahymena pyriformis]
 [DB:genpept] [DE:Tetrahymena pyriformis mitochondrial DNA, complete genome.]
 [NT:Open reading frame ymf71 (CPGN); ATT initiation] [LE:37598] [RE:37894]
 [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_6643751_c1_859	3229	7001	270	89		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_6644537_f1_178	3230	7002	258	85		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_6650267_f3_611	3231	7003	123	40		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_6715_c3_1123	3232	7004	510	169		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_6728178_f1_176	3233	7005	129	42		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_6728578_c2_942	3234	7006	1893	630	678	1.1e-66

Description

pir:[LN:B70001] [AC:B70001] [PN:ABC transporter (permease) homolog ytsD] [GN:ytsD] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1185910:g2635521] [LN:BSUB0016] [AC:Z99119:AL009126] [GN:ytsD] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.] [NT:similar to ABC transporter (permease)] [LE:110708] [RE:112648] [DI:complement] >gp:[GI:g2293178] [LN:AF008220] [AC:AF008220] [PN:YtsD] [GN:ytsD] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis rrnB-dnaB genomic region.] [NT:similarity to NADH dehydrogenase] [LE:67779] [RE:69719] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_6819462_f1_9	3235	7007	1491	496	1508	1.2e-154

Description

gp:[GI:e1299584:g3687418] [LN:BLY17554] [AC:Y17554] [PN:permease] [GN:arcD] [OR:Bacillus licheniformis] [DB:genpept-bct1] [DE:Bacillus licheniformis arcA, arcB, arcC and arcD genes.] [LE:2579] [RE:3985] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_6828125_c1_788	3236	7008	252	83	398	5.0e-37

Description

gp:[GI:d1046032:g5360856] [LN:D86934] [AC:D86934] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus (strain:N315) DNA, clone_lib:library of N31] [DB:genpept] [DE:Staphylococcus aureus genes, mec region, partial and complete cds.] [NT:ORF CN040] [LE:47301] [RE:>47552] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_6834501_c1_828	3237	7009	231	76		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_6929627_c2_1064	3238	7010	1146	381	756	5.7e-75

Description

pir:[LN:F70903] [AC:F70903] [PN:probable adhE'protein] [GN:adhE]
[CL:long-chain alcohol dehydrogenase homology] [OR:Mycobacterium
tuberculosis] [DB:pir2] >gp:[GI:e322878:g2213499] [LN:MTCI28]
[AC:Z97050:AL123456] [PN:adhE] [GN:adhE] [OR:Mycobacterium tuberculosis]
[DB:genpept-bct1] [DE:Mycobacterium tuberculosis H37Rv complete genome;
segment 10/162.] [NT:Rv0162c, (MTCI28.02c), len: 383,adhE, alcohol]
[LE:1482] [RE:2633] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_6929642_f1_14	3239	7011	243	80		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_6929686_c2_1081	3240	7012	264	87	368	7.5e-34

Description

pir:[LN:A60634] [AC:A60634:C30471:S26349] [PN:probable transposase]
[OR:Staphylococcus aureus] [DB:pir2] >gp:[GI:g46597] [LN:SAIS2571]
[AC:X53952] [PN:transposase] [OR:Staphylococcus aureus] [DB:genpept-bct1]
[DE:S.aureus plasmid pSH6 DNA for insertion sequences IS257-1 andIS256.]
[LE:188] [RE:862] [DI:direct] >gp:[GI:g3676452] [LN:AF051917]
[AC:AF051917:L19570] [PN:putative transposase TnpE] [GN:tnpE]
[OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus
plasmid pSK41, complete sequence.] [LE:40946] [RE:41620] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_6929686_f1_111	3241	7013	693	230	1195	1.7e-121

Description

sp:[LN:TRA2_STAAU] [AC:P19380] [OR:STAPHYLOCOCCUS AUREUS] [DE:TRANSPOSASE FOR INSERTION SEQUENCE-LIKE ELEMENT IS431MEC] [SP:P19380] [DB:swissprot]
 >pir:[LN:S12093] [AC:S12093:JU0116] [PN:probable transposase]
 [OR:Staphylococcus aureus] [DB:pir2] >gp:[GI:g46602] [LN:SAIS431M]
 [AC:X53818:M18438] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:S. aureus IS431mec gene associated with methicillin resistance.] [NT:putative transposase (AA 1 - 224)] [SP:P19380] [LE:272] [RE:946] [DI:direct]
 >gp:[GI:e1237900:g2791991] [LN:SAMECAR1I] [AC:Y14051] [PN:putative transposase] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:Staphylococcus aureus mecA, mecR1, mecI genes and ORF168, ORF142, ORF44, ORF145 and ORF224.] [NT:ORF224] [LE:8096] [RE:8770] [DI:direct] >gp:[GI:d1046034:g5360858] [LN:D86934] [AC:D86934] [PN:transposase for insertion sequence-like element] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus (strain:N315) DNA, clone_lib:library of N31] [DB:genpept] [DE:Staphylococcus aureus genes, mec region, partial and complete cds.] [NT:ORF N062] [LE:48054] [RE:48728] [DI:direct] >gp:[GI:d1046044:g5360868] [LN:D86934] [AC:D86934] [PN:transposase for insertion sequence-like element] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus (strain:N315) DNA, clone_lib:library of N31] [DB:genpept] [DE:Staphylococcus aureus genes, mec region, partial and complete cds.] [NT:ORF N070] [LE:53400] [RE:54074] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_7031563_c1_763	3242	7014	243	80	358	8.6e-33

Description

pir:[LN:S54709] [AC:S54709] [PN:hypothetical protein 81] [OR:Staphylococcus aureus] [DB:pir2]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_7223587_c3_1174	3243	7015	1401	466	218	4.9e-15

Description

gp:[GI:d1011960:g1064812] [LN:BACGNTZA] [AC:D78193] [GN:yycH] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:168) DNA] [DB:genpept-bct1]
 [DE:Bacillus subtilis 36kb sequence between gntZ and trnY genes encoding 34 ORFs.] [LE:32039] [RE:33415] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_7297338_f1_190	3244	7016	213	70		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_791307_c3_1273	3245	7017	156	51		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_862927_c3_1289	3246	7018	195	64		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_87562_f3_550	3247	7019	162	53		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_892142_f2_249	3248	7020	198	65		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_898550_f3_629	3249	7021	126	41		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_917550_c1_869	3250	7022	216	71	143	5.2e-10

Description

gp:[GI:g929968] [LN:BAU30713] [AC:U30713] [OR:Bacillus anthracis]
[SR:plasmid pXO1] [DB:genpept-bct1] [DE:Bacillus anthracis Sterne toxin
plasmid pXO1 right inverted repeatelement (SterneR) bordering the
toxin-encoding region, ORFA and truncated ORFB genes, complete cds.]
[NT:ORFA; similar to B. anthracis WeyAR element ORFA;] [LE:171] [RE:491]
[DI:direct] >gp:[GI:g929971] [LN:BAU30714] [AC:U30714] [OR:Bacillus
anthracis] [SR:plasmid pXO1] [DB:genpept-bct1] [DE:Bacillus anthracis
Weybridge A toxin plasmid pXO1 right inverted repeat element (WeyAR)
bordering the toxin-encoding region, ORFA and ORFB genes, complete cds.]
[NT:ORFA; similar to B. anthracis SterneR element ORFA;] [LE:171] [RE:491]
[DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_969050_c2_1031	3251	7023	162	53		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_970077_c3_1098	3252	7024	135	44	52	0.040

Description

gp:[GI:e264333:g1050454] [LN:CHRFBFPGE] [AC:X91081] [GN:rfbP]
[OR:Campylobacter hyoilei] [DB:genpept-bct1] [DE:C.hyoilei rfbF and rfbP
genes.] [LE:1896] [RE:2498] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_970250_c2_1057	3253	7025	912	303	446	4.1e-42

Description

pir:[LN:E69219] [AC:E69219] [PN:conserved hypothetical protein MTH894]
[GN:MTH894] [OR:Methanobacterium thermoautotrophicum] [DB:pir2]
>gp:[GI:g2621989] [LN:AE000865] [AC:AE000865:AE000666] [PN:conserved
protein] [GN:MTH894] [OR:Methanobacterium thermoautotrophicum]
[DB:genpept-bct1] [DE:Methanobacterium thermoautotrophicum from bases 808939
to 820180(section 71 of 148) of the complete genome.] [NT:Function
Code:14.01 - Unknown, Conserved protein;] [LE:4427] [RE:5410] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_970386_f1_60	3254	7026	333	110	270	5.2e-23

Description

pir:[LN:D70073] [AC:D70073] [PN:metabolite transport protein homolog yxC] [GN:yx] [CL:glucose transport protein] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1184706:g2636527] [LN:BSUB0021] [AC:Z99124:AL009126] [GN:yx] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.] [NT:similar to metabolite transport protein] [LE:87516] [RE:88901] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_9765951_c1_816	3255	7027	144	47		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_9773385_c1_687	3256	7028	816	271	303	5.8e-27

Description

gp:[GI:g757830] [LN:EC4HPADNA] [AC:Z37980] [PN:2-oxo-hept-3-ene-1,7-dioate hydratase] [GN:hpaH] [OR:Escherichia coli] [DB:genpept-bct1] [DE:E.coli hpa[G,R,E,D,F,H,I,X,A,B,C] genes.] [LE:4957] [RE:5760] [DI:direct] >gp:[GI:g2695682] [LN:AF036583] [AC:AF036583] [PN:2-oxo-hept-4-ene-1,7-dioate hydratase] [GN:hpcG] [OR:Escherichia coli] [DB:genpept-bct2] [DE:Escherichia coli 2-oxo-hept-4-ene-1,7-dioate hydratase (hpcG) gene,complete cds.] [NT:OHED hydratase] [LE:1] [RE:804] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_979178_c3_1277	3257	7029	243	80		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_9792842_c1_711	3258	7030	1851	616	1480	1.1e-151

Description

pir:[LN:C69840] [AC:C69840] [PN:conserved hypothetical protein yitJ]
 [GN:yitJ] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1183103:g2633437]
 [LN:BSUB0006] [AC:Z99109:AL009126] [GN:yitJ] [FN:unknown] [OR:Bacillus
 subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 6
 of 21): from 999501 to1209940.] [NT:similar to hypothetical proteins]
 [LE:178731] [RE:180569] [DI:complement] >gp:[GI:e1173535:g2145402]
 [LN:BSY09476] [AC:Y09476] [PN:YitJ] [OR:Bacillus subtilis] [DB:genpept-bct1]
 [DE:B.subtilis 54kb genomic DNA fragment.] [NT:putative - Some homology with
 Meth2 (S. cerevisae)] [LE:35957] [RE:37795] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_9800000_c3_1090	3259	7031	228	75		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_9806332_f3_491	3260	7032	450	149	237	9.3e-20

Description

pir:[LN:A71175] [AC:A71175] [PN:probable dehydrogenase] [GN:PH0597]
 [OR:Pyrococcus horikoshii] [DB:pir2] >gp:[GI:d1030629:g3257003]
 [LN:AP000002]
 [AC:AP000002:AB009475:AB009476:AB009477:AB009478:AB009479:AB009480]
 [PN:376aa long hypothetical dehydrogenase] [GN:PH0597] [OR:Pyrococcus
 horikoshii] [SR:Pyrococcus horikoshii (strain:OT3) DNA] [DB:genpept-bct1]
 [DE:Pyrococcus horikoshii OT3 genomic DNA, 287001-544000 nt. position(2/7).]
 [NT:similar to owl:BSZ9404317 percent identity: 49.821] [LE:248539]
 [RE:249669] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_9806692_c3_1251	3261	7033	1374	457	907	5.7e-91

Description

sp:[LN:YMER STAAU] [AC:P08655] [OR:STAPHYLOCOCCUS AUREUS] [DE:HYPOTHETICAL 19.7 KD PROTEIN IN MERCURIC RESISTANCE OPERON] [SP:P08655] [DB:swissprot] >pir:[LN:G29504] [AC:G29504] [PN:hypothetical 20K protein (mer regulatory region)] [OR:Staphylococcus aureus] [DB:pir2] >gp:[GI:g459902] [LN:L29436] [AC:L29436:M15048:N00048] [PN:regulatory protein] [GN:merR] [OR:Plasmid pI258] [SR:Plasmid pI258 DNA] [DB:genpept-bct1] [DE:Plasmid pI258 (from S.aureus strain RN23 8325) mercury resistance(mer) operon encoding mercuric reductase (merA), organomercuriallyase (merB), regulatory protein (merR) and membrane transportprotein (merT), complete cds.] [LE:188] [RE:730] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_9847811_c1_698	3262	7034	162	53		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000999_991500_f1_182	3263	7035	135	44		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001000_11955055_c1_45	3264	7036	192	64		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001000_1214635_c2_48	3265	7037	387	128	469	1.5e-44

Description

gp:[GI:d1036080:g4001724] [LN:AB015981] [AC:AB015981] [PN:OrfA] [GN:orfA] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus (strain:209P) DNA] [DB:genpept-bct1] [DE:Staphylococcus aureus genes for OrfA, MnhA, MnhB, MnhC, MnhD, MnhE,MnhF and MnhG, complete cds.] [LE:302] [RE:685] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503001000_13089052_c2_46	3266	7038	123	40		
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Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503001000_1378550_f3_34	3267	7039	144	47		
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Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503001000_14460932_f2_21	3268	7040	294	97	451	1.2e-42
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Description

gp:[GI:g1022726] [LN:SHU35635] [AC:U35635] [PN:unknown] [OR:Staphylococcus haemolyticus] [SR:Staphylococcus haemolyticus strain=Y176] [DB:genpept-bct1] [DE:Staphylococcus haemolyticus IS1272 ORF1 and ORF2 genes, completedcs.] [NT:ORF1] [LE:1101] [RE:1922] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503001000_14500036_c3_66	3269	7041	129	42		
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Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503001000_15041078_f2_13	3270	7042	279	92	319	1.2e-28
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Description

pir:[LN:G70012] [AC:G70012] [PN:conserved hypothetical protein yuiF] [GN:yuiF] [CL:conserved integral membrane protein HP0758] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1184283:g2635701] [LN:BSUB0017] [AC:Z99120:AL009126] [GN:yuiF] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.] [NT:similar to hypothetical proteins] [LE:96999] [RE:98327] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001000_21646015_f3_36	3271	7043	201	66	198	7.8e-16

Description

gp:[GI:g1022725] [LN:SHU35635] [AC:U35635] [PN:unknown] [OR:Staphylococcus haemolyticus] [SR:Staphylococcus haemolyticus strain=Y176] [DB:genpept-bct1] [DE:Staphylococcus haemolyticus IS1272 ORF1 and ORF2 genes, completecds.] [NT:ORF2] [LE:394] [RE:1083] [DI:complement] >gp:[GI:g295162] [LN:STAMECRA] [AC:L14017] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus (strain COL) DNA] [DB:genpept-bct1] [DE:Staphylococcus aureus methicillin-resistance protein (mecR) geneand unknown ORF, complete cds.] [NT:unknown ORF1; putative] [LE:1492] [RE:2181] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001000_22136087_c2_53	3272	7044	1512	503	2102	1.3e-217

Description

gp:[GI:d1036084:g4001728] [LN:AB015981] [AC:AB015981] [PN:MnhD] [GN:mnhD] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus (strain:209P) DNA] [DB:genpept-bct1] [DE:Staphylococcus aureus genes for OrfA, MnhA, MnhB, MnhC, MnhD, MnhE,MnhF and MnhG, complete cds.] [LE:3976] [RE:5472] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001000_22457312_f1_9	3273	7045	126	41		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001000_23456932_f3_26	3274	7046	153	50		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001000_23859843_f1_10	3275	7047	393	130	212	2.5e-17

Description

sp:[LN:GS13_BACSU] [AC:P80870:O05238] [GN:YUGI] [OR:BACILLUS SUBTILIS] [DE:GENERAL STRESS PROTEIN 13 (GSP13)] [SP:P80870:O05238] [DB:swissprot]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001000_23947132_f3_23	3276	7048	378	125	269	2.3e-23

Description

gp:[GI:e291128:g1834379] [LN:BLCOMAB] [AC:Y10551] [GN:ComAB] [FN:positive activator of lichenysin synthetase] [OR:Bacillus licheniformis] [DB:genpept-bct1] [DE:B.licheniformis comAB gene.] [LE:617] [RE:>963] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001000_24644702_cl_41	3277	7049	435	144	647	2.0e-63

Description

gp:[GI:d1036082:g4001726] [LN:AB015981] [AC:AB015981] [PN:MnhB] [GN:mnhB] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus (strain:209P) DNA] [DB:genpept-bct1] [DE:Staphylococcus aureus genes for OrfA, MnhA, MnhB, MnhC, MnhD, MnhE, MnhF and MnhG, complete cds.] [LE:3214] [RE:3642] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001000_26756252_c3_61	3278	7050	2427	808	3318	0.0

Description

gp:[GI:d1036081:g4001725] [LN:AB015981] [AC:AB015981] [PN:MnhA] [GN:mnhA] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus (strain:209P) DNA] [DB:genpept-bct1] [DE:Staphylococcus aureus genes for OrfA, MnhA, MnhB, MnhC, MnhD, MnhE, MnhF and MnhG, complete cds.] [LE:816] [RE:3221] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001000_29742890_f2_22	3279	7051	189	62		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001000_32689812_c2_54	3280	7052	312	103	386	9.3e-36

Description

gp:[GI:d1036086:g4001730] [LN:AB015981] [AC:AB015981] [PN:MnhF] [GN:mnhF] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus (strain:209P) DNA] [DB:genpept-bct1] [DE:Staphylococcus aureus genes for OrfA, MnhA, MnhB, MnhC, MnhD, MnhE, MnhF and MnhG, complete cds.] [LE:5953] [RE:6246] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001000_33397338_c3_64	3281	7053	492	163	635	3.8e-62

Description

gp:[GI:d1036085:g4001729] [LN:AB015981] [AC:AB015981] [PN:MnhE] [GN:mnhE]
[OR:Staphylococcus aureus] [SR:Staphylococcus aureus (strain:209P) DNA]
[DB:genpept-bct1] [DE:Staphylococcus aureus genes for OrfA, MnhA, MnhB,
MnhC, MnhD, MnhE,MnhF and MnhG, complete cds.] [LE:5474] [RE:5953]
[DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001000_34384380_c1_42	3282	7054	333	110	468	1.9e-44

Description

gp:[GI:d1036083:g4001727] [LN:AB015981] [AC:AB015981] [PN:MnhC] [GN:mnhC]
[OR:Staphylococcus aureus] [SR:Staphylococcus aureus (strain:209P) DNA]
[DB:genpept-bct1] [DE:Staphylococcus aureus genes for OrfA, MnhA, MnhB,
MnhC, MnhD, MnhE,MnhF and MnhG, complete cds.] [LE:3642] [RE:3983]
[DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001000_34617286_f2_19	3283	7055	612	203	304	3.9e-35

Description

sp:[LN:YDJ3_SCHPO] [AC:P87051] [GN:SPAC57A10.03] [OR:SCHIZOSACCHAROMYCES
POMBE] [SR:,FISSION YEAST] [EC:5.2.1.8] [DE:PROBABLE PEPTIDYL-PROLYL
CIS-TRANS ISOMERASE C57A10.03,] [SP:P87051] [DB:swissprot]
>gp:[GI:e313994:g2058370] [LN:SPAC57A10] [AC:Z94864] [PN:peptidyl-prolyl
cis-trans isomerase] [GN:SPAC57A10.03] [OR:Schizosaccharomyces pombe]
[SR:fission yeast] [DB:genpept-plnl] [DE:S.pombe chromosome I cosmid
c57A10.] [NT:SPAC57A10.03, len:155, SIMILARITY:Caenorhabditis] [SP:P87051]
[LE:5344:5414:5521:5779] [RE:5373:5455:5574:5858] [DI:directJoin]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001000_36604587_c1_44	3284	7056	1173	390		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001000_4017050_c3_59	3285	7057	126	41		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001000_5114680_c3_65	3286	7058	363	120	463	6.4e-44

Description

gp:[GI:d1036087:g4001731] [LN:AB015981] [AC:AB015981] [PN:MnhG] [GN:mnhG]
[OR:Staphylococcus aureus] [SR:Staphylococcus aureus (strain:209P) DNA]
[DB:genpept-bct1] [DE:Staphylococcus aureus genes for OrfA, MnhA, MnhB,
MnhC, MnhD, MnhE, MnhF and MnhG, complete cds.] [LE:6224] [RE:6580]
[DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001000_6672886_f3_35	3287	7059	1173	390	914	1.0e-91

Description

sp:[LN:YQIG_BACSU] [AC:P54524] [GN:YQIG] [OR:BACILLUS SUBTILIS] [EC:1.-.-.-]
[DE:PROBABLE NADH-DEPENDENT FLAVIN OXIDOREDUCTASE YQIG,] [SP:P54524]
[DB:swissprot] >pir:[LN:C69961] [AC:C69961] [PN:NADH-dependent flavin
oxidoreductase homolog yqiG] [GN:yqiG] [OR:Bacillus subtilis] [DB:pir2]
>gp:[GI:d1013261:g1303926] [LN:BACJH642] [AC:D84432:D82370] [PN:YqiG]
[OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:JH642(trpC2 PheA1))
DNA] [DB:genpept-bct1] [DE:Bacillus subtilis DNA, 283 Kb region containing
skin element.] [LE:202096] [RE:203214] [DI:complement]
>gp:[GI:e1185689:g2634855] [LN:BSUB0013] [AC:Z99116:AL009126] [GN:yqiG]
[FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
complete genome (section 13 of 21): from 2395261to 2613730.] [NT:similar to
NADH-dependent flavin oxidoreductase] [SP:P54524] [LE:120407] [RE:121525]
[DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001000_783125_c3_56	3288	7060	183	60		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_10000312_c3_1340	3289	7061	165	54		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503001001_10006340_f2_492	3290	7062	501	166	85	0.0011

Description

gp:[GI:g160616] [LN:PFAR45B] [AC:M83791] [PN:trophozoite antigen] [GN:R45]
[OR:Plasmodium falciparum] [SR:Plasmodium falciparum (strain Tak 9.96)
(library: lambda-gt11] [DB:genpept-inv1] [DE:Plasmodium falciparum
trophozoite antigen gene (repeat region),partial cds.] [LE:<1] [RE:>327]
[DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503001001_10265677_f2_556	3291	7063	150	49		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503001001_10267016_c2_1133	3292	7064	789	262	210	4.1e-17

Description

sp:[LN:TIPA_STRLI] [AC:P32184] [GN:TIPA] [OR:STREPTOMYCES LIVIDANS]
[DE:TRANSCRIPTIONAL ACTIVATOR TIPA] [SP:P32184] [DB:swissprot]
>pir:[LN:S35354] [AC:S35354:A45923] [PN:tipA protein] [GN:tipA] [CL:tipA
protein] [OR:Streptomyces lividans] [DB:pir2] >gp:[GI:g408223] [LN:S64314]
[AC:S64314] [PN:TipAL-AS] [GN:tipA] [OR:Streptomyces lividans]
[DB:genpept-bct1] [DE:tipAL-AS complex: tipA=TipAL-AS [Streptomyces
lividans, Genomic,1146 nt].] [NT:thiostrepton-specific recognition protein;
Method:] [LE:120] [RE:881] [DI:direct] >gp:[GI:e1453008:g4808352] [LN:SCE9]
[AC:AL049841] [PN:transcriptional regulator] [GN:SCE9.20] [OR:Streptomyces
coelicolor] [DB:genpept-bct1] [DE:Streptomyces coelicolor cosmid E9.]
[NT:SCE9.20c, tipA, transcriptional regulator, len: 253] [LE:21108]
[RE:21869] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503001001_10268818_f3_803	3293	7065	234	77		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503001001_10343756_f3_840	3294	7066	174	57		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_10439005_f1_44	3295	7067	516	171	157	1.7e-11

Description

gp:[GI:d1044366:g5105267] [LN:AP000062] [AC:AP000062] [PN:114aa long hypothetical protein] [GN:APE1580] [OR:Aeropyrum pernix] [SR:Aeropyrum pernix (strain:K1) DNA] [DB:genpept] [DE:Aeropyrum pernix genomic DNA, section 5/7.] [NT:similar to OWL:AB00946832 percent identity:37.500] [LE:13911] [RE:14255] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_10548187_f3_766	3296	7068	162	53		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_10581693_f2_490	3297	7069	684	227	842	4.4e-84

Description

pir:[LN:A69868] [AC:A69868] [PN:ykvJ protein] [GN:ykvJ] [CL:conserved hypothetical protein HI1191] [OR:Bacillus subtilis] [DB:pir2]
>gp:[GI:e1184962:g2633743] [LN:BSUB0008] [AC:Z99111:AL009126] [GN:ykvJ] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.] [NT:similar to hypothetical proteins] [LE:44124] [RE:44783] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_10589818_f2_358	3298	7070	201	66	58	0.0051

Description

gp:[GI:e321942:g2664263] [LN:EFAS48C] [AC:Y12234] [PN:hypothetical protein] [OR:Enterococcus faecalis] [DB:genpept-bct1] [DE:E.faecalis plasmid DNA containing gene cluster involved in production and immunity to peptide antibiotic AS-48.] [NT:ORF6] [LE:4556] [RE:5065] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_10667002_c3_1423	3299	7071	201	66		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503001001_10667002_c3_1504	3300	7072	168	55		
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Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503001001_10737818_f1_230	3301	7073	471	156	223	1.7e-18
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Description

sp:[LN:YP17_LISMO] [AC:P52309] [OR:Listeria monocytogenes] [DE:HYPOTHETICAL 17.1 KD PROTEIN IN DNAG/DNAE 5'REGION (P17)] [SP:P52309] [DB:swissprot]
>gp:[GI:g664754] [LN:LMU13165] [AC:U13165] [PN:P17] [OR:Listeria monocytogenes] [DB:genpept-bct2] [DE:Listeria monocytogenes P17 (orfP17), DNA primase (dnaG) and sigma43 subunit of RNA polymerase (rpoD) genes, complete cds.] [NT:orfP17] [LE:196] [RE:645] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503001001_10976387_c3_1503	3302	7074	210	69		
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Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503001001_11023402_f3_781	3303	7075	273	90	127	2.6e-08
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Description

pir:[LN:A71007] [AC:A71007] [PN:hypothetical protein PH1351] [GN:PH1351] [OR:Pyrococcus horikoshii] [DB:pir2] >gp:[GI:d1031400:g3257774]
[LN:AP000006]
[AC:AP000006:AB005215:AB009510:AB009511:AB009512:AB009513:AB009514]
[PN:101aa long hypothetical protein] [GN:PH1351] [OR:Pyrococcus horikoshii]
[SR:Pyrococcus horikoshii (strain:OT3) DNA, clone:Pyrococcus horikoshi]
[DB:genpept-bct1] [DE:Pyrococcus horikoshii OT3 genomic DNA, 1166001-1485000 nt. position(6/7).] [LE:50986] [RE:51291] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503001001_110275_f2_577	3304	7076	276	91	292	8.5e-26
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Description

gp:[GI:e255528:g1617429] [LN:SEABCTS] [AC:X99127] [PN:membrane protein]
[FN:iron repressible ABC transport system] [OR:Staphylococcus epidermidis]
[DB:genpept-bct1] [DE:S.epidermidis gene encoding ABC transport system.]
[LE:878] [RE:1624] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_11152176_c1_967	3305	7077	1029	342	1111	1.4e-112

Description

pir:[LN:A69855] [AC:A69855] [PN:low-affinity inorganic phosphate transport homolog ykaB] [GN:ykaB] [OR:Bacillus subtilis] [DB:pir2]
 >gp:[GI:e1181485:g2632005] [LN:BSAJ2571] [AC:AJ002571] [PN:YkaB] [GN:ykaB] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis 168 56 kb DNA fragment between xlyA and ykoR.] [NT:homologous to low affinity phosphate transporter] [LE:1614] [RE:2600] [DI:complement] >gp:[GI:e1183304:g2633638] [LN:BSUB0007] [AC:Z99110:AL009126] [GN:ykaB] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.] [NT:similar to low-affinity inorganic phosphate] [LE:154563] [RE:155549] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_112561_f1_99	3306	7078	138	45		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_116383_f2_590	3307	7079	165	54		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_11728376_c2_1327	3308	7080	249	82	241	2.2e-20

Description

pir:[LN:A70026] [AC:A70026] [PN:hypothetical protein yuzB] [GN:yuzB] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1184298:g2635716] [LN:BSUB0017] [AC:Z99120:AL009126] [GN:yuzB] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.] [LE:110425] [RE:110661] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_11831433_f2_602	3309	7081	159	52	48	0.031

Description

gp:[GI:g554799] [LN:HIVB54CH] [AC:M96497] [PN:envelope protein] [GN:env]
[OR:Human immunodeficiency virus type 1] [SR:Human immunodeficiency virus
type 1 (individual isolate) RNA] [DB:genpept-vrl] [DE:Human
immunodeficiency virus type 1 (clone B5-4) V1 & V2 regions ofthe envelope
protein (env) gene, partial cds.] [NT:hypervariable regions V1 and V2;
putative] [LE:<1] [RE:>296] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_11883557_f1_292	3310	7082	195	64		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_1199063_f1_135	3311	7083	510	169	165	5.3e-12

Description

sp:[LN:YJJP_HAEIN] [AC:P44520] [GN:HI0108] [OR:HAEMOPHILUS INFLUENZAE]
[DE:HYPOTHETICAL PROTEIN HI0108] [SP:P44520] [DB:swissprot] >pir:[LN:I64142]
[AC:I64142] [PN:hypothetical protein HI0108] [OR:Haemophilus influenzae]
[DB:pir2] >gp:[GI:g1573061] [LN:U32696] [AC:U32696:L42023] [PN:conserved
hypothetical protein] [GN:HI0108] [OR:Haemophilus influenzae Rd]
[DB:genpept-bct2] [DE:Haemophilus influenzae Rd section 11 of 163 of the
complete genome.] [NT:similar to GB:U14003 SP:P39402 PID:537207 GB:U00096]
[LE:4095] [RE:4988] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_1214688_f1_146	3312	7084	939	312	526	1.4e-50

Description

sp:[LN:MURB_BACSU] [AC:P18579:P16669:P37581] [GN:MURB] [OR:BACILLUS SUBTILIS] [EC:1.1.1.158] [DE:ACETYLMURAMATE DEHYDROGENASE)] [SP:P18579:P16669:P37581] [DB:swissprot] >pir:[LN:A43727] [AC:S26500:PC1128:A43727:B69662] [PN:UDP-N-acetylenolpyruvoylglucosamine reductase murB:hypothetical protein (murG 3' region)] [GN:murB] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:g142833] [LN:BACDDSA] [AC:M31827] [OR:Bacillus subtilis] [SR:Bacillus subtilis (clone: lambda-BS1) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis (clone lambda-BS1) cell division and sporulationprotein (dds) gene, complete cds.] [NT:ORF2] [LE:479] [RE:1390] [DI:direct] >gp:[GI:e1185113:g2633894] [LN:BSUB0008] [AC:Z99111:AL009126] [PN:UDP-N-acetylenolpyruvoylglucosamine reductase] [GN:murB] [FN:peptidoglycan biosynthesis] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:1.1.1.158] [DE:Bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.] [NT:alternate gene name: ylxC] [SP:P18579] [LE:197268] [RE:198179] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_12616018_f2_357	3313	7085	270	89	84	0.0027

Description

gp:[GI:g48992] [LN:ECINCI2] [AC:X62169:S47694] [GN:pilU] [OR:Escherichia coli] [DB:genpept-bct1] [DE:E.coli IncI2 plasmid R721 pilU, plV, shf, rci genes.] [LE:29] [RE:664] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_12617827_c1_1083	3314	7086	762	253	1160	8.9e-118

Description

gp:[GI:e1393156:g4490615] [LN:SAU133520] [AC:AJ133520] [PN:triosephosphate isomerase] [GN:tpi] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:Staphylococcus aureus gap operon (gapR, gap, pgk and tpi genes).] [LE:4307] [RE:5068] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503001001_12789077_c3_1469	3315	7087	1107	368	1311	8.9e-134

Description

sp:[LN:UVRA_BACSU] [AC:O34863] [GN:UVRA] [OR:BACILLUS SUBTILIS]
 [DE:EXCINUCLEASE ABC SUBUNIT A] [SP:O34863] [DB:swissprot] >pir:[LN:F69729]
 [AC:F69729] [PN:excinuclease ABC chain A:excision endonuclease ABC,, chain
 A:uvrA protein] [GN:uvrA] [CL:excinuclease ABC chain A:ATP-binding cassette
 homology] [OR:Bacillus subtilis] [EC:3.1.-.-] [DB:pir2]
 >gp:[GI:e1184422:g2636042] [LN:BSUB0019] [AC:Z99122:AL009126]
 [PN:excinuclease ABC (subunit A)] [GN:uvrA] [FN:excision of ultraviolet
 light-induced] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus
 subtilis complete genome (section 19 of 21): from 3597091to 3809700.]
 [SP:O34863] [LE:12034] [RE:14907] [DI:complement] >gp:[GI:g2618842]
 [LN:AF017113] [AC:AF017113] [PN:excinuclease ABC subunit A] [GN:uvrA]
 [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis 300-304
 degree genomic sequence.] [LE:15386] [RE:18259] [DI:direct]
 >gp:[GI:e1184422:g2636042] [LN:BSUB0019] [AC:Z99122:AL009126]
 [PN:excinuclease ABC (subunit A)] [GN:uvrA] [FN:excision of ultraviolet
 light-induced] [OR:Bacillus subtilis] [DB:genpept] [DE:Bacillus subtilis
 complete genome (section 19 of 21): from 3597091to 3809700.] [SP:O34863]
 [LE:12034] [RE:14907] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503001001_12929631_f2_529	3316	7088	156	51		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503001001_12948336_c3_1475	3317	7089	273	90	316	2.4e-28

Description

sp:[LN:CLPP_BACSU] [AC:P80244:O08433] [GN:CLPP] [OR:BACILLUS SUBTILIS]
 [EC:3.4.21.92] [DE:(ENDOPEPTIDASE CLP) (CASEINOLYTIC PROTEASE) (PROTEASE
 TI)] [SP:P80244:O08433] [DB:swissprot] >pir:[LN:B69601] [AC:B69601:A47683]
 [PN:ATP-dependent clp proteinase, chain P:stress protein G7] [GN:clpP]
 [CL:ATP-dependent Clp proteinase chain P] [OR:Bacillus subtilis]
 [EC:3.4.21.-] [DB:pir2] >gp:[GI:e1186142:g2635967] [LN:BSUB0018]
 [AC:Z99121:AL009126] [PN:ATP-dependent Clp protease proteolytic subunit]
 [GN:clpP] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:3.4.21.92]
 [DE:Bacillus subtilis complete genome (section 18 of 21): from 3399551to
 3609060.] [NT:alternate gene name: yvdN] [SP:P80244] [LE:145744] [RE:146337]
 [DI:direct] >gp:[GI:e313044:g1945673] [LN:BSZ94043] [AC:Z94043]
 [PN:hypothetical protein] [GN:yvdN] [OR:Bacillus subtilis] [DB:genpept-bct1]
 [DE:B.subtilis genomic DNA fragment (88 kb).] [NT:similar to CLPP_ECOLI
 ATP-dependent clp protease] [SP:P80244] [LE:35334] [RE:35927]
 [DI:complement] >gp:[GI:g2668494] [LN:BSU59754] [AC:U59754] [PN:ClpP]
 [GN:clpP] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis Clp
 protease proteolytic component (clpP) gene,complete cds.] [NT:proteolytic
 component of Clp protease] [LE:140] [RE:733] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503001001_1351533_c2_1261	3318	7090	2571	856	3966	0.0

Description

sp:[LN:SECA_STAAU] [AC:O06446] [GN:SECA] [OR:STAPHYLOCOCCUS AUREUS]
 [DE:PREPROTEIN TRANSLOCASE SECA SUBUNIT] [SP:O06446] [DB:swissprot]
 >gp:[GI:g2078390] [LN:SAU97062] [AC:U97062] [PN:SecA] [GN:secA]
 [FN:secretion] [OR:Staphylococcus aureus] [DB:genpept-bct1]
 [DE:Staphylococcus aureus NCTC 8325 SecA (secA) gene, complete cds.]
 [LE:440] [RE:2971] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503001001_1362705_c1_960	3319	7091	123	40		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503001001_1366018_f3_723	3320	7092	135	44		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_13710887_c2_1298	3321	7093	753	250	315	3.1e-28

Description

pir:[LN:I39522] [AC:I39522] [PN:3-dehydroquinate dehydratase,, catabolic]
 [GN:quiB] [CL:3-dehydroquinate dehydratase:3-dehydroquinate dehydratase
 homology] [OR:Acinetobacter calcoaceticus] [EC:4.2.1.10] [DB:pir2]
 >gp:[GI:g3172120] [LN:ACCPAOP]
 [AC:L05770:U04359:M33798:U20284:U11554:L13114:L03407] [PN:catabolic
 dehydroquinate dehydratase] [GN:quiB] [FN:dehydration of dehydroquinate to]
 [OR:Acinetobacter sp. ADP1] [DB:genpept-bct2] [DE:Acinetobacter sp. ADP1
 pca-qui-pob supraoperonic cluster, complete sequence.] [LE:10923] [RE:11795]
 [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_13714193_c3_1456	3322	7094	582	193	583	1.2e-56

Description

sp:[LN:YSEA_STACA] [AC:P47995] [OR:STAPHYLOCOCCUS CARNOSUS] [DE:HYPOTHETICAL
 PROTEIN IN SECA 5'REGION (ORF1) (FRAGMENT)] [SP:P47995] [DB:swissprot]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_13727318_f1_246	3323	7095	813	270	348	9.9e-32

Description

gp:[GI:g2735506] [LN:SCU96107] [AC:U96107] [PN:SceB precursor] [GN:sceB]
 [OR:Staphylococcus carnosus] [DB:genpept-bct2] [DE:Staphylococcus carnosus
 N5,N10-methylenetetrahydromethanopterin reductase homolog, SceB precursor
 (sceB) and putative transmembrane protein genes, complete cds, and putative
 Na⁺/H⁺ antiporter NhaC(nhaC) gene, partial cds.] [NT:major secreted protein]
 [LE:1894] [RE:2685] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503001001_1376577_f2_374	3324	7096	675	224	77	0.0044

Description

pir:[LN:F70141] [AC:F70141] [PN:probable oligopeptide transport ATP-binding protein oppF] [GN:oppF] [CL:inner membrane protein malK:ATP-binding cassette homology] [OR:Borrelia burgdorferi] [SR:, Lyme disease spirochete] [DB:pir2] >gp:[GI:g2688242] [LN:AE001140] [AC:AE001140:AE000783] [PN:oligopeptide ABC transporter, ATP-binding] [GN:BB0335] [OR:Borrelia burgdorferi] [SR:Lyme disease spirochete] [DB:genpept-bct2] [DE:Borrelia burgdorferi (section 26 of 70) of the complete genome.] [NT:similar to SP:P24137 percent identity: 56.81;] [LE:3216] [RE:4187] [DI:direct].
>gp:[GI:g2281463] [LN:AF000366] [AC:AF000366] [PN:oligopeptide permease homolog F] [GN:oppF] [OR:Borrelia burgdorferi] [SR:Lyme disease spirochete] [DB:genpept-bct2] [DE:Borrelia burgdorferi oligopeptide permease homologs AI (oppAI), AII (oppAII), AIII (oppAIII), B (oppB), C (oppC), D (oppD), and F (oppF), P26 (p26) and enolase homolog (eno) genes, complete cds.] [NT:OppF] [LE:9017] [RE:9988] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503001001_13803167_f2_373	3325	7097	552	183	157	8.0e-11

Description

pir:[LN:A69774] [AC:A69774] [PN:integrase homolog ydcL] [GN:ydcL] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:d1020071:g1881291] [LN:AB001488] [AC:AB001488] [GN:ydcL] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:168) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.] [NT:PROBABLE INTEGRASE.] [LE:62741] [RE:63847] [DI:complement] >gp:[GI:e1182446:g2632780] [LN:BSUB0003] [AC:Z99106:AL009126] [GN:ydcL] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.] [NT:similar to integrase] [LE:126486] [RE:127592] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503001001_13834425_c2_1291	3326	7098	126	41		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503001001_13921942_c3_1483	3327	7099	1554	517	1690	6.1e-174

Description

pir:[LN:D69675] [AC:D69675:I40024] [PN:phosphoglycerate mutase,, 2, 3-diphosphoglycerate-independent] [GN:pgm] [CL:phosphoglycerate mutase, 2, 3-bisphosphoglycerate-independent] [OR:Bacillus subtilis] [EC:5.4.2.1] [DB:pir2] >gp:[GI:e1186079:g2635904] [LN:BSUB0018] [AC:Z99121:AL009126] [PN:phosphoglycerate mutase] [GN:pgm] [FN:glycolysis] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:5.4.2.1] [DE:Bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.] [SP:P39773] [LE:77390] [RE:78925] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503001001_13931527_c3_1337	3328	7100	723	240	87	0.011

Description

pir:[LN:S49604] [AC:S49604] [PN:hypothetical protein 126 (rps12 3' region)] [OR:plastid Astasia longa] [DB:pir2] >gp:[GI:e156256:g1334340] [LN:ALRPS12] [AC:X82630] [GN:orf126] [OR:Chloroplast Astasia longa] [SR:euglenophycean alga] [DB:genpept-pln1] [DE:A.longa plastid rps12, orf126 and orf288 genes.] [NT:ata start] [LE:<1424] [RE:1801] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503001001_1408438_f1_283	3329	7101	948	315	110	8.1e-06

Description

sp:[LN:YDCZ_ECOLI] [AC:P76111] [GN:YDCZ] [OR:ESCHERICHIA COLI] [DE:HYPOTHETICAL 15.9 KD PROTEIN IN TEHB-ANSP INTERGENIC REGION] [SP:P76111] [DB:swissprot] >pir:[LN:B64897] [AC:B64897] [PN:probable membrane protein b1447] [OR:Escherichia coli] [DB:pir2] >gp:[GI:g1787718] [LN:AE000241] [AC:AE000241:U00096] [PN:orf, hypothetical protein] [GN:b1447] [FN:orf; Unknown] [OR:Escherichia coli] [DB:genpept-bct2] [DE:Escherichia coli K-12 MG1655 section 131 of 400 of the completegenome.] [NT:f149; This 149 aa ORF is 31 pct identical (11 gaps)] [LE:9124] [RE:9573] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503001001_14097163_f1_50	3330	7102	138	45		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503001001_14120465_f1_56	3331	7103	513	170		
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Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503001001_14454632_f1_194	3332	7104	177	58	225	1.1e-18
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Description

gp:[GI:g1022726] [LN:SHU35635] [AC:U35635] [PN:unknown] [OR:Staphylococcus haemolyticus] [SR:Staphylococcus haemolyticus strain=Y176] [DB:genpept-bct1] [DE:Staphylococcus haemolyticus IS1272 ORF1 and ORF2 genes, completecds.] [NT:ORF1] [LE:1101] [RE:1922] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503001001_14460882_c1_1104	3333	7105	177	58	234	1.2e-19
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Description

gp:[GI:g1022726] [LN:SHU35635] [AC:U35635] [PN:unknown] [OR:Staphylococcus haemolyticus] [SR:Staphylococcus haemolyticus strain=Y176] [DB:genpept-bct1] [DE:Staphylococcus haemolyticus IS1272 ORF1 and ORF2 genes, completecds.] [NT:ORF1] [LE:1101] [RE:1922] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503001001_14460882_f3_776	3334	7106	183	60	128	6.0e-08
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Description

gp:[GI:g1022726] [LN:SHU35635] [AC:U35635] [PN:unknown] [OR:Staphylococcus haemolyticus] [SR:Staphylococcus haemolyticus strain=Y176] [DB:genpept-bct1] [DE:Staphylococcus haemolyticus IS1272 ORF1 and ORF2 genes, completecds.] [NT:ORF1] [LE:1101] [RE:1922] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503001001_14478377_c3_1383	3335	7107	1149	382	637	2.3e-62

Description

sp:[LN:HMPA_BACSU] [AC:P49852] [GN:HMP:ANE3] [OR:BACILLUS SUBTILIS]
[DE:FLAVOHEMOPROTEIN (HAEMOGLOBIN-LIKE PROTEIN) (FLAVOHEMOGLOBIN)]
[SP:P49852] [DB:swissprot] >pir:[LN:B69642] [AC:B69642] [PN:flavohemoglobin
hmp] [GN:hmp] [CL:flavohemoglobin:cytochrome-b5 reductase homology:globin
homology] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:d1011920:g1063247]
[LN:BAC168TRP2] [AC:D78189] [OR:Bacillus subtilis] [SR:Bacillus subtilis
(strain:168trpC2) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis hmp DNA for 7
ORFs, complete cds.] [NT:high homology to flavohemoprotein
(Haemoglobin-like) [LE:999] [RE:2198] [DI:direct] >gp:[GI:e1181505:g2632025]
[LN:BSAJ2571] [AC:AJ002571] [PN:Ykia] [GN:ykia] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis 168 56 kb DNA fragment between xlyA
and ykoR.] [NT:Flavohemoprotein] [SP:P49852] [LE:24916] [RE:26115]
[DI:direct] >gp:[GI:e1183324:g2633658] [LN:BSUB0007] [AC:Z99110:AL009126]
[PN:flavohemoglobin] [GN:hmp] [OR:Bacillus subtilis] [DB:genpept-bct1]
[DE:Bacillus subtilis complete genome (section 7 of 21): from 1194391to
1411140.] [NT:alternate gene name: ykia] [SP:P49852] [LE:177865] [RE:179064]
[DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503001001_14494461_c2_1178	3336	7108	168	55		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503001001_14500052_f1_64	3337	7109	204	67		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503001001_14538202_c3_1510	3338	7110	762	253	1034	2.0e-104

Description

sp:[LN:V296_BACSU] [AC:P80866] [GN:YURI] [OR:BACILLUS SUBTILIS]
[DE:VEGETATIVE PROTEIN 296 (VEG296)] [SP:P80866] [DB:swissprot]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_14564005_f2_456	3339	7111	249	82	87	0.0016

Description

pir:[LN:B69341] [AC:B69341] [PN:cobalt transport protein (cbiQ-1) homolog]
[OR:Archaeoglobus fulgidus] [DB:pir2] >gp:[GI:g2649885] [LN:AE001054]
[AC:AE001054:AE000782] [PN:cobalt transport protein (cbiQ-1)] [GN:AF0730]
[OR:Archaeoglobus fulgidus] [DB:genpept-bct2] [DE:Archaeoglobus fulgidus
section 53 of 172 of the complete genome.] [NT:similar to GP:1419077 percent
identity: 32.61;] [LE:978] [RE:1700] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_14642203_c3_1363	3340	7112	834	277	772	1.2e-76

Description

pir:[LN:G70080] [AC:G70080] [PN:conserved hypothetical protein yxkD]
[GN:yxkD] [CL:conserved hypothetical protein yitT] [OR:Bacillus subtilis]
[DB:pir2] >gp:[GI:e1186383:g2636419] [LN:BSUB0020] [AC:Z99123:AL009126]
[GN:yxkD] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus
subtilis complete genome (section 20 of 21): from 3798401to 4010550.]
[NT:similar to hypothetical proteins] [LE:188319] [RE:189155]
[DI:complement] >gp:[GI:d1012387:g1783243] [LN:D83026] [AC:D83026:D45911]
[GN:yxkD] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:BGSC 1A1)
DNA] [DB:genpept-bct1] [DE:Bacillus subtilis genome sequence covering
lic-cel region.] [NT:homologous to jojC gene product (B. subtilis;]
[LE:35310] [RE:36146] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_14648452_c3_1464	3341	7113	801	266	346	1.6e-31

Description

gp:[GI:e244971:g1340128] [LN:SA1234] [AC:X97985] [OR:Staphylococcus aureus]
[DB:genpept-bct1] [DE:S.aureus orfs 1,2,3 & 4.] [NT:ORF1] [LE:537] [RE:1304]
[DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_14875890_c3_1412	3342	7114	846	281	734	1.2e-72

Description

gp:[GI:e1359127:g4007669] [LN:SC4B5] [AC:AL034443] [PN:putative
oxidoreductase] [GN:SC4B5.01c] [OR:Streptomyces coelicolor]
[DB:genpept-bct1] [DE:Streptomyces coelicolor cosmid 4B5.] [NT:SC4B5.01c,
probable oxidoreductase, len; 277aa,] [LE:52] [RE:885] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503001001_14878807_f2_599	3343	7115	960	319	162	2.8e-09

Description

gp:[GI:e321943:g2664264] [LN:EFAS48C] [AC:Y12234] [PN:hypothetical protein]
[OR:Enterococcus faecalis] [DB:genpept-bct1] [DE:E.faecalis plasmid DNA
containing gene cluster involved in production and immunity to peptide
antibiotic AS-48.] [NT:ORF7] [LE:5043] [RE:6266] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503001001_14886052_c3_1386	3344	7116	495	164	307	2.2e-27

Description

sp:[LN:YQGC_BACSU] [AC:P54486] [GN:YQGC] [OR:BACILLUS SUBTILIS]
[DE:HYPOTHETICAL 17.3 KD PROTEIN IN CCCA-SODA INTERGENIC REGION] [SP:P54486]
[DB:swissprot] >pir:[LN:G69955] [AC:G69955] [PN:hypothetical protein yqgC]
[GN:yqgC] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:d1013185:g1303850]
[LN:BACJH642] [AC:D84432:D82370] [PN:YqgC] [OR:Bacillus subtilis]
[SR:Bacillus subtilis (strain:JH642(trpC2 PheA1)) DNA] [DB:genpept-bct1]
[DE:Bacillus subtilis DNA, 283 Kb region containing skin element.]
[LE:132903] [RE:133385] [DI:direct] >gp:[GI:e1185770:g2634936] [LN:BSUB0013]
[AC:Z99116:AL009126] [GN:yqgC] [FN:unknown] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 13 of 21):
from 2395261to 2613730.] [SP:P54486] [LE:190236] [RE:190718] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503001001_14970251_f3_623	3345	7117	294	97		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503001001_15057762_c2_1198	3346	7118	1575	524	1194	2.2e-121

Description

sp:[LN:MEMP_ALCEU] [AC:Q07252] [OR:ALCALIGENES EUTROPHUS] [DE:MEMBRANE
PROTEIN] [SP:Q07252] [DB:swissprot] >pir:[LN:I39534] [AC:I39534:S33452]
[PN:hypothetical protein] [OR:Alcaligenes eutrophus] [DB:pir2]
>gp:[GI:g311309] [LN:AELACDEH] [AC:Z22737] [PN:putative membrane-bound
protein with four times] [OR:Ralstonia eutropha] [DB:genpept-bct1]
[DE:A.eutrophus genes for lactate dehydrogenase, putativemembrane-bound
protein with four times repetition of Pro-Ser-Ala at the N-terminus (function
unknown) and transglycosidase (partial).] [SP:Q07252] [LE:962] [RE:2503]
[DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503001001_1561_c1_1025	3347	7119	1944	647	1406	7.6e-144

Description

pir:[LN:A69814] [AC:A69814] [PN:ABC transporter (ATP-binding protein) homolog yfmR] [GN:yfmR] [CL:ATP-binding cassette homology] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1182716:g2633050] [LN:BSUB0004] [AC:Z99107:AL009126] [GN:yfmR] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.] [NT:similar to ABC transporter (ATP-binding protein)] [LE:208365] [RE:210254] [DI:direct] >gp:[GI:e1182727:g2633061] [LN:BSUB0005] [AC:Z99108:AL009126] [GN:yfmR] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.] [NT:similar to ABC transporter (ATP-binding protein)] [LE:6245] [RE:8134] [DI:direct] >gp:[GI:d1020922:g2116756] [LN:D86418] [AC:D86418] [PN:YfmR] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:AC327) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis genomic DNA 69-70 degree region, partialsequence.] [LE:2937] [RE:4826] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503001001_15661088_c2_1162	3348	7120	513	170		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503001001_15751312_f1_164	3349	7121	2136	711	1980	1.1e-204

Description

sp:[LN:ADH2_ENTHI] [AC:Q24803:Q27649] [GN:ADH2] [OR:ENTAMOEBA HISTOLYTICA] [EC:1.1.1.1:1.2.1.10] [DE:DEHYDROGENASE, (ACDH)] [SP:Q24803:Q27649] [DB:swissprot] >gp:[GI:g488430] [LN:EHU04863] [AC:U04863] [PN:alcohol dehydrogenase 2] [OR:Entamoeba histolytica] [DB:genpept-inv1] [DE:Entamoeba histolytica HM1:IMSS alcohol dehydrogenase 2 (EhADH2)mRNA, complete cds.] [NT:The derived amino acid sequence of EhADH2 is] [LE:3] [RE:2615] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503001001_15752262_f3_666	3350	7122	153	50		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_15756542_c2_1195	3351	7123	201	66		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_157767_c3_1366	3352	7124	1077	358	534	1.9e-51

Description

gp:[GI:d1045428:g5106360] [LN:AB028629] [AC:AB028629] [PN:lipase] [GN:lipA] [OR:Clostridium perfringens] [SR:Clostridium perfringens (strain:13) DNA, clone:pSB235] [DB:genpept] [DE:Clostridium perfringens metB, cysK, ygaG, lipA genes forcystathionine beta-synthase, cysteine synthase, hypotheticalprotein, lipase, partial and complete cds.] [NT:esterase] [LE:3248] [RE:4183] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_15781336_c2_1131	3353	7125	471	156	150	9.5e-11

Description

pir:[LN:C70059] [AC:C70059] [PN:hypothetical protein ywiB] [GN:ywiB] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1186235:g2636271] [LN:BSUB0020] [AC:Z99123:AL009126] [GN:ywiB] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.] [LE:35970] [RE:36398] [DI:complement] >gp:[GI:e324352:g2224755] [LN:BSZ97024] [AC:Z97024] [GN:ywiB] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis ywiA, sbo, ywiB, argS and narK genes.] [LE:1255] [RE:1683] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_16522890_f1_189	3354	7126	171	56		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_16603207_f3_710	3355	7127	378	125	217	7.5e-18

Description

pir:[LN:S72776] [AC:S72776] [PN:B1496_F1_41 protein] [OR:Mycobacterium leprae] [DB:pir2] >gp:[GI:g466873] [LN:U00013] [AC:U00013] [PN:B1496_F1_41] [OR:Mycobacterium leprae] [DB:genpept-bct1] [DE:Mycobacterium leprae cosmid B1496.] [LE:29815] [RE:30312] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503001001_166062_c2_1287	3356	7128	123	40	50	0.030

Description

pir:[LN:S73871] [AC:S73871] [PN:type I restriction enzyme ecokI specificity protein homolog:hypothetical protein H10_orf145L:hypothetical protein H10_orf145L] [OR:Mycoplasma pneumoniae] [SR:ATCC 29342, , ATCC 29342] [SR:ATCC 29342,] [DB:pir2] >gp:[GI:g1674242] [LN:MPAE000053] [AC:AE000053:U00089] [GN:H10_orf145L] [OR:Mycoplasma pneumoniae] [DB:genpept-bct2] [DE:Mycoplasma pneumoniae section 53 of 63 of the complete genome.] [NT:type I restriction enzyme ecokI specificity protein] [LE:3554] [RE:3991] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503001001_166713_c2_1263	3357	7129	2001	666	2697	1.2e-280

Description

sp:[LN:UVRB_BACSU] [AC:P37954:O34455] [GN:UVRB:DINA:UVR] [OR:BACILLUS SUBTILIS] [DE:EXCINUCLEASE ABC SUBUNIT B (DINA PROTEIN)] [SP:P37954:O34455] [DB:swissprot] >pir:[LN:G69729] [AC:G69729:I39817:B37317] [PN:excinnuclease ABC chain B:DNA repair protein DinA:excision endonuclease ABC,, chain B:hypothetical protein (DNA damage-inducible A76 promoter 3' region):UrvB homolog DinA] [GN:uvrB:uvr:dinA] [CL:excinnuclease ABC chain B:DEAD/H box helicase homology] [OR:Bacillus subtilis] [EC: 3.1.-.-] [DB:pir2] >gp:[GI:e1184423:g2636043] [LN:BSUB0019] [AC:Z99122:AL009126] [PN:excinnuclease ABC (subunit B)] [GN:uvrB] [FN:excision of ultraviolet light-induced] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.] [NT:alternate gene name: dinA, uvrA] [SP:P37954] [LE:14915] [RE:16900] [DI:complement] >gp:[GI:g2618841] [LN:AF017113] [AC:AF017113] [PN:excinnuclease ABC subunit B] [GN:uvrB] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis 300-304 degree genomic sequence.] [LE:13393] [RE:15378] [DI:direct] >gp:[GI:e1184423:g2636043] [LN:BSUB0019] [AC:Z99122:AL009126] [PN:excinnuclease ABC (subunit B)] [GN:uvrB] [FN:excision of ultraviolet light-induced] [OR:Bacillus subtilis] [DB:genpept] [DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.] [NT:alternate gene name: dinA, uvrA] [SP:P37954] [LE:14915] [RE:16900] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503001001_16677343_c1_925	3358	7130	447	148	107	3.4e-06

Description

sp:[LN:Y357_METJA] [AC:Q57803] [GN:MJ0357] [OR:METHANOCOCCUS JANNASCHII]
 [DE:HYPOTHETICAL PROTEIN MJ0357] [SP:Q57803] [DB:swissprot] >pir:[LN:E64344]
 [AC:E64344] [PN:hypothetical protein MJ0357] [OR:Methanococcus jannaschii]
 [DB:pir2] [MP:REV326407-325940] >gp:[GI:g1591066] [LN:U67489]
 [AC:U67489:L77117] [PN:M. jannaschii predicted coding region MJ0357]
 [GN:MJ0357] [OR:Methanococcus jannaschii] [DB:genpept-bct2]
 [DE:Methanococcus jannaschii section 31 of 150 of the complete genome.]
 [NT:hypothetical protein; identified by GeneMark;] [LE:1632] [RE:2099]
 [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503001001_16834512_c3_1401	3359	7131	1380	459	661	6.7e-65

Description

sp:[LN:PHR_BACFI] [AC:Q04449] [GN:PHR] [OR:BACILLUS FIRMUS] [EC:4.1.99.3]
 [DE:(PHOTOREACTIVATING ENZYME) (FRAGMENT)] [SP:Q04449] [DB:swissprot]
 >gp:[GI:g142783] [LN:BACCTA] [AC:M94110] [PN:DNA photolyase] [GN:phr]
 [OR:Bacillus firmus] [SR:Bacillus firmus (strain OF4) DNA] [DB:genpept-bct1]
 [EC:4.1.99.3] [DE:Bacillus firmus DNA photolyase (phr) gene, 3' end, and
 cytochromeoxidase (cta) operon.] [NT:putative] [LE:1] [RE:1020] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503001001_16850303_c1_1090	3360	7132	477	158	510	6.7e-49

Description

sp:[LN:SMPB_BACSU] [AC:O32230] [GN:SMPB] [OR:BACILLUS SUBTILIS] [DE:SMALL
 PROTEIN B' HOMOLOG] [SP:O32230] [DB:swissprot] >pir:[LN:F70027] [AC:F70027]
 [PN:conserved hypothetical protein yvaI] [GN:yvaI] [CL:small protein smpB]
 [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1186048:g2635873] [LN:BSUB0018]
 [AC:Z99121:AL009126] [GN:yvaI] [FN:unknown] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 18 of 21):
 from 3399551to 3609060.] [NT:similar to hypothetical proteins] [SP:O32230]
 [LE:50760] [RE:51230] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503001001_17011562_c3_1354	3361	7133	168	55		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503001001_181500_c3_1353	3362	7134	798	265	415	7.8e-39

Description

sp:[LN:TAGA_BACSU] [AC:P27620] [GN:TAGA] [OR:BACILLUS SUBTILIS] [DE:TEICHOIC ACID BIOSYNTHESIS PROTEIN A] [SP:P27620] [DB:swissprot] >pir:[LN:B49757] [AC:B49757:B69720] [PN:polyglycerol phosphate techoic acid biosynthesis protein tagA] [GN:tagA] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:g143724] [LN:BACTAGABCD] [AC:M57497] [GN:tagA] [OR:Bacillus subtilis] [SR:B.subtilis (strain 168) DNA] [DB:genpept-bct1] [DE:B.subtilis tagA, tagB, tagC and tagD genes, complete cds.] [NT:putative] [LE:800] [RE:1570] [DI:direct] >gp:[GI:e1184481:g2636101] [LN:BSUB0019] [AC:Z99122:AL009126] [GN:tagA] [FN:polyglycerol phosphate assembly and export] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.] [SP:P27620] [LE:83340] [RE:84110] [DI:direct] >gp:[GI:e1184481:g2636101] [LN:BSUB0019] [AC:Z99122:AL009126] [GN:tagA] [FN:polyglycerol phosphate assembly and export] [OR:Bacillus subtilis] [DB:genpept] [DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.] [SP:P27620] [LE:83340] [RE:84110] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503001001_187568_c2_1149	3363	7135	327	108	178	1.0e-13

Description

pir:[LN:F70008] [AC:F70008] [PN:hypothetical protein yufC] [GN:yufC] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1184242:g2635660] [LN:BSUB0017] [AC:Z99120:AL009126] [GN:yufC] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.] [LE:53800] [RE:54084] [DI:direct] >gp:[GI:e311513:g1934775] [LN:BSZ93932] [AC:Z93932] [PN:unknown] [GN:yufC] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis genomic DNA fragment from yufA to yufE.] [LE:7444] [RE:7728] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503001001_187916_c2_1189	3364	7136	612	203	344	2.6e-31

Description

gp:[GI:e1314177:g3395518] [LN:PMAJ84] [AC:AJ000084] [PN:putative acetyl transferase] [GN:pat] [OR:Proteus mirabilis] [DB:genpept-bct1] [DE:Proteus mirabilis ccm and pat genes and partial ygbA gene.] [LE:949] [RE:1506] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503001001_189187_c1_1040	3365	7137	132	43		
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Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503001001_19532277_c1_1120	3366	7138	126	41		
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Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503001001_19537812_c2_1293	3367	7139	150	49	39	0.0042
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Description

pir:[LN:A70221] [AC:A70221] [PN:conserved hypothetical protein BBC08]
 [OR:Borrelia burgdorferi] [SR:, Lyme disease spirochete] [DB:pir2]
 >gp:[GI:g2689920] [LN:AE000791] [AC:AE000791] [PN:conserved hypothetical
 protein] [GN:BBC08] [OR:Borrelia burgdorferi] [SR:Lyme disease spirochete]
 [DB:genpept-bct2] [DE:Borrelia burgdorferi plasmid cp9, complete plasmid
 sequence.] [NT:similar to GB:U03641 PID:458212 percent identity:] [LE:5534]
 [RE:5980] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503001001_19547783_f2_493	3368	7140	771	256	448	2.5e-42
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Description

gp:[GI:g4481749] [LN:AF007865] [AC:AF007865] [PN:BacR] [GN:bacR]
 [OR:Bacillus licheniformis] [DB:genpept-bct2] [DE:Bacillus licheniformis
 bacitracin synthetase operon, complete sequence; BacS (bacS), BcrA (bcrA),
 BcrB (bcrB), and BcrC (bcrC) genes, complete cds.] [NT:44488] [LE:44497]
 [RE:45213] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503001001_195885_f2_436	3369	7141	165	54		
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Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503001001_19589187_f3_689	3370	7142	207	68	57	0.019

Description

pir:[LN:F71027] [AC:F71027] [PN:hypothetical protein PH1514] [GN:PH1514]
 [OR:Pyrococcus horikoshii] [DB:pir2] >gp:[GI:d1031565:g3257939]
 [LN:AP000006]
 [AC:AP000006:AB005215:AB009510:AB009511:AB009512:AB009513:AB009514]
 [PN:310aa long hypothetical protein] [GN:PH1514] [OR:Pyrococcus horikoshii]
 [SR:Pyrococcus horikoshii (strain:OT3) DNA, clone:Pyrococcus horikoshi]
 [DB:genpept-bct1] [DE:Pyrococcus horikoshii OT3 genomic DNA, 1166001-1485000
 nt. position(6/7).] [LE:183119] [RE:184051] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503001001_19696951_c3_1486	3371	7143	183	60	193	2.6e-15

Description

pir:[LN:A70028] [AC:A70028] [PN:hypothetical protein yvaL] [GN:yvaL]
 [CL:protein-export protein secG] [OR:Bacillus subtilis] [DB:pir2]
 >gp:[GI:e1186051:g2635876] [LN:BSUB0018] [AC:Z99121:AL009126] [GN:yvaL]
 [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
 complete genome (section 18 of 21): from 3399551to 3609060.] [LE:54605]
 [RE:54835] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503001001_19704062_f2_538	3372	7144	183	60		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503001001_197127_c3_1411	3373	7145	132	43		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503001001_19714012_c1_939	3374	7146	144	47		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_197152_c3_1343	3375	7147	348	115	257	4.3e-22

Description

gp:[GI:d1036083:g4001727] [LN:AB015981] [AC:AB015981] [PN:MnhC] [GN:mnhC]
 [OR:Staphylococcus aureus] [SR:Staphylococcus aureus (strain:209P) DNA]
 [DB:genpept-bct1] [DE:Staphylococcus aureus genes for OrfA, MnhA, MnhB,
 MnhC, MnhD, MnhE, MnhF and MnhG, complete cds.] [LE:3642] [RE:3983]
 [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_19726575_c1_942	3376	7148	144	47		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_19765965_c1_1098	3377	7149	249	82	323	4.4e-29

Description

gp:[GI:g2226349] [LN:AF003593] [AC:AF003593] [PN:CspC] [GN:cspC]
 [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:Staphylococcus aureus CspC
 (cspC) gene, complete cds.] [NT:similar to major cold-shock protein]
 [LE:444] [RE:644] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_19766886_f1_59	3378	7150	435	144	167	1.9e-12

Description

gp:[GI:e1294701:g3171734] [LN:BTPGI2XX] [AC:X13481] [OR:Bacillus
 thuringiensis] [DB:genpept-bct1] [DE:Bacillus thuringiensis plasmid pGI2
 with transposon Tn4430.] [NT:ORF 2] [LE:6037] [RE:6849] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_19804502_f2_364	3379	7151	144	47		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_19814387_c1_966	3380	7152	135	44		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_19929556_f2_545	3381	7153	129	42		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_2007677_f2_513	3382	7154	144	47		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_2007767_c2_1199	3383	7155	126	41		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_20110186_f3_688	3384	7156	153	50		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_20322153_c2_1212	3385	7157	219	72		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_20350875_c3_1515	3386	7158	123	40		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_20485663_f2_563	3387	7159	210	69		
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_20491385_f1_252	3388	7160	144	47		
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_20604832_f3_692	3389	7161	558	185	106	0.0012
<u>Description</u>						

gp:[GI:g552163] [LN:PFA10B] [AC:J03986] [OR:Plasmodium falciparum]
 [SR:P.falciparum (strain IMTM22) asexual erythrocytic form DNA, clon]
 [DB:genpept-invl] [DE:P.falciparum 10b antigen gene, partial cds.] [NT:10b
 antigen] [LE:<1] [RE:>1124] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_20707877_c3_1457	3390	7162	123	40		
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_20734387_f3_640	3391	7163	159	52		
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_20830417_c3_1332	3392	7164	147	48		
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_20893828_c1_974	3393	7165	219	72		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_20900017_c2_1239	3394	7166	2169	722	3396	0.0

Description

gp:[GI:e1393150:g4490609] [LN:SAU133495] [AC:AJ133495] [PN:ribonucleotide reductase major subunit] [GN:rir1] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:Staphylococcus aureus ribonucleotide reductase operon.] [LE:448] [RE:2604] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_209452_f1_276	3395	7167	648	215	754	9.4e-75

Description

gp:[GI:e255528:g1617429] [LN:SEABCTS] [AC:X99127] [PN:membrane protein] [FN:iron repressible ABC transport system] [OR:Staphylococcus epidermidis] [DB:genpept-bct1] [DE:S.epidermidis gene encoding ABC transport system.] [LE:878] [RE:1624] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_209627_c3_1444	3396	7168	1032	343	1571	2.5e-161

Description

gp:[GI:e1393151:g4490610] [LN:SAU133495] [AC:AJ133495] [PN:ribonucleotide reductase minor subunit] [GN:rir2] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:Staphylococcus aureus ribonucleotide reductase operon.] [LE:2722] [RE:3693] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_21490925_c1_1005	3397	7169	126	41		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_21509430_c1_962	3398	7170	132	43		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_21525061_c1_1016	3399	7171	681	226	110	0.00014

Description

sp:[LN:YB69_HAEIN] [AC:P44118] [GN:HI1169] [OR:HAEMOPHILUS INFLUENZAE] [DE:HYPOTHETICAL PROTEIN HI1169] [SP:P44118] [DB:swissprot] >pir:[LN:A64021] [AC:A64021] [PN:hypothetical protein HI1169] [OR:Haemophilus influenzae] [DB:pir2] >gp:[GI:g1574096] [LN:U32797] [AC:U32797:L42023] [PN:H. influenzae predicted coding region HI1169] [GN:HI1169] [OR:Haemophilus influenzae Rd] [DB:genpept-bct2] [DE:Haemophilus influenzae Rd section 112 of 163 of the completegenome.] [NT:hypothetical protein; identified by GeneMark;] [LE:511] [RE:1077] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_21537811_c1_1007	3400	7172	1137	378	925	7.1e-93

Description

sp:[LN:CSBB_BACSU] [AC:Q45539] [GN:CSBB] [OR:BACILLUS SUBTILIS] [DE:CSBB PROTEIN] [SP:Q45539] [DB:swissprot] >pir:[LN:JC5173] [AC:JC5173:G69607] [PN:stress response protein csbB] [GN:csbB] [CL:stress response protein csbB] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:g1387979] [LN:BACCSBB] [AC:L77099] [GN:csbB] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis csbB gene, complete cds.] [NT:similar to hypothetical protein from Synechocystis] [LE:310] [RE:1299] [DI:direct] >gp:[GI:e1182849:g2633183] [LN:BSUB0005] [AC:Z99108:AL009126] [PN:stress response protein] [GN:csbB] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.] [NT:alternate gene name: yfhN] [SP:Q45539] [LE:127505] [RE:128494] [DI:direct] >gp:[GI:d1025396:g2804544] [LN:D85082] [AC:D85082] [PN:YfhN] [OR:Bacillus subtilis] [SR:Bacillus subtilis DNA] [DB:genpept-bct1] [DE:Bacillus subtilis DNA, genome sequence, 79 to 81 degree region.] [LE:20396] [RE:21385] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_21617215_f1_36	3401	7173	150	49		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_21726510_f2_612	3402	7174	126	41		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_21751287_f3_684	3403	7175	123	40		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_21883512_c3_1512	3404	7176	225	74		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_21897308_f2_541	3405	7177	261	86		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_21963877_c2_1273	3406	7178	123	40		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_22265936_c3_1452	3407	7179	1128	375	1557	7.6e-160

Description

pir:[LN:A55856] [AC:A55856] [PN:llm protein] [GN:llm] [CL:lipophilic protein lim] [OR:Staphylococcus aureus] [DB:pir2] >gp:[GI:d1023388:g4433370] [LN:STASRM551A] [AC:D21131] [PN:lipophilic protein which affects bacterial lysis] [GN:llm] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus (strain:SRM551) DNA, clone_lib:lambda ZapII] [DB:genpept-bct1] [DE:Staphylococcus aureus gene for a participant in homogeneous expression of high-level methicillin resistance, complete cds.] [LE:148] [RE:1203] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503001001_22381693_c3_1472	3408	7180	852	283	1187	1.2e-120

Description

sp:[LN:LGT_STAAU] [AC:P52282] [GN:LGT] [OR:STAPHYLOCOCCUS AUREUS]
[EC:2.4.99.-] [DE:PROLIPOPROTEIN DIACYLGLYCERYL TRANSFERASE,] [SP:P52282]
[DB:swissprot] >gp:[GI:g1016770] [LN:SAU35773] [AC:U35773]
[PN:prolipoprotein diacylglycerol transferase] [GN:lgt] [FN:transfer of
diglyceride moiety to SH Group of] [OR:Staphylococcus aureus]
[DB:genpept-bct1] [DE:Staphylococcus aureus prolipoprotein diacylglycerol
transferase(lgt) gene, complete cds.] [LE:297] [RE:1136] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503001001_22391068_c1_1046	3409	7181	1056	351	1284	6.4e-131

Description

gp:[GI:e1330455:g3724158] [LN:SAA005352] [AC:AJ005352] [PN:lipoprotein]
[GN:sssD] [FN:iron transporter] [OR:Staphylococcus aureus] [DB:genpept-bct1]
[DE:Staphylococcus aureus, Sst putative iron transport operon.] [LE:3066]
[RE:4095] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503001001_22446053_c2_1132	3410	7182	726	241	335	2.4e-30

Description

pir:[LN:A64479] [AC:A64479] [PN:DNA-(apurinic or apyrimidinic site)
lyase,;endonuclease III] [CL:Methanococcus jannaschii conserved
DNA-(apurinic or apyrimidinic site) lyase] [OR:Methanococcus jannaschii]
[EC:4.2.99.18] [DB:pir2] [MP:FOR1403656-1404318] >gp:[GI:g1592082]
[LN:U67584] [AC:U67584:L77117] [PN:endonuclease III, putative (nth2)]
[GN:MJ1434] [OR:Methanococcus jannaschii] [DB:genpept-bct2]
[DE:Methanococcus jannaschii section 126 of 150 of the complete genome.]
[NT:similar to GB:U11289 SP:P39788 PID:533099] [LE:7078] [RE:7740]
[DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503001001_22462926_c1_1122	3411	7183	783	260	669	9.5e-66

Description

pir:[LN:H70023] [AC:H70023] [PN:N-acetyl-glucosamine catabolism homolog
yutF] [GN:yutF] [CL:nagD protein] [OR:Bacillus subtilis] [DB:pir2]
>gp:[GI:e1184308:g2635726] [LN:BSUB0017] [AC:Z99120:AL009126] [GN:yutF]
[FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
complete genome (section 17 of 21): from 3197001to 3414420.] [NT:similar to
N-acetyl-glucosamine catabolism] [LE:120087] [RE:120857] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_22687900_c3_1369	3412	7184	681	226	685	1.9e-67

Description

pir:[LN:G70000] [AC:G70000] [PN:two-component response regulator [YtsB] homolog ytsA] [GN:ytsA] [CL:ompR protein:response regulator homology] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1185913:g2635524] [LN:BSUB0016] [AC:Z99119:AL009126] [GN:ytsA] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.] [NT:similar to two-component response regulator [YtsB]] [LE:114498] [RE:115193] [DI:complement] >gp:[GI:g2293175] [LN:AF008220] [AC:AF008220] [PN:signal transduction regulator] [GN:ytsA] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis rrnB-dnaB genomic region.] [LE:65234] [RE:65929] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_22776938_c2_1323	3413	7185	156	51		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_22895400_f3_753	3414	7186	138	45		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_23437750_c1_938	3415	7187	171	56		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_23438461_c1_926	3416	7188	687	228	103	0.029

Description

gp:[GI:g5306158] [LN:AF160864] [AC:AF160864] [PN:orf1386] [GN:orf1386] [OR:Mitochondrion Tetrahymena pyriformis] [SR:Tetrahymena pyriformis] [DB:genpept] [DE:Tetrahymena pyriformis mitochondrial DNA, complete genome.] [NT:Open reading frame ymf77 (CPGN); ATA initiation] [LE:22317] [RE:26477] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_23439005_f1_6	3417	7189	141	46		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_23439061_c1_984	3418	7190	531	176	258	3.4e-22

Description

pir:[LN:F69927] [AC:F69927] [PN:hypothetical protein yosT] [GN:yosT]
[OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1185472:g2634393] [LN:BSUB0011]
[AC:Z99114:AL009126] [GN:yosT] [FN:unknown] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 11 of 21):
from 2000171to 2207900.] [LE:157797] [RE:158246] [DI:complement]
>gp:[GI:g3025644] [LN:AF020713] [AC:AF020713] [PN:unknown] [GN:yosT]
[OR:Bacteriophage SPBc2] [DB:genpept-phg] [DE:Bacteriophage SPBc2 complete
genome.] [LE:127274] [RE:127723] [DI:direct] >gp:[GI:g2522410] [LN:AF012906]
[AC:AF012906:U80600] [PN:unknown] [GN:yojV] [OR:Bacillus subtilis]
[DB:genpept-bct2] [DE:Bacillus subtilis yojP gene, partial cds; yojQ/S,
yojR, yojT,yojU, yojV, yojW, yojX, yojY, yojZ, and yokA genes, complete
cds.] [LE:4921] [RE:5370] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_23444838_c2_1267	3419	7191	264	87	373	2.2e-34

Description

gp:[GI:e1387399:g4379428] [LN:SAAJ3781] [AC:AJ223781] [PN:thioredoxin
reductase] [GN:trxB] [OR:Staphylococcus aureus] [DB:genpept-bct1]
[EC:1.6.4.5] [DE:Staphylococcus aureus trxB gene.] [LE:1262] [RE:2197]
[DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_23445175_f3_674	3420	7192	135	44		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_23445890_c2_1177	3421	7193	492	163	333	3.8e-30

Description

pir:[LN:S74709] [AC:S74709] [PN:hypothetical protein sll1188]
 [OR:Synechocystis sp.] [SR:PCC 6803, , PCC 6803] [SR:PCC 6803,] [DB:pir2]
 >gp:[GI:d1017593:g1651934] [LN:D90901] [AC:D90901:AB001339] [PN:hypothetical
 protein] [OR:Synechocystis sp.] [SR:Synechocystis sp. (strain:PCC6803) DNA]
 [DB:genpept-bct1] [DE:Synechocystis sp. PCC6803 complete genome, 3/27,
 271600-402289.] [NT:ORF_ID:sll1188] [LE:42106] [RE:42600] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_23446912_f2_597	3422	7194	123	40		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_2345062_f3_639	3423	7195	171	56		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_23450_c3_1490	3424	7196	189	62		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_23469552_c1_923	3425	7197	207	68		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503001001_23475892_c1_1121	3426	7198	1362	453	707	9.0e-70

Description

pir:[LN:G70015] [AC:G70015] [PN:conserved hypothetical protein yunD]
 [GN:yunD] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1184316:g2635734]
 [LN:BSUB0017] [AC:Z99120:AL009126] [GN:yunD] [FN:unknown] [OR:Bacillus
 subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section
 17 of 21): from 3197001to 3414420.] [NT:similar to hypothetical proteins]
 [LE:125728] [RE:127116] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503001001_23476517_c2_1259	3427	7199	1296	431	638	1.8e-62

Description

sp:[LN:CMF1 BACSU] [AC:P39145] [GN:COMFA:COMF1] [OR:BACILLUS SUBTILIS]
 [DE:COMF OPERON PROTEIN 1] [SP:P39145] [DB:swissprot] >pir:[LN:G69602]
 [AC:G69602:S77620:S35011:I40387:S28597] [PN:late competence protein
 required for DNA uptake comFA:ATP-dependent DNA helicase/translocase comF1]
 [GN:comFA:comF1] [CL:DEAD/H box helicase homology] [OR:Bacillus subtilis]
 [DB:pir2] >gp:[GI:g580841] [LN:BSCOMFG] [AC:Z18629] [PN:F1] [GN:comForf1]
 [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis comF gene.]
 [SP:P39145] [LE:952] [RE:2343] [DI:direct] >gp:[GI:e1184453:g2636073]
 [LN:BSUB0019] [AC:Z99122:AL009126] [PN:late competence protein] [GN:comFA]
 [FN:required for DNA uptake (competence)] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 19 of 21):
 from 3597091to 3809700.] [SP:P39145] [LE:44137] [RE:45528] [DI:complement]
 >gp:[GI:g1762332] [LN:BSU56901] [AC:U56901] [GN:comFA] [OR:Bacillus
 subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis putative transcriptional
 regulator (yvhJ),Ycr59c/YigZ homolog (yvhK), histidine kinase
 (degS),transcriptionalregulator of degradation enzyme (degU), (degV),
 (comFA), (comFB),(comFC), flagellar protein (yviB), negative regulator of
 flagellin(flzM), flagellar protein (yviC), flagellar-hook associated
 protein1 (flgK), flagellar-hook associated protein 3 (flgL),
 (yviE),transmembrane protein (yviF), (csrA), flagellin (hag),
 flagellarprotein (yviH), flagellar hook-associated protein 2
 (fliD),flagellar protein (fliS), flagellar protein (fliT), sigma-54modulator
 homolog (yviI), and (secA) genes, complete cds.] [NT:involved in
 transformation] [LE:5065] [RE:6456] [DI:direct] >gp:[GI:e1184453:g2636073]
 [LN:BSUB0019] [AC:Z99122:AL009126] [PN:late competence protein] [GN:comFA]
 [FN:required for DNA uptake (competence)] [OR:Bacillus subtilis]
 [DB:genpept] [DE:Bacillus subtilis complete genome (section 19 of 21): from
 3597091to 3809700.] [SP:P39145] [LE:44137] [RE:45528] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_23492127_f2_368	3428	7200	453	150		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_23494051_f2_444	3429	7201	1101	366	336	1.8e-30

Description

sp:[LN:YHCK_BACSU] [AC:P54595] [GN:YHCK] [OR:BACILLUS SUBTILIS]
 [DE:HYPOTHETICAL 40.7 KD PROTEIN IN CSPB-GLPP INTERGENIC REGION] [SP:P54595]
 [DB:swissprot] >pir:[LN:G69822] [AC:G69822] [PN:conserved hypothetical
 protein yhcK] [GN:yhcK] [OR:Bacillus subtilis] [DB:pir2]
 >gp:[GI:e233892:g1239987] [LN:BS75DGREG] [AC:X96983] [PN:hypothetical
 protein] [GN:yhcK] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis
 chromosomal DNA (region 75 degrees: cspB upstream of glpPFD operon).]
 [NT:similarity to hypothetical proteins from] [SP:P54595] [LE:6616]
 [RE:7695] [DI:complement] >gp:[GI:e1182901:g2633235] [LN:BSUB0005]
 [AC:Z99108:AL009126] [GN:yhcK] [FN:unknown] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 5 of 21):
 from 802821 to1011250.] [NT:similar to hypothetical proteins] [SP:P54595]
 [LE:182422] [RE:183501] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_235042_c1_1064	3430	7202	141	46		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503001001_2352140_f3_902	3431	7203	156	51		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503001001_23523326_c3_1385	3432	7204	1242	413	416	6.1e-39

Description

sp:[LN:YICK_ECOLI] [AC:P31436] [GN:YICK] [OR:ESCHERICHIA COLI]
 [DE:HYPOTHETICAL 43.5 KD PROTEIN IN SELC-NLPA INTERGENIC REGION] [SP:P31436]
 [DB:swissprot] >pir:[LN:D65167] [AC:D65167] [PN:probable membrane protein
 yicK] [GN:yicK] [OR:Escherichia coli] [DB:pir2] >gp:[GI:g290508]
 [LN:ECOUW82] [AC:L10328] [GN:o394] [FN:unknown] [OR:Escherichia coli]
 [SR:Escherichia coli K12 strain MG1655; lambda clones EC14-52]
 [DB:genpept-bct1] [DE:E. coli; the region from 81.5 to 84.5 minutes.]
 [NT:similar to unidentified ORF near 47 minutes] [LE:26345] [RE:27529]
 [DI:direct] >gp:[GI:g1790091] [LN:AE000443] [AC:AE000443:U00096]
 [PN:two-module transport protein] [GN:yicK] [FN:putative transport; Not
 classified] [OR:Escherichia coli] [DB:genpept-bct2] [DE:Escherichia coli
 K-12 MG1655 section 333 of 400 of the completegenome.] [NT:o394; 100 pct
 identical to YICK_ECOLI SW:] [LE:8286] [RE:9470] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503001001_23572177_c3_1482	3433	7205	1194	397	1792	9.5e-185

Description

gp:[GI:e1393155:g4490614] [LN:SAU133520] [AC:AJ133520] [PN:phosphoglycerate
 kinase] [GN:pgk] [OR:Staphylococcus aureus] [DB:genpept-bct1]
 [DE:Staphylococcus aureus gap operon (gapR, gap, pgk and tpi genes).]
 [LE:2995] [RE:4185] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503001001_23600175_f2_616	3434	7206	123	40		

Description

NO-HIT